

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
18 November 2004 (18.11.2004)

PCT

(10) International Publication Number
WO 2004/099242 A2

(51) International Patent Classification⁷: **C07K 14/315**

(21) International Application Number:
PCT/EP2004/004856

(22) International Filing Date: 6 May 2004 (06.05.2004)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
03450112.2 7 May 2003 (07.05.2003) EP
03450266.6 28 November 2003 (28.11.2003) EP

(71) Applicant (for all designated States except US): **INTER-CELL AG** [AT/AT]; Campus Vienna Biocenter 6, A-1030 Vienna (AT).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **MEINKE, Andreas** [DE/AT]; Pietteggasse 26/1, A-3013 Pressbaum (AT). **NAGY, Eszter** [HU/AT]; Taborstrasse 9, A-1020 Vienna (AT). **HANNER, Markus** [AT/AT]; Jacquingasse 5/6, A-1030 Vienna (AT). **HORKY, Markus** [AT/AT]; Wehlisstrasse 51/2a/20, A-1200 Vienna (AT). **KALLEDA, Sabine** [AT/AT]; Roseggergasse 37/1, A-1160 Vienna (AT). **PRUSTOMERSKY, Sonja** [AT/AT]; Kreuzbrunn 10/4, A-3001 Mauerbach (AT).

(74) Agent: **SONN & PARTNER**; Riemergasse 14, A-1010 Vienna (AT).

(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declarations under Rule 4.17:

- as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii)) for all designations
- of inventorship (Rule 4.17(iv)) for US only

Published:

- without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: S. AGALACTIAE ANTIGENS I + II

(57) Abstract: The present invention discloses isolated nucleic acid molecules encoding a hyperimmune serum reactive antigen or a fragment thereof as well as hyperimmune serum reactive antigens or fragments thereof from *S. agalactiae*, methods for isolating such antigens and specific uses thereof.



WO 2004/099242 A2

S. *agalactiae* antigens I + II

The present invention relates to isolated nucleic acid molecules, which encode antigens for *Streptococcus agalactiae*, which are suitable for use in preparation of pharmaceutical medicaments for the prevention and treatment of bacterial infections caused by *Streptococcus agalactiae*.

Streptococcus agalactiae is a gram-positive bacterium, and belongs to the Group B Streptococci (GBS) based on its hemolysis pattern in blood agar. The organism is encapsulated, and capsule is an important element of pathogenicity. Capsules are antigenic and form the basis for classifying GBS by serotypes. Nine distinct GBS serotypes have been identified: Ia, Ib, II, III, IV, V, VI, VII and VIII. Most *S. agalactiae* serotypes have been shown to cause serious disease, and the two most common serotypes - type III and V - are estimated to account for the majority of invasive disease worldwide. The ranking and serotype prevalence differs by age group and geographic area. In the US, GBS type III causes more than 50% of infant disease, type V about 40% of nonpregnant adult disease, and type Ia about a third of disease in any patient population.

Streptococcus agalactiae is an important agent of human disease at the extremities of age and in those who have underlying disease. Group B *Streptococci* are the major cause of generalized and focal infections in the newborn infant. GBS is the predominant pathogen in newborns in the US since the 1970's. Bacterial infection can lead to life threatening diseases, such as sepsis, pneumonia and meningitis. Survivors can become permanently handicapped with hearing, learning and visual disabilities. Newborns usually acquire the organism intrapartum or during delivery from their GBS-colonized mothers. In addition, GBS are also a frequent cause of infections in pregnant women and in chronically ill and elderly patients, such as those suffering from diabetes, malignancies, immunodeficiencies, etc., (reviewed by Balter, S. et al. in Gram positive pathogens ed. by Fischetti V.A. et al. ASM Press 2000, pp 154-160).

10-35% of pregnant women are colonized with GBS, but are asymptomatic. However, GBS colonization is important because of the risk of vertical transmission. 50-70% of neonates born to colonized women - that is 5-15% of all newborns - become colonized by GBS during delivery. Colonization is a prerequisite for infection and disease. The most preterm infants are at the highest risk for invasive disease due to low maternal transfer of antibodies and immature immune system. GBS carriage during pregnancy may be chronic, intermittent, or transient. It is difficult to assess the duration of carriage, since women are screened once during a prenatal visit from the late trimester. Several studies suggest that there is a correlation (~90%) between the colonization status in the third trimester and at the time of delivery. Serotyping of the isolates indicates that persistence of the same type is most common (reviewed by Balter, S. et al. in Gram positive pathogens ed. by Fischetti V.A. et al. ASM Press 2000, pp 154-160).

Without preventive intervention, 1 to 2% of all neonates and 15% of neonates born to heavily colonized women develop invasive disease (sepsis, pneumonia and/or meningitis). In the US, GBS infections affect 1-5 newborns/1000 live birth. About 17,000 cases of invasive GBS disease occurred in the US annually, and 7,500 occurred in newborns before prevention. GBS is the most common cause of bacterial meningitis accounting for ~ 40 % of all cases reported in this age group. The overall incidence of invasive GBS disease is 0.2-0.7/100,000 in the US. It is somewhat lower in Europe. Mortality without preventive intervention is 6% with invasive disease, every 16. infected newborn dies and 20% of survivors become permanently handicapped.

The rates of serious group B strep infections are much higher among newborns than among any other age group. Nonetheless, serious group B strep infections occur in other age groups in both men and women. Among non-pregnant adults, rates of serious disease range from 4.1 to 7.2 cases per 100,000 populations. The average death rate for invasive infections (infections where the bacteria have entered a part of the body that is normally not exposed to bacteria) is 8-10% for adult's ages 18-64 and 15-25% for adults 65 years of age and over. Mortality rates are lower among younger adults, and adults who do not have other medical conditions. The rate of serious group B strep disease increases with age. The average age of cases

CONFIRMATION COPY

- 2 -

in non-pregnant adults is about 60 years old. Most adult group B strep disease occurs in adults who have serious medical conditions. These include: diabetes mellitus; liver disease; history of stroke; history of cancer; or bedsores. Among the elderly, rates of serious group B strep disease are more common among residents of nursing facilities, and among bedridden hospitalized patients. Group B strep disease among non-pregnant adults may often be acquired after recent trauma, or after having certain invasive hospital procedures like surgery ([Farley, M., 2001]; [Jackson, L. et al., 1995]; www.cdc.gov/groupbstrep/).

Direct medical costs of neonatal disease before prevention were \$294 million annually and GBS continues to pose a considerable economic burden.

A definitive diagnosis of infection with *Streptococcus agalactiae* generally relies on isolation of the organism from cervical swabs, blood or other normally sterile body sites. Tests are also available to detect capsular polysaccharide antigen in body fluids.

Penicillin G is the treatment of choice for established cases of GBS. Ten days of treatment is recommended for bacteremia, pneumonia and soft tissue infections, while 2-3 weeks is recommended for meningitis and 3-4 weeks for osteomyelitis.

Prevention has been established since 1994 in North America by screening pregnant women for carriage of GBS, taking vaginal and anorectal swabs at 35-37 weeks' gestation, or by identifying risk factors at admission for delivery without cultures. Women who are candidates for prophylaxis are given intrapartum antibiotic therapy during labor to prevent early-onset neonatal disease. This prevention method has decreased the incidence of GBS disease from 1.7 to 0.4/1000 live births between 1993 and 1999 in the US. Although most neonatal GBS disease can be prevented through intrapartum prophylaxis (Penicillin G or Ampicillin), currently available strategies are not ideal, especially for the prevention of late-onset (>7 days of age) infections and disease in premature babies. There are always individuals who escape of screening for carriage due to several reasons, such as intermittent carriers, who are tested negative at wks 32-35, but become positive during delivery, unattendance, negligence, or delivery before screening date (32-35 wks).

In the long run, widespread use of antibiotics usually induces resistant strains that appear after a period of time. Extensive use of Penicillin (every 3-5th women are treated with high dose), and other antibiotics has already been shown to steadily increase the percentage of antibiotic resistant clinical isolates (ref). Moreover, efficiency of antibiotic based prevention is not that effective for late onset disease, as it is for early onset (within 48 hrs after delivery). An additional concern is that prevention in susceptible adult populations has not been addressed.

Vaccine development is hindered by the lack of sufficient knowledge about the elements of protective immunity against GBS carriage and disease. The relationship of carriage to the development of natural immunity is poorly understood. In addition, the immunologic mechanism that allows disease to occur in a carrier is ill defined. However, it is suggested that the maternal serum levels of pathogen-specific antibodies are correlated with neonatal GBS disease. It has been firmly established that there is an inverse correlation between maternal anti-capsular polysaccharide antibody levels at delivery and the frequency of invasive neonatal diseases [Campbell, J. et al., 2000].

Although the group B carbohydrate antigen is common to all strains of GBS, unfortunately, it is not strongly immunogenic and antibodies are not protective from lethal challenge in experimental models. The GBS capsule itself that is made of polysaccharides, is immunogenic and is able to induce protective antibodies. However, this protection is type-specific. Although capsular specific antibodies have been shown to be highly protective, it remains unclear what concentration of these serotype-specific antibodies protect against disease and more recently it has become clear that opsonic activity and avidity of these

antibodies are more critical determinants of protection than concentration.

The importance of surface proteins in human immunity to *S. agalactiae* already has been appreciated. It is apparent that all serotypes express surface proteins with activity relevant to host immune defense. The alpha C protein, beta C protein, Rib and Sip proteins are well-characterized biochemically and genetically, and have also been shown to be immunogenic and protective in animal models ({Michel, J. et al., 1991}; {Brodeur, B. et al., 2000}; {Larsson, C. et al., 1999}; {Cheng, Q. et al., 2002}). The major problem with these proteins as vaccine candidates seems to be their variability in prevalence among the different clinical isolates of GBS. The Rib protein for example is present in serotype III GBS, but missing from type V, which is responsible for a significant portion of disease worldwide. Some other surface proteins are characterized as being immunogenic, but there is a limited systematic work done to identify most of the immunogenic proteins of GBS.

Thus, there remains a need for an effective treatment to prevent or ameliorate GBS infections. A vaccine could not only prevent infections by GBS, but more specifically prevent or ameliorate colonization of host tissues (esp. in the birth canal), thereby reducing the incidence of transmission from mother to fetus. Reducing the incidence of acute infection and carriage of the organism would lead to prevention of invasive diseases in newborns - pneumonia, bacteremia, meningitis, and sepsis. Vaccines capable of showing cross-protection against the majority of *S. agalactiae* strains causing human infections could also be useful to prevent or ameliorate infections caused by all other streptococcal species, namely groups A, C and G.

A vaccine can contain a whole variety of different antigens. Examples of antigens are whole-killed or attenuated organisms, subfractions of these organisms/tissues, proteins, or, in their most simple form, peptides. Antigens can also be recognized by the immune system in form of glycosylated proteins or peptides and may also be or contain polysaccharides or lipids. Short peptides can be used since for example cytotoxic T-cells (CTL) recognize antigens in form of short usually 8-11 amino acids long peptides in conjunction with major histocompatibility complex (MHC). B-cells can recognize linear epitopes as short as 4-5 amino acids, as well as three-dimensional structures (conformational epitopes). In order to obtain sustained, antigen-specific immune responses, adjuvants need to trigger immune cascades that involve all cells of the immune system. Primarily, adjuvants are acting, but are not restricted in their mode of action, on so-called antigen presenting cells (APCs). These cells usually first encounter the antigen(s) followed by presentation of processed or unmodified antigen to immune effector cells. Intermediate cell types may also be involved. Only effector cells with the appropriate specificity are activated in a productive immune response. The adjuvant may also locally retain antigens and co-injected other factors. In addition the adjuvant may act as a chemoattractant for other immune cells or may act locally and/or systemically as a stimulating agent for the immune system.

Vaccine development since the late 1970s has focused on the capsular polysaccharides, but a safe, effective product is still not available. However, vaccine against *S. agalactiae* is ranked as one of the most important for development and administration to infants and high-risk adults. Currently vaccines against this infection are only in the research stages of development. Efforts are focused on using capsular polysaccharide (CPS) as immunogens, either with or without conjugation to protein {Paoletti, L. et al., 2002}. However, there are several arguments against the use of polysaccharide-based vaccine. Polysaccharides induce IgG2 antibodies, which cross the placenta less efficiently than IgG1 or IgG3 antibodies. It is especially a problem for the most susceptible neonates, the still-borns since placental antibody transfer is low before weeks 32-34. It is estimated that ~10% of deliveries occur before the 34th pregnancy week.

Protein conjugate vaccines are no doubt a great new addition to the armamentarium in the battle against GBS disease, but the vaccine can contain only a limited number of GBS serotypes and given adequate ecological pressure, replacement disease by non-vaccine serotypes remains a real threat, particularly in

areas with very high disease burden. Moreover polysaccharide antigens used for active immunization do not provide immunological memory in humans. Conjugation of CPS to non-GBS related immunogenic protein carriers (e.g. tetanus toxoid, cholera toxin B subunit, etc.) has been shown to be beneficial in inducing higher concentrations of antibodies in vaccinees, but it does not provide pathogen-specific B cell and T cell epitopes which would recruit memory B and T cells during a real infection to support the most effective host response. To be able to supplement the CPS vaccines with proteins fulfilling these criteria it is necessary to identify conserved immunogenic GBS-specific surface proteins.

All these insufficiencies suggest that there is a need to develop new generation vaccines composed of proteins, or their derivatives, expressed by all strains under *in vivo* conditions with the ability to induce opsonizing and/or neutralizing antibodies in humans.

There is a great potential for passive antibody-based therapy. There have been already attempts to use human intravenous immunoglobulin (IVIG) preparations for prevention. Recent advances in the technology of monoclonal antibody production provide the means to generate human antibody reagents and reintroduce antibody therapies, while avoiding the toxicities associated with serum therapy. Immunoglobulins are an extremely versatile class of antimicrobial proteins that can be used to prevent and treat emerging infectious diseases. Antibody therapy has been effective against a variety of diverse microorganisms (reviewed in {Burnie, J. et al., 1998}). Anti-GBS mAbs could be given therapeutically to every newborn that develop invasive diseases or preventively to low birth-weight and premature neonates.

During the last decade the immunogenicity and protective capacity of several GBS proteins have been described in animal models and these are now being explored for the development of species-common protein based vaccines. Such proteins are the GBS surface proteins Sip {Brodeur, B. et al., 2000}, rib, ϕ -protein and {Michel, J. et al., 1991}.

Certain proteins or enzymes displayed on the surface of gram-positive organisms significantly contribute to pathogenesis, are involved in the disease process caused by these pathogens. Often, these proteins are involved in direct interactions with host tissues or in concealing the bacterial surface from the host defense mechanisms {Navarre, W. et al., 1999}. *S. agalactiae* is not an exception in this regard. Several surface proteins are characterized as virulence factors, important for GBS pathogenicity ((reviewed in {Paoletti L.C. et al. in Gram positive pathogens, ed. by Fischetti V.A et al., ASM Press 2000, pp 137-153}; {Paoletti, L. et al., 2002}). If antibodies to these proteins could offer better protection to humans than polysaccharides, they could provide the source of a novel, protein-based GBS vaccine to be used in conjunction with or in place of the more traditional capsular polysaccharide vaccine. The use of some of the above-described proteins as antigens for a potential vaccine as well as a number of additional candidates resulted mainly from a selection based on easiness of identification or chance of availability. There is a demand to identify relevant antigens for *S. agalactiae* in a more comprehensive way.

The present inventors have developed a method for identification, isolation and production of hyperimmune serum reactive antigens from a specific pathogen, especially from *Staphylococcus aureus* and *Staphylococcus epidermidis* (WO 02/059148). However, given the differences in biological property, pathogenic function and genetic background, *Streptococcus agalactiae* is distinctive from *Staphylococcus* strains. Importantly, the selection of sera for the identification of antigens from *S. agalactiae* is different from that applied to the *S. aureus* screens. Four major types of human antibody sources were collected for that purpose. First, healthy pregnant women who were tested negative for cervical and anorectal carriage of GBS. This donor group represents the most important source of antibodies. In addition to their serum samples, human cervical secretions collected with cervical wicks, containing secretory IgA (sIgA) were also used for antigen identification and validation. The main value of this collection is that sIgA can be considered the major immune effector molecule on mucosal surfaces. Second, healthy pregnant women

colonized with GBS whos newborn remained GBS-free (although with antibiotic prevention). Third, adults below <45 years of age without clinical disease. Four, naïve individuals, youg children between 5 and 10 months of age, after they already lost maternal antibodies and have not acquired GBS-specific ones due to the lack of GBS disease.

To be able to select for relevant serum sources, a series of ELISAs and immunoblotting experiments measuring anti-*S. agalactiae* IgG and IgA antibody levels were performed with bacterial lysates and culture supernatant proteins. Sera from high titer carriers and non-carriers were included in the genomic-based antigen identification. This approach for selection of human sera is basically very different from that used for *S. aureus*, where carriage or non-carriage state couldn't be associated with antibody levels.

The present invention uses high throughput genomic method to identify *in vivo* expressed pathogen-specific proteins with the ability to induce antibodies in humans during the course of infections and colonization.

The genomes of the two bacterial species *S. agalactiae* and *S. aureus* by itself show a number of important differences. The genome of *S. agalactiae* contains app. 2.2 Mb, while *S. aureus* harbours 2.85 Mb. They have an average GC content of 35.7 and 33%, respectively and approximately 30 to 45% of the encoded genes are not shared between the two pathogens. In addition, the two bacterial species require different growth conditions and media for propagation. A list of the most important diseases, which can be inflicted by the two pathogens is presented below. *S. aureus* causes mainly nosocomial, opportunistic infections: impetigo, folliculitis, abscesses, boils, infected lacerations, endocarditis, meningitis, septic arthritis, pneumonia, osteomyelitis, scalded skin syndrome (SSS), toxic shock syndrome. *S. agalactiae* causes mainly neonatal infections and diseases in elderly, such as bacteremia, sepsis, wound infection, osteomyelitis and meningitis.

The complete genome sequence of a capsular serotype III isolate of *S. agalactiae*, designated NEM316 (ATCC 12403) was determined by the random shotgun sequencing strategy (GenBank accession number AL732656; see www.tigr.org/tigrscripts/CMR2/CMRHomePage.spl). {Glaser, P. et al., 2002}.

The problem underlying the present invention was to provide means for the development of medicaments such as vaccines against *S. agalactiae* infection. More particularly, the problem was to provide an efficient, relevant and comprehensive set of nucleic acid molecules or hyperimmune serum reactive antigens from *S. agalactiae* that can be used for the manufacture of said medicaments.

Therefore, the present invention provides an isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence, which is selected from the group consisting of:

- a) a nucleic acid molecule having at least 70% sequence identity to a nucleic acid molecule selected from **Seq ID No 14, 90, 157-216**.
- b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
- c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
- d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b), or c)
- e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid molecule defined in a), b), c) or d).

According to a preferred embodiment of the present invention the sequence identity is at least 80%, preferably at least 95%, especially 100%.

Furthermore, the present invention provides an isolated nucleic acid molecule encoding a hyperimmune

serum reactive antigen or a fragment thereof comprising a nucleic acid sequence selected from the group consisting of

- a) a nucleic acid molecule having 96 % or more than 96 %, preferably at least 98 %, especially 100 % sequence identity to a nucleic acid molecule selected from **Seq ID No** 1, 3, 5-13, 15, 18-25, 27-31, 33-36, 39-68, 70-85, 92-100, 103-126, 128-145, 147, 149-156, 217, 435-448 and 463-474.
- b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
- c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
- d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b) or c),
- e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).

According to another aspect, the present invention provides an isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence selected from the group consisting of

- a) a nucleic acid molecule having 98 % or more than 98%, especially 100 % sequence identity to a nucleic acid molecule selected from **Seq ID No** 32, 86, 91, 101, 127.
- b) a nucleic acid molecule which is complementary to the nucleic acid of a),
- c) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).

Preferably, the nucleic acid molecule is DNA or RNA.

According to a preferred embodiment of the present invention, the nucleic acid molecule is isolated from a genomic DNA, especially from a *S. agalactiae* genomic DNA.

According to the present invention a vector comprising a nucleic acid molecule according to any of the present invention is provided.

In a preferred embodiment the vector is adapted for recombinant expression of the hyperimmune serum reactive antigens or fragments thereof encoded by the nucleic acid molecule according to the present invention.

The present invention also provides a host cell comprising the vector according to the present invention.

According to another aspect the present invention further provides a hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to the present invention.

In a preferred embodiment the amino acid sequence (polypeptide) is selected from the group consisting of **Seq ID No** 231, 307, 374-433.

In another preferred embodiment the amino acid sequence (polypeptide) is selected from the group consisting of **Seq ID No** 218, 220, 222-230, 232, 235-242, 244-248, 250-253, 256-285, 287-302, 309-317, 320-343, 345-362, 364, 366-373, 434, 449-462 and 475-486.

In a further preferred embodiment the amino acid sequence (polypeptide) is selected from the group consisting of **Seq ID No** 249, 303, 308, 318, 344.

According to a further aspect the present invention provides fragments of hyperimmune serum-reactive antigens selected from the group consisting of peptides comprising amino acid sequences of column

“predicted immunogenic aa” and “location of identified immunogenic region” of Table 1A, especially **peptides comprising amino acid** 4-20, 35-44, 65-70, 73-87, 92-98, 112-137, 152-161, 177-186, 193-200, 206-213, 229-255, 282-294, 308-313, 320-326, 349-355, 373-384, 388-406, 420-425 and 115-199 of **Seq ID No 218**; 5-24, 35-41, 44-70, 73-89, 103-109, 127-143, 155-161, 185-190, 192-207, 212-219, 246-262, 304-336, 372-382, 384-393, 398-407, 412-418, 438-444, 1-75, 76-161 and 164-239 of **Seq ID No 219**; 4-10, 16-58, 60-71, 77-92, 100-126, 132-146, 149-164, 166-172, 190-209, 214-220, 223-229, 241-256, 297-312, 314-319, 337-343, 351-359, 378-387, 398-418, 421-428, 430-437, 440-448, 462-471, 510-519, 525-536, 552-559, 561-568, 573-582, 596-602, 608-630, 637-649, 651-665, 681-702, 714-732, 739-745, 757-778, 790-805, 807-815, 821-829, 836-842, 846-873, 880-903, 908-914, 916-923, 931-940, 943-948, 956-970, 975-986, 996-1015, 1031-1040, 1051-1069, 1072-1095, 1114-1119, 1130-1148, 1150-1157, 1169-1176, 1229-1238 and 802-812 of **Seq ID No 220**; 5-12, 14-26, 35-47, 52-67, 72-78, 83-98, 121-141, 152-159, 163-183, 186-207, 209-257, 264-277, 282-299, 301-309, 312-318, 324-339, 358-368, 372-378, 387-397, 425-431 and 46-291 of **Seq ID No 221**; 29-38, 44-64, 70-76, 78-87, 94-100, 102-112, 119-134, 140-149, 163-173, 178-186, 188-194, 207-234, 247-262, 269-290 and 73-92 of **Seq ID No 222**; 10-28, 36-63, 77-87, 103-119, 127-136, 141-169, 171-183, 195-200, 207-232, 236-246, 251-265, 268-283, 287-297, 314-322, 335-343, 354-363, 384-390, 405-411, 419-436, 443-455, 467-473, 480-513, 518-529, 550-557, 565-585, 602-608, 616-625, 632-660, 665-677, 685-701, 726-736, 738-747, 752-761, 785-796, 801-813, 838-853, 866-871 and 757-774 of **Seq ID No 223**; 31-38, 61-66, 74-81, 90-115, 123-145, 154-167, 169-179, 182-193, 200-206, 238-244, 267-272 and 235-251 of **Seq ID No 224**; 19-25, 38-54, 56-64, 66-72, 74-92, 94-100, 116-129, 143-149, 156-183, 204-232, 253-266, 269-275, 294-307 and 241-313 of **Seq ID No 225**; 5-34, 50-56, 60-65, 74-85, 89-97, 108-119, 159-165, 181-199, 209-225, 230-240, 245-251, 257-262, 274-282, 300-305 and 64-75 of **Seq ID No 226**; 5-13, 16-21, 27-42, 45-52, 58-66, 74-87, 108-114, 119-131 and 39-51 of **Seq ID No 227**; 6-23, 46-54, 59-65, 78-84, 100-120, 128-133, 140-146, 159-165, 171-183, 190-204, 224-232, 240-248, 250-259, 274-280, 288-296, 306-315 and 267-274 of **Seq ID No 228**; 5-12, 15-24, 26-36, 42-65, 68-80, 82-104, 111-116, 125-144, 159-167, 184-189, 209-218, 235-243, 254-265, 269-283, 287-300, 306-316, 318-336, 338-352, 374-392 and 162-174 of **Seq ID No 229**; 30-42, 45-54 and 25-37 of **Seq ID No 230**; 10-30, 53-59, 86-95, 116-130, 132-147, 169-189, 195-201, 212-221, 247-256, 258-265, 278-283, 291-298, 310-316, 329-339, 341-352, 360-367, 388-396, 398-411, 416-432, 443-452, 460-466, 506-512, 515-521, 542-548 and 419-431 of **Seq ID No 231**; 4-27, 30-53, 60-67, 70-90, 92-151, 159-185, 189-195, 198-210, 215-239 and 173-189 of **Seq ID No 232**; 4-26, 41-54, 71-78, 116-127, 140-149, 151-158, 161-175, 190-196, 201-208, 220-226, 240-252, 266-281, 298-305, 308-318, 321-329, 344-353, 372-378, 384-405, 418-426, 429-442, 457-463, 494-505, 514-522 and 174-188 of **Seq ID No 233**; 17-25, 27-39, 61-67, 81-89, 99-110, 120-131, 133-139, 147-161, 167-172, 179-185, 192-198, 203-213, 226-238, 243-258, 261-267, 284-290, 296-307, 311-328, 340-352, 356-371 and 239-256 of **Seq ID No 234**; 8-30, 40-49, 67-80, 114-123, 126-142, 152-162, 188-194 and 57-70 of **Seq ID No 235**; 4-23, 28-34, 36-47, 50-61, 76-81, 89-94, 96-104, 112-119, 126-146, 155-181, 195-200, 208-214, 220-229, 244-260, 263-276, 282-288, 292-300, 317-323, 336-351, 353-359, 363-375, 382-399, 415-432, 444-455, 458-471, 476-481, 484-492, 499-517, 522-529, 535-541, 543-568, 572-584, 586-600, 607-617, 626-637, 656-675 and 282-297 of **Seq ID No 236**; 6-24, 30-35, 38-45, 63-91, 134-140, 146-160, 167-188, 214-220, 226-234, 244-250, 260-270, 286-301, 316-329, 340-371, 429-446, 448-459, 474-481, 485-491, 512-526, 537-544, 550-565, 573-583, 596-613, 621-630, 652-658 and 87-97 of **Seq ID No 237**; 8-20, 26-48, 56-67, 76-86, 94-109, 115-121, 123-129, 143-160, 178-186, 191-198, 201-208, 221-236, 238-244, 260-268 and 237-247 of **Seq ID No 238**; 4-40, 42-57, 73-87, 98-117, 126-135, 150-156, 166-174, 196-217, 231-236, 248-258, 276-284, 293-301, 307-313, 339-347, 359-365, 375-387, 395-402, 428-440, 445-456, 485-490, 497-505, 535-541, 547-555, 610-625, 648-656, 665-671 and 448-528 of **Seq ID No 239**; 10-18, 39-45, 51-61, 80-96, 98-106, 110-115, 158-172, 174-183, 191-200, 220-237, 249-255, 274-289, 308-324, 331-341, 372-381, 384-397, 405-414 and 322-338 of **Seq ID No 240**; 30-36, 38-56, 85-108, 134-147, 149-160, 163-183, 188-201, 206-211, 219-238, 247-254 and 5-13 of **Seq ID No 241**; 11-40, 98-103, 110-115, 133-145, 151-159, 172-179, 192-201, 204-212, 222-228, 235-245, 258-268, 283-296, 298-309, 322-329, 342-351, 354-362, 372-378, 385-393, 407-418, 495-516 and 1-148 of **Seq ID No 242**; 5-19, 21-36, 73-94, 112-119, 122-137, 139-145, 152-167, 184-190, 198-204, 208-224, 249-265, 267-281, 299-304, 309-317, 326-333, 356-364, 368-374, 381-389, 391-414, 419-425, 430-435 and 113-140 of **Seq ID No 243**; 45-54, 59-67, 78-91 and 15-23 of **Seq ID No 244**; 11-22, 33-47, 52-80, 88-112, 124-129 and 6-25 of **Seq ID No 245**; 26-41, 51-63, 80-89, 93-115, 150-163, 187-193, 220-237, 240-249, 286-294, 296-306, 316-329, 345-353, 361-370, 407-425, 428-437, 474-482, 484-494, 504-517, 533-541, 549-558, 595-613, 616-625, 660-668, 673-685, 711-726, 736-744, 749-761, 787-802, 812-820, 825-837, 863-878, 888-896, 901-913, 939-954, 964-972,

977-989, 1003-1008, 1016-1022, 1028-1034, 1041-1053, 1059-1074, 1101-1122, 420-511 and 581-704 of **Seq ID No 246**; 18-25, 27-55, 71-83, 89-95, 102-113, 120-146, 150-156, 174-185 and 159-175 of **Seq ID No 247**; 24-30, 38-56, 63-68, 87-93, 136-142, 153-164, 183-199, 213-219, 226-234, 244-261, 269-278, 283-289, 291-297, 320-328, 330-336, 340-346, 348-356, 358-366, 382-387, 401-408, 414-419, 449-455, 468-491, 504-512, 531-537, 554-560, 597-608, 621-627, 632-643, 650-662, 667-692, 703-716, 724-737, 743-758, 783-794, 800-818, 846-856 and 806-884 of **Seq ID No 248**; 4-14, 21-39, 86-92, 99-107, 121-131, 136-144, 147-154, 158-166, 176-185, 193-199, 207-222, 224-230 and 117-136 of **Seq ID No 249**; 65-76, 85-97, 103-109, 115-121, 125-146, 163-169, 196-205, 212-219, 228-237, 241-247, 254-262, 269-288, 294-303, 305-313, 328-367, 395-401, 405-412, 418-429, 437-447, 481-488, 506-513, 519-524, 530-541, 546-557 and 266-284 of **Seq ID No 250**; 5-14, 37-42, 49-71, 78-92, 97-112, 127-136, 147-154, 156-163, 186-198, 216-225, 233-243, 248-253, 295-307, 323-332, 359-366, 368-374, 380-398 and 194-223 of **Seq ID No 251**; 4-11, 33-39, 45-72, 100-113, 119-129, 136-144, 169-175, 177-185, 200-208, 210-219, 262-276, 278-297, 320-326, 336-344, 347-362, 381-394, 443-453 and 438-454 of **Seq ID No 252**; 4-29, 31-52, 55-61, 95-110, 138-158, 162-171, 179-187, 202-229, 239-248, 251-256, 262-267, 269-285, 304-310, 351-360, 362-368, 381-388, 415-428, 435-440, 448-458 and 161-178 of **Seq ID No 253**; 4-17, 19-28, 32-43, 47-59, 89-110, 112-126, 128-134, 140-148, 152-161, 169-184, 191-204, 230-235, 255-264, 328-338, 341-347, 401-409, 413-419, 433-441, 449-458, 463-468, 476-482, 486-492, 500-506, 529-545 and 305-381 of **Seq ID No 254**; 10-29, 38-45, 53-61, 134-145, 152-160, 163-170, 202-208, 219-229, 248-258, 266-275, 282-288, 315-320, 328-334, 377-385, 392-402, 418-424, 447-453, 460-471, 479-487, 491-497, 500-507, 531-537, 581-594, 615-623, 629-635, 644-652, 659-666, 668-678, 710-717, 719-728, 736-741, 747-760, 766-773, 784-789, 794-800, 805-817, 855-861, 866-887 and 698-715 of **Seq ID No 255**; 16-26, 29-37, 44-58, 62-68, 74-80, 88-95, 97-120, 125-144, 165-196 and 58-72 of **Seq ID No 256**; 14-21, 23-46, 49-60, 63-74, 78-92, 96-103, 117-129, 134-161, 169-211, 217-231, 239-248, 252-281, 292-299, 313-343 and 243-257 of **Seq ID No 257**; 11-27, 46-52, 67-72, 76-84, 91-112, 116-153, 160-175, 187-196, 202-211, 213-220 and 43-76 of **Seq ID No 258**; 5-29, 37-56, 78-86, 108-118, 152-161 and 120-130 of **Seq ID No 259**; 8-14, 19-41, 52-66, 75-82, 87-92, 106-121, 127-133, 136-143, 158-175, 180-187, 196-204, 221-228, 239-245, 259-265, 291-306, 318-323, 328-340, 352-358, 361-368, 375-381, 391-399, 411-418, 431-442, 446-455, 484-496, 498-510, 527-533, 541-549, 558-565, 575-585, 587-594, 644-655, 661-668, 671-677 and 184-196 of **Seq ID No 260**; 4-22, 29-38, 55-62, 75-81, 102-107, 110-134, 143-150, 161-167, 172-179, 191-215, 223-233, 241-247, 251-264, 266-272, 288-309, 340-352, 354-366, 394-402, 414-438 and 198-218 of **Seq ID No 261**; 24-44, 49-70, 80-91, 105-118, 128-136, 140-154 and 77-92 of **Seq ID No 262**; 5-22, 31-36, 41-47, 67-74, 83-90, 105-122, 135-143, 160-167 and 118-129 of **Seq ID No 263**; 4-25, 33-73, 81-93, 96-106, 114-120, 122-128, 130-172, 179-208, 210-241, 251-283, 296-301 and 92-100 of **Seq ID No 264**; 14-24, 29-38, 43-50, 52-72, 86-97, 101-107, 110-125, 127-141, 145-157, 168-175, 177-184, 186-195, 205-226, 238-250, 255-261, 284-290, 293-304, 307-314, 316-323, 325-356, 363-371, 383-390, 405-415, 423-432, 442-454, 466-485, 502-511, 519-527, 535-556, 558-565, 569-574, 612-634, 641-655, 672-686, 698-709, 715-722, 724-732, 743-753, 760-769, 783-792, 818-825, 830-839, 842-849, 884-896, 905-918, 926-940, 957-969, 979-1007, 1015-1021, 1049-1057 and 336-349 of **Seq ID No 265**; 6-16, 26-31, 33-39, 62-73, 75-85, 87-100, 113-123, 127-152, 157-164, 168-181, 191-198, 208-214, 219-226, 233-254, 259-266, 286-329 and 181-195 of **Seq ID No 266**; 4-13, 32-39, 53-76, 99-108, 110-116, 124-135, 137-146, 149-157, 162-174, 182-190, 207-231, 242-253, 255-264, 274-283, 291-323, 334-345, 351-360, 375-388, 418-425, 456-474, 486-492, 508-517, 520-536, 547-560, 562-577, 31-45 and 419-443 of **Seq ID No 267**; 15-26, 30-37, 42-49, 58-90, 93-99, 128-134, 147-154, 174-179, 190-197, 199-205, 221-230, 262-274, 277-287, 300-314, 327-333, 343-351, 359-377, 388-396, 408-413, 416-425, 431-446 and 246-256 of **Seq ID No 268**; 5-26, 34-42, 47-54, 61-67, 71-104, 107-115, 131-138, 144-153, 157-189, 196-202, 204-210, 228-245, 288-309, 316-329, 332-341, 379-386, 393-399, 404-412, 414-421, 457-468, 483-489, 500-506, 508-517, 523-534, 543-557, 565-580, 587-605, 609-617, 619-627, 631-636, 640-646, 662-668, 675-682, 705-710, 716-723, 727-732, 750-758, 784-789, 795-809, 869-874, 14-138, 166-286, 372-503, 674-696 and 754-859 of **Seq ID No 269**; 5-17, 32-38, 40-47, 80-89, 113-119, 125-137, 140-154, 157-163, 170-177, 185-199, 213-225, 228-236, 242-248, 277-290, 292-305, 323-333, 347-353, 364-370, 385-394, 399-406, 423-433, 441-451, 462-474, 477-487 and 116-124 of **Seq ID No 270**; 7-16, 18-30, 32-49, 53-61, 63-85, 95-101, 105-115, 119-134, 143-150, 159-178, 185-202, 212-229, 236-250, 254-265, 268-294 and 63-72 of **Seq ID No 271**; 4-12, 19-47, 73-81, 97-103, 153-169, 188-198, 207-213, 217-223, 236-242, 255-265, 270-278, 298-305, 309-317, 335-347, 354-363, 373-394, 419-424, 442-465, 486-492, 500-507, 542-549, 551-558, 560-572, 580-589, 607-614, 617-623, 647-653, 666-676, 694-704, 706-714, 748-754, 765-772, 786-792, 795-806 and 358-370 of **Seq ID No 272**; 18-28, 30-38, 40-46, 49-55, 69-78, 82-98, 104-134, 147-153, 180-190, 196-202, 218-236,

244-261, 266-273, 275-286, 290-295, 301-314, 378-387, 390-395, 427-434 and 290-305 of **Seq ID No 273**; 4-13, 20-31, 39-51, 54-61, 69-84, 87-105, 117-124 and 108-125 of **Seq ID No 274**; 24-34, 43-54, 56-66, 68-79 and 50-69 of **Seq ID No 275**; 5-43, 71-77, 102-131, 141-148, 150-156, 159-186, 191-207, 209-234, 255-268, 280-286, 293-299, 317-323, 350-357, 363-372, 391-397, 406-418, 428-435, 455-465, 484-497, 499-505, 525-531, 575-582, 593-607, 621-633, 638-649, 655-673, 684-698, 711-725, 736-741, 743-752, 759-769, 781-793, 813-831, 843-853, 894-905, 908-916, 929-946, 953-963, 970-978, 1001-1007, 1011-1033, 165-178 and 818-974 of **Seq ID No 276**; 16-44, 63-86, 98-108, 185-191, 222-237, 261-274, 282-294, 335-345, 349-362, 374-384, 409-420, 424-430, 440-447, 453-460, 465-473, 475-504, 522-534, 538-551, 554-560, 567-582, 598-607, 611-619, 627-640, 643-653, 655-661, 669-680, 684-690, 701-707, 715-731, 744-750, 756-763, 768-804, 829-837, 845-853, 855-879, 884-890, 910-928, 77-90, 144-212, 279-355, 434-536, 782-810 and 875-902 of **Seq ID No 277**; 4-22, 29-41, 45-51, 53-66, 70-77, 86-95, 98-104, 106-124, 129-135, 142-151, 153-161, 169-176, 228-251, 284-299, 331-337, 339-370, 380-387, 393-398, 406-411, 423-433, 440-452, 461-469, 488-498, 501-516, 523-530, 532-559, 562-567, 570-602, 612-628, 630-645, 649-659, 666-672, 677-696, 714-723, 727-747 and 212-227 of **Seq ID No 278**; 4-9, 17-31, 35-41, 56-61, 66-75, 81-87, 90-124, 133-138, 149-163, 173-192, 213-219, 221-262, 265-275, 277-282, 292-298, 301-307, 333-346, 353-363, 371-378, 419-430, 435-448, 456-469, 551-570, 583-599, 603-612 and 275-291 of **Seq ID No 279**; 28-34, 53-58, 72-81, 100-128, 145-154, 159-168, 172-189, 217-225, 227-249, 256-263, 299-309, 322-330, 361-379, 381-388, 392-401, 404-417, 425-436, 440-446, 451-464, 469-487, 502-511, 543-551, 559-564, 595-601, 606-612, 615-626, 633-642, 644-650, 664-670, 674-684, 692-701, 715-723, 726-734, 749-756, 763-771, 781-787, 810-843, 860-869, 882-889, 907-917, 931-936, 941-948, 951-958, 964-971, 976-993, 1039-1049, 1051-1065, 1092-1121, 1126-1132, 1145-1151, 1158-1173, 1181-1192, 1194-1208, 1218-1223, 1229-1243, 1249-1254, 1265-1279, 1287-1297, 1303-1320, 1334-1341, 1343-1358, 1372-1382, 1406-1417, 1419-1425, 1428-1434, 1441-1448, 1460-1473, 1494-1504, 1509-1514, 1529-1550, 654-669 and 1400-1483 of **Seq ID No 280**; 10-16, 20-25, 58-65, 97-109, 118-132, 134-146, 148-155, 186-195, 226-233, 244-262, 275-284, 295-310, 317-322, 330-339, 345-351, 366-375, 392-403, 408-415, 423-430, 435-444, 446-457, 467-479, 486-499, 503-510, 525-537, 540-585, 602-612, 614-623, 625-634, 639-645, 650-669, 700-707, 717-724, 727-739, 205-230 and 733-754 of **Seq ID No 281**; 5-22, 37-43, 72-81, 105-113, 128-133, 148-160, 188-194, 204-230, 238-245, 251-257 and 194-213 of **Seq ID No 282**; 16-21, 35-41, 56-72, 74-92, 103-109 and 62-68 of **Seq ID No 283**; 4-15, 17-82, 90-104, 107-159, 163-170, 188-221, 234-245, 252-265 and 220-235 of **Seq ID No 284**; 16-22, 36-46, 61-75, 92-107, 113-121, 139-145, 148-160 and 30-42 of **Seq ID No 285**; 4-12, 20-26, 43-49, 55-62, 66-78, 121-127, 135-141, 146-161, 164-170, 178-189, 196-205, 233-238, 269-279, 288-318, 325-332, 381-386, 400-407 and 328-346 of **Seq ID No 286**; 5-12, 31-49, 57-63, 69-79, 89-97, 99-114, 116-127, 134-142, 147-154, 160-173, 185-193, 199-204, 211-222, 229-236, 243-249, 256-274 and 58-68 of **Seq ID No 287**; 10-20, 28-34, 39-53, 68-79, 84-90, 99-106 and 73-79 of **Seq ID No 288**; 14-37, 45-50, 61-66, 77-82, 93-98, 109-114, 125-130, 141-146, 157-162, 173-178, 189-194, 205-210, 221-226, 237-242, 253-258, 269-274, 285-290, 301-306, 316-332, 349-359, 371-378, 385-406, 34-307 and 312-385 of **Seq ID No 289**; 4-10, 17-38, 50-85, 93-99, 109-116, 128-185, 189-197, 199-210, 223-256, 263-287, 289-312, 327-337, 371-386, 389-394, 406-419, 424-432, 438-450, 458-463, 475-502, 507-513, 519-526, 535-542, 550-567 and 361-376 of **Seq ID No 290**; 10-39, 42-93, 100-144, 155-176, 178-224, 230-244, 246-255, 273-282, 292-301, 308-325, 332-351, 356-361, 368-379, 386-393, 400-421 and 138-155 of **Seq ID No 291**; 5-11, 17-34, 40-45, 50-55, 72-80, 101-123, 145-151, 164-172, 182-187, 189-195, 208-218, 220-241, 243-252, 255-270, 325-331, 365-371, 391-398, 402-418, 422-428, 430-435, 443-452, 463-469, 476-484, 486-494, 503-509, 529-553, 560-565, 570-590, 608-614, 619-627, 654-661, 744-750, 772-780, 784-790, 806-816, 836-853, 876-885, 912-918, 926-933, 961-975, 980-987, 996-1006, 1016-1028, 1043-1053, 1057-1062, 994-1003 and 1033-1056 of **Seq ID No 292**; 17-45, 64-71, 73-81, 99-109, 186-192, 223-238, 262-275, 283-295, 336-346, 350-363, 375-385, 410-421, 425-431, 441-448, 454-463, 468-474, 476-512, 523-537, 539-552, 568-583, 599-608, 612-620, 628-641, 644-654, 656-662, 670-681, 685-695, 702-708, 716-723, 725-735, 757-764, 769-798, 800-806, 808-816, 826-840, 846-854, 856-862, 874-881, 885-902, 907-928, 274-350 and 443-513 of **Seq ID No 293**; 4-22, 29-41, 45-51, 53-61, 70-76, 85-92, 99-104, 111-122, 134-140, 142-154, 163-174, 224-232, 255-265, 273-279, 283-297, 330-335, 337-348, 356-367, 373-385, 391-396, 421-431, 442-455, 475-485, 493-505, 526-538, 544-561, 587-599, 605-620, 622-651, 662-670, 675-681, 687-692, 697-712, 714-735 and 252-262 of **Seq ID No 294**; 4-12, 15-35, 40-46, 50-59, 67-94, 110-128, 143-169, 182-188, 207-215, 218-228, 238-250 and 74-90 of **Seq ID No 295**; 9-18, 42-58, 78-85, 88-95, 97-106, 115-122, 128-134, 140-145, 154-181, 186-202, 204-223, 261-267, 269-278, 284-293, 300-336, 358-368 and 12-29 of **Seq ID No 296**; 7-34, 46-53, 62-72, 82-88, 100-105, 111-117, 132-137, 144-160, 166-180, 183-189, 209-221, 231-236, 246-253, 268-282, 286-293,

323-336, 364-372, 378-392, 422-433 and 388-405 of **Seq ID No 297**; 21-27, 34-50, 72-77, 80-95, 164-177, 192-198, 202-220, 226-236, 239-247, 270-279, 285-292, 315-320, 327-334, 348-355, 364-371, 388-397, 453-476, 488-497, 534-545, 556-576, 582-588, 601-607, 609-616, 642-662, 674-681, 687-697, 709-715, 721-727, 741-755 and 621-739 of **Seq ID No 298**; 4-14, 16-77, 79-109 and 25-99 of **Seq ID No 299**; 4-9, 17-23, 30-37, 44-55, 65-72, 77-93, 102-121, 123-132, 146-153 and 17-29 of **Seq ID No 300**; 4-18, 25-41, 52-60, 83-92, 104-112, 117-123, 149-155, 159-167, 170-192, 201-210, 220-227, 245-250 and 124-137 of **Seq ID No 301**; 8-25, 50-55, 89-95, 138-143, 148-153, 159-169, 173-179, 223-238, 262-268, 288-295, 297-308, 325-335, 403-409, 411-417, 432-446, 463-475, 492-501, 524-530, 542-548, 561-574, 576-593, 604-609, 612-622, 637-654, 665-672, 678-685, 720-725, 731-739, 762-767, 777-783, 820-838, 851-865, 901-908, 913-920, 958-970, 1000-1006, 1009-1015, 1020-1026, 1043-1052, 1055-1061, 1-128, 252-341, 771-793 and 1043-1058 of **Seq ID No 302**; 16-26, 33-46 and 64-76 of **Seq ID No 303**; 4-27, 69-77, 79-101, 117-123, 126-142, 155-161, 171-186, 200-206, 213-231, 233-244, 267-273, 313-329, 335-344, 347-370, 374-379, 399-408, 422-443, 445-453, 461-468, 476-482, 518-534, 544-553, 556-567, 578-595, 601-620, 626-636, 646-658, 666-681, 715-721, 762-768, 778-785, 789-803, 809-819, 22-108, 153-318, 391-527 and 638-757 of **Seq ID No 304**; 6-21, 32-43, 62-92, 104-123, 135-141, 145-152, 199-216, 218-226, 237-247, 260-269, 274-283, 297-303, 1-72 and 127-211 of **Seq ID No 305**; 6-26, 50-56, 83-89, 108-114, 123-131, 172-181, 194-200, 221-238, 241-247, 251-259, 263-271, 284-292, 304-319, 321-335, 353-358, 384-391, 408-417, 424-430, 442-448, 459-466, 487-500, 514-528, 541-556, 572-578, 595-601, 605-613, 620-631, 635-648, 660-670, 673-679, 686-693, 702-708, 716-725, 730-735, 749-755, 770-777, 805-811, 831-837, 843-851, 854-860, 863-869, 895-901, 904-914, 922-929, 933-938, 947-952, 956-963, 1000-1005, 1008-1014, 1021-1030, 1097-1103, 1120-1130, 1132-1140, 1-213, 269-592 and 992-1120 of **Seq ID No 306**; 9-16, 33-39, 47-59, 65-79, 81-95, 103-108, 115-123, 138-148, 163-171, 176-185, 191-196, 205-211, 213-221, 224-256, 261-276, 294-302, 357-363, 384-390, 95-111 and 161-189 of **Seq ID No 307**; 21-27, 35-45, 70-76, 92-105, 129-143, 145-155, 161-166, 170-191, 204-211, 214-231, 234-246, 249-255, 259-275 and 1-18 of **Seq ID No 308**; 21-35, 45-53, 56-64, 69-97 and 1-16 of **Seq ID No 309**; 25-33, 41-47, 61-68, 86-101, 106-114, 116-129, 134-142, 144-156, 163-176, 181-190, 228-251, 255-261, 276-292, 295-305, 334-357, 368-380, 395-410, 424-429, 454-460, 469-482, 510-516, 518-527, 531-546, 558-570, 579-606, 628-636, 638-645, 651-656, 668-674, 691-698, 717-734, 742-754, 765-770, 792-797, 827-835, 847-859, 874-881, 903-909, 926-933, 942-961, 964-977, 989-1004, 1010-1028, 1031-1047, 1057-1075, 1081-1095, 1108-1117, 1138-1144, 1182-1189, 1193-1206, 1220-1229, 1239-1246, 1257-1267, 1271-1279, 1284-1301, 1312-1320, 1329-1335, 1341-1347, 1358-1371, 1399-1404, 1417-1426, 1458-1463, 1468-1476, 1478-1485, 1493-1506, 1535-1541, 1559-1574, 1583-1590, 1595-1601, 1603-1611, 1622-1628, 1634-1644, 1671-1685, 1689-1696, 1715-1720, 1734-1746, 1766-1775, 1801-1806, 1838-1844, 1858-1871, 1910-1917, 1948-1955, 1960-1974, 2000-2015, 2019-2036, 2041-2063, 748-847 and 1381-1391 of **Seq ID No 310**; 5-12, 18-24, 27-53, 56-63, 96-113, 119-124, 131-136, 157-163, 203-209, 215-223, 233-246, 264-273, 311-316, 380-389, 393-399, 425-433, 445-450, 457-462, 464-470, 475-482, 507-513, 527-535, 542-548, 550-565, 591-602, 607-613, 627-642, 644-664, 673-712, 714-732, 739-764, 769-782, 812-818, 826-838, 848-854, 860-871, 892-906, 930-938, 940-954, 957-973, 990-998, 1002-1021, 1024-1033, 1037-1042, 1050-1060, 1077-1083, 1085-1092, 1100-1129, 1144-1161, 1169-1175, 1178-1189, 1192-1198, 1201-1207, 1211-1221, 1229-1239, 1250-1270, 1278-1292, 1294-1300, 1314-1335, 1344-1352, 1360-1374, 1394-1405, 1407-1414, 1416-1424, 1432-1452, 1456-1462, 1474-1497, 1500-1510, 1516-1522, 1534-1542, 1550-1559, 1584-1603, 1608-1627, 187-273 and 306-441 of **Seq ID No 311**; 70-80, 90-97, 118-125, 128-140, 142-148, 154-162, 189-202, 214-222, 224-232, 254-260, 275-313, 317-332, 355-360, 392-398, 425-432, 448-456, 464-470, 476-482, 491-505, 521-528, 533-546, 560-567, 592-597, 605-614, 618-626, 637-644, 646-653, 660-666, 677-691 and 207-227 of **Seq ID No 312**; 5-19, 26-34, 37-55, 57-66, 69-83, 86-102, 115-134, 138-143, 154-172, 178-195, 209-246, 251-257, 290-302, 306-311 and 256-266 of **Seq ID No 313**; 10-20, 22-28, 35-57, 72-79, 87-103, 108-128, 130-144, 158-171, 190-198, 225-242, 274-291, 301-315, 317-324, 374-385 and 353-365 of **Seq ID No 314**; 4-9, 17-30, 34-54, 59-66, 73-94, 118-130, 135-150, 158-171, 189-198, 219-239, 269-275, 283-301, 89-106 and 176-193 of **Seq ID No 315**; 14-20, 22-74, 77-86, 89-99, 104-109, 126-135, 154-165, 181-195, 197-212, 216-224, 264-275 and 107-118 of **Seq ID No 316**; 4-18, 21-38, 63-72, 101-109, 156-162, 165-179, 183-192, 195-210, 212-218, 230-239, 241-256, 278-290, 299-311, 313-322, 332-341, 348-366, 386-401, 420-426, 435-450, 455-460, 468-479, 491-498, 510-518, 532-538, 545-552, 557-563, 567-573, 586-595, 599-609, 620-626, 628-636, 652-657, 665-681 and 1-198 of **Seq ID No 317**; 4-10, 16-38, 51-68, 73-79, 94-115, 120-125, 132-178, 201-208, 216-223, 238-266, 269-295, 297-304, 337-342, 347-356, 374-401, 403-422, 440-447, 478-504, 510-516, 519-530, 537-544 and 191-206 of **Seq ID No 318**; 12-40, 42-48, 66-71, 77-86, 95-102, 113-120, 129-137, 141-148, 155-174, 208-214, 218-225, 234-240,

256-267, 275-283, 300-306, 313-321, 343-350, 359-367, 370-383, 398-405, 432-439, 443-461, 492-508, 516-526, 528-535 and 370-478 of **Seq ID No 319**; 6-14, 20-37, 56-62, 90-95, 97-113, 118-125, 140-145, 161-170, 183-202, 237-244, 275-284, 286-305, 309-316, 333-359, 373-401, 405-412 and 176-187 of **Seq ID No 320**; 33-44, 50-55, 59-80, 86-101, 129-139, 147-153, 157-163, 171-176, 189-201, 203-224, 239-245, 257-262, 281-287, 290-297, 304-320, 322-331, 334-350, 372-390, 396-401, 71-88 and 353-372 of **Seq ID No 321**; 5-11, 15-24, 26-33, 40-47, 75-88, 95-103, 105-112 and 17-30 of **Seq ID No 322**; 5-11, 16-39, 46-54, 62-82, 100-107, 111-124, 126-150, 154-165, 167-183, 204-238, 245-295, 301-313, 316-335 and 8-16 of **Seq ID No 323**; 4-19, 34-48, 69-74, 79-107, 115-127, 129-135, 143-153, 160-169, 171-182 and 142-153 of **Seq ID No 324**; 4-30, 65-74, 82-106, 110-120, 124-132, 135-140, 146-175, 179-184, 190-196, 217-223, 228-233, 250-267, 275-292, 303-315, 322-332 and 174-186 of **Seq ID No 325**; 9-16, 29-41, 47-57, 68-84, 87-109, 113-119, 162-180, 186-193, 195-201, 203-208, 218-230, 234-243, 265-271, 281-292, 305-312, 323-332, 341-347, 349-363, 368-374, 383-390, 396-410, 434-440, 446-452, 455-464, 466-473, 515-522, 529-542, 565-570, 589-600, 602-613, 618-623, 637-644, 1019-1027, 1238-1244, 1258-1264, 1268-1276, 1281-1292, 1296-1302 and 883-936 of **Seq ID No 326**; 10-17, 23-32, 39-44, 54-72, 75-81, 88-111, 138-154, 160-167, 178-185, 201-210, 236-252, 327-334, 336-342, 366-376, 388-400, 410-430, 472-482, 493-526, 552-558, 586-592, 598-603, 612-621, 630-635, 641-660 and 384-393 of **Seq ID No 327**; 4-22, 24-39, 50-59, 73-84, 100-105, 111-117, 130-138, 155-161, 173-178, 182-189, 205-215, 266-284, 308-313, 321-328, 330-337, 346-363, 368-374, 388-395, 397-405, 426-434, 453-459, 482-492, 501-507, 509-515, 518-523, 527-544, 559-590, 598-612, 614-629, 646-659, 663-684, 686-694, 698-721 and 445-461 of **Seq ID No 328**; 14-22, 27-33 and 3-17 of **Seq ID No 329**; 29-41, 66-73, 81-87, 90-108, 140-146, 150-159, 165-184, 186-196, 216-226, 230-238, 247-253, 261-269 and 126-140 of **Seq ID No 330**; 5-12, 16-25, 27-33, 36-45, 60-68, 83-88, 103-126 and 86-101 of **Seq ID No 331**; 14-23, 36-47, 56-66, 84-89, 94-105, 111-127, 140-153, 160-174, 176-183, 189-203, 219-225, 231-237, 250-257 and 194-227 of **Seq ID No 332**; 4-25, 54-60, 64-71, 73-82, 89-106, 117-124, 157-169, 183-188, 199-210, 221-232, 236-244, 255-264 and 58-98 of **Seq ID No 333**; 13-19, 26-36, 41-53, 55-71, 77-84, 86-108, 114-135, 157-172, 177-183, 187-194, 208-213, 218-226, 110-125 and 156-170 of **Seq ID No 334**; 5-24, 63-69, 77-85, 94-112, 120-137, 140-146, 152-159, 166-172, 179-187, 193-199, 206-212, 222-228, 234-240, 244-252, 257-264, 270-289, 298-309, 316-328, 337-348, 363-375, 1-56 and 340-352 of **Seq ID No 335**; 18-39, 42-71, 78-120, 124-144, 152-173, 179-189, 199-209, 213-222, 228-258, 269-304, 329-361, 364-372, 374-389, 396-441 and 313-327 of **Seq ID No 336**; 19-25, 91-98, 108-120, 156-162, 168-174, 191-204, 211-216, 232-266, 272-278, 286-308, 316-321, 327-333, 344-355, 358-364, 384-391, 395-428, 464-476, 487-495, 497-511, 544-561, 563-573, 575-582, 588-594, 10-25 and 322-338 of **Seq ID No 337**; 14-26, 32-49, 51-57, 59-72, 80-91, 102-112, 119-125, 147-161, 164-173, 175-183, 188-213, 217-222, 246-254, 260-276, 282-303, 308-318, 321-328, 333-350, 352-359, 371-378, 392-401, 407-414, 416-443, 448-463, 471-484, 490-497, 501-514, 519-527, 539-551, 557-570, 578-590, 592-598, 600-610, 618-629, 633-647, 654-667, 676-689, 702-709, 718-726, 728-737, 741-760, 764-780, 786-795, 808-826, 836-842, 845-852, 865-874, 881-887, 931-945, 949-957, 968-974, 979-986, 1003-1009, 1023-1029 and 90-103 of **Seq ID No 338**; 11-16, 37-56, 60-66, 69-77, 80-88, 93-106, 117-139, 166-171 and 72-90 of **Seq ID No 339**; 59-84, 123-133, 145-150, 161-167, 178-189 and 115-128 of **Seq ID No 340**; 15-33, 39-46, 52-64, 74-87, 108-124, 127-144, 150-156, 173-179, 184-194, 201-208, 219-236, 243-269, 272-295, 302-309, 343-349, 356-361, 370-379, 405-411, 414-423, 430-451, 457-464, 466-475, 477-483, 496-502, 507-522, 541-548, 557-563, 571-577, 579-585, 590-605, 626-642, 650-662, 671-691, 704-710, 751-769, 775-781, 786-791, 794-829, 851-858, 868-878, 884-904, 913-919, 931-939 and 132-142 of **Seq ID No 341**; 33-58, 64-71, 74-80, 83-88, 96-120, 122-139, 146-157, 167-177, 207-213, 220-225, 236-242, 264-279, 300-305, 326-336, 340-347, 350-360, 97-115 and 199-211 of **Seq ID No 342**; 4-26, 43-57, 70-99, 102-117, 121-133, 142-148, 151-168, 170-183, 192-220, 235-249, 258-279 and 30-41 of **Seq ID No 343**; 34-42, 48-58, 70-94, 110-130, 154-160, 164-172, 178-183, 195-203, 211-222, 229-250, 256-261, 274-284, 286-292, 312-323 and 222-233 of **Seq ID No 344**; 4-9, 15-36, 38-45, 49-74, 78-88, 100-112, 136-191, 211-220, 226-233, 239-246, 254-274, 287-307, 316-322, 342-353, 356-366, 373-378, 384-393, 405-431, 449-457, 459-468, 487-511, 515-524, 529-541, 544-552, 562-568, 571-576 and 208-280 of **Seq ID No 345**; 10-27, 31-37, 39-54, 71-108, 124-143 and 2-107 of **Seq ID No 346**; 16-27, 38-57, 64-70, 90-102, 104-113, 116-137, 160-166 and 1-80 of **Seq ID No 347**; 13-21, 31-36, 56-67, 127-136, 153-171, 173-180, 184-200, 214-222, 225-231, 239-263, 267-273 and 135-159 of **Seq ID No 348**; 12-27, 31-51, 68-74, 77-87, 94-101, 108-114, 117-123, 127-134, 138-168, 173-196, 201-207, 212-217, 227-237, 247-257, 264-280 and 205-223 of **Seq ID No 349**; 17-22, 25-54, 70-76, 92-100 and 98-110 of **Seq ID No 350**; 7-29, 40-50, 60-67, 87-96, 105-111, 119-164, 172-199, 206-212, 220-227, 237-259, 272-279, 282-293, 295-309, 313-319, 321-328, 345-363, 376-386 and 159-176 of **Seq ID No 351**; 4-19, 24-

30, 36-43, 50-68, 71-89, 93-106, 141-152, 154-172, 179-197, 199-215, 229-239, 246-252, 255-263, 281-298, 319-325, 329-356, 358-368, 374-390, 397-409, 420-429, 432-444, 450-456, 459-475, 483-494, 496-502, 520-528, 532-556 and 362-377 of **Seq ID No 352**; 18-25, 40-62, 77-85, 91-97, 105-116, 123-133, 139-184, 189-197 and 122-140 of **Seq ID No 353**; 4-49, 52-58, 62-70, 79-105, 109-133, 142-150, 163-168, 206-214, 220-228, 233-240, 243-254, 274-281, 303-311, 327-338, 357-373, 378-396, 403-413, 420-436, 441-453, 461-467, 475-481, 484-498, 506-512, 514-521, 523-529, 562-579, 589-595, 598-603, 615-648, 714-722, 728-742, 749-758, 777-792, 795-807 and 643-658 of **Seq ID No 354**; 8-27, 37-48, 51-56, 72-79, 87-106, 120-138, 140-147, 167-176, 187-197, 205-216, 222-229, 234-239, 243-249, 277-288, 292-315, 334-343, 347-353, 363-391, 398-404, 430-447, 461-467, 478-492, 498-507 and 456-470 of **Seq ID No 355**; 5-12, 18-24, 59-69, 80-93, 95-109, 119-125, 130-137, 139-147, 158-163, 168-176, 182-202, 206-215, 222-239, 241-249, 267-277, 291-298, 311-318, 321-327, 338-344, 348-355, 373-386, 393-406, 411-417, 434-443, 446-465, 473-484, 514-521, 532-553, 584-594 and 221-237 of **Seq ID No 356**; 4-14, 27-34, 50-58, 63-72, 79-106, 109-114, 121-142, 146-154, 161-167, 169-175, 178-201, 223-238, 249-254, 259-264, 278-292, 294-312, 319-330 and 167-191 of **Seq ID No 357**; 7-28, 36-42, 50-61, 63-80, 122-152, 161-174, 176-191 and 140-190 of **Seq ID No 358**; 20-57, 59-65, 70-78, 86-102, 119-133, 142-161, 163-173, 177-188, 192-202, 204-220, 222-236, 240-253, 279-319, 326-331, 337-383, 390-399, 406-412, 420-427, 431-438 and 381-395 of **Seq ID No 359**; 13-18, 28-34, 37-43, 50-59, 75-81, 83-97, 105-121, 139-147, 200-206, 209-227, 231-247, 260-271, 318-327, 366-381, 388-394, 399-406 and 182-201 of **Seq ID No 360**; 6-29, 37-43, 51-56, 70-77, 82-102, 110-119, 127-143, 178-190, 201-209, 216-243, 261-269, 281-292, 305-313, 327-339, 341-354, 356-373, 391-397, 423-429, 438-445, 450-478 and 21-314 of **Seq ID No 361**; 4-12, 15-21, 32-41, 59-76, 80-89, 96-104 and 90-103 of **Seq ID No 362**; 9-28, 30-41, 44-54, 69-74, 77-82, 90-97, 104-123, 125-135, 149-155, 164-173, 177-184, 217-226, 230-235, 238-244, 258-272, 282-297, 300-305, 309-315, 317-322, 327-336, 348-362, 368-374, 380-387, 400-411, 414-424, 451-458, 460-466, 483-494, 497-503, 506-511, 521-528, 540-553, 569-587, 598-606, 628-642, 661-681, 688-700, 718-733, 740-749, 752-764, 769-783, 823-834, 848-854, 862-872, 878-884, 886-898, 915-920, 938-951, 954-961, 963-972, 982-989, 996-1003, 1010-1016, 1021-1032, 1038-1044, 1047-1057, 1060-1070, 1079-1088, 1094-1102, 1117-1127, 1129-1135, 1142-1153, 1158-1204, 1212-1229, 1234-1263, 1269-1277, 1308-1313, 1327-1338, 1344-1376, 1400-1415, 1436-1443, 1448-1458, 1497-1504, 1511-1522, 1544-1566, 3-82 and 509-576 of **Seq ID No 363**; 8-36, 40-64, 71-79, 88-94, 102-109, 118-127, 138-148, 151-159, 163-174, 192-198, 200-206, 220-233, 268-273, 290-301, 304-309, 316-323, 331-349, 378-391, 414-420, 427-437, 455-475, 494-510, 541-547, 549-555, 616-640, 1-60, 55-139, 212-308, 386-458 and 458-624 of **Seq ID No 364**; 16-31, 35-42, 70-77, 91-101, 120-130, 132-140, 143-153, 185-190, 195-202, 215-222, 228-238, 241-251, 257-264, 268-277, 288-302, 312-324, 326-333, 341-348, 364-382, 415-429, 438-454, 458-466, 491-499, 501-521 and 273-281 of **Seq ID No 365**; 8-14, 32-57, 74-149, 155-177, 179-212, 221-266, 271-296, 304-324, 329-346, 349-359, 368-401, 413-419, 426-454, 465-478, 493-510 and 466-490 of **Seq ID No 366**; 22-28, 33-51, 64-89, 96-119, 126-132, 138-146, 152-159, 161-169, 172-179, 193-198, 205-211, 221-231, 235-254, 273-280, 297-303, 312-320, 328-346, 351-373, 378-384, 391-398, 448-454, 460-468, 470-481, 516-558, 574-593, 597-602, 613-623, 626-646, 649-656, 668-673, 675-683, 696-708, 715-722, 724-739, 745-751, 759-777, 780-804, 816-822 and 102-113 of **Seq ID No 367**; 12-28, 41-91, 98-107, 112-120, 125-131, 151-193, 215-221, 240-250, 263-280 and 128-138 of **Seq ID No 368**; 16-24, 32-38, 46-62, 68-81, 90-105, 127-133, 144-150, 160-166, 178-184, 186-202, 210-219, 232-240, 252-258, 264-273, 293-324, 337-344, 349-357, 360-369, 385-398, 410-416, 419-427, 441-449, 458-476, 508-515, 523-539, 544-549, 562-569, 571-579, 96-109 and 127-139 of **Seq ID No 369**; 19-25, 28-34, 56-61, 85-97, 110-116 and 39-53 of **Seq ID No 370**; 4-37, 41-50, 62-72, 91-97, 99-109, 114-125, 136-141, 149-158, 160-166, 201-215 and 27-225 of **Seq ID No 371**; 15-31, 44-51, 96-105, 122-130, 149-157, 162-168, 178-183, 185-192, 198-204, 206-213, 221-234, 239-245, 248-255, 257-266, 289-335, 349-357, 415-422, 425-441, 448-454, 462-468 and 463-481 of **Seq ID No 372**; 5-31, 39-55, 63-72, 76-99, 106-155, 160-177, 179-199, 207-217, 223-240, 245-255, 261-267, 294-316, 321-343, 354-378, 382-452, 477-488, 529-536, 555-569, 584-591, 593-612, 620-627, 632-640, 647-654, 671-680, 698-704, 723-730, 732-750, 769-775, 781-788, 822-852 and 505-525 of **Seq ID No 373**; 3-18 of **Seq ID No 374**; 4-14 and 12-24 of **Seq ID No 375**; 4-11, 22-30 and 12-25 of **Seq ID No 376**; 5-12 and 4-18 of **Seq ID No 377**; 4-28 and 7-14 of **Seq ID No 378**; 6-16 and 8-16 of **Seq ID No 379**; 4-15, 18-33 and 24-36 of **Seq ID No 380**; 4-10, 16-21 and 20-31 of **Seq ID No 381**; 6-19 of **Seq ID No 382**; 11-18 and 3-10 of **Seq ID No 383**; 13-24 and 3-15 of **Seq ID No 384**; 15-27 and 7-16 of **Seq ID No 385**; 11-16 and 1-15 of **Seq ID No 386**; 4-16 and 9-21 of **Seq ID No 387**; 4-24, 40-48, 54-67 and 22-39 of **Seq ID No 388**; 6-30, 34-55, 62-68, 78-106 and 68-74 of **Seq ID No 389**; 3-14 of **Seq ID No 390**; 9-19 and 6-21 of **Seq ID No 391**; 4-17 and 1-9 of **Seq ID No 392**; 5-30 and 1-8 of **Seq ID No**

393; 4-16, 23-46, 51-56 and 45-55 of Seq ID No 394; 7-16 of Seq ID No 395; 2-14 of Seq ID No 396; 4-36, 43-65 and 50-62 of Seq ID No 397; 10-30 and 14-21 of Seq ID No 398; 9-17 and 1-10 of Seq ID No 399; 4-12 and 3-16 of Seq ID No 400; 4-15 and 5-23 of Seq ID No 401; 10-21 of Seq ID No 402; 6-16 of Seq ID No 403; 4-29, 31-38 and 2-14 of Seq ID No 404; 4-35 and 33-42 of Seq ID No 405; 2-17 of Seq ID No 406; 9-18, 30-35 and 15-33 of Seq ID No 407; 4-9 and 6-12 of Seq ID No 408; 3-17 of Seq ID No 409; 12-21, 37-44, 52-61, 72-80 and 38-48 of Seq ID No 410; 4-10, 29-44, 54-61, 69-78 and 13-27 of Seq ID No 411; 13-23, 36-53 and 2-15 of Seq ID No 412; 4-25, 28-46, 56-72, 81-99, 120-132, 134-142, 154-160 and 129-141 of Seq ID No 413; 4-15, 24-33, 35-41, 64-86 and 21-33 of Seq ID No 414; 9-15 and 4-13 of Seq ID No 415; 4-11, 13-19, 34-48 and 15-32 of Seq ID No 416; 4-21 and 11-31 of Seq ID No 417; 23-57 and 38-50 of Seq ID No 418; 4-32 and 3-13 of Seq ID No 419; 4-10, 13-25, 32-42, 56-68, 72-84 and 26-38 of Seq ID No 420; 4-20, 31-48, 52-58, 65-71, 80-93, 99-108, 114-123 and 37-49 of Seq ID No 421; 6-12, 14-20 and 3-25 of Seq ID No 422; 14-25, 27-38 and 5-14 of Seq ID No 423; 4-41, 57-105, 109-118, 123-136, 144-152 and 86-99 of Seq ID No 424; 6-19 of Seq ID No 425; 2-19 of Seq ID No 426; 14-47 and 1-14 of Seq ID No 427; 4-21, 29-44 and 2-18 of Seq ID No 428; 23-29 and 10-28 of Seq ID No 429; 6-16, 22-36 and 11-22 of Seq ID No 430; 4-19, 30-44 and 18-27 of Seq ID No 431; 5-15, 37-45, 58-65 and 38-47 of Seq ID No 432; 4-15, 23-34 and 4-15 of Seq ID No 433; 30-36, 44-54, 79-85, 101-114, 138-152, 154-164, 170-175, 179-200, 213-220, 223-240, 243-255, 258-264, 268-284 and 10-28 of Seq ID No 434; the peptides comprising amino acid sequences of column "Identical region" of the Table 1B, especially peptides comprising amino acid 210-226 and 738-753 of Seq ID No 449; 326-344, 326-348, 338-354, 371-392, 801-809 and 877-901 of Seq ID No 450; 893-906 of Seq ID No 451; 51-69 of Seq ID No 452; 110-125 of Seq ID No 453; 291-305 of Seq ID No 454; 210-226 and 738-753 of Seq ID No 455; 326-344, 326-348, 338-354, 371-392, 801-809 and 877-901 of Seq ID No 456; 893-906 of Seq ID No 457; 51-69 of Seq ID No 458; 110-125 of Seq ID No 459; 291-305 of Seq ID No 460; 32-44 of Seq ID No 461; 399-410 of Seq ID No 462; the serum reactive epitopes as specified in the column of "aa from" to "aa to" of Table 2, especially peptides comprising amino acid 120-143, 138-161 and 156-179 of Seq ID No 218; 110-129 and 168-184 of Seq ID No 219; 74-90 of Seq ID No 222; 759-773 of Seq ID No 223; 237-260 of Seq ID No 224; 265-284 of Seq ID No 225; 65-74 of Seq ID No 226; 41-50 of Seq ID No 227; 163-174 of Seq ID No 229; 26-37 of Seq ID No 230; 174-189 of Seq ID No 232; 240-256 of Seq ID No 234; 285-297 of Seq ID No 236; 238-247 of Seq ID No 238; 491-519 of Seq ID No 239; 114-140 of Seq ID No 243; 267-284 of Seq ID No 250; 439-453 of Seq ID No 252; 162-178 of Seq ID No 253; 347-364 of Seq ID No 254; 699-715 of Seq ID No 255; 60-71 of Seq ID No 256; 244-257 of Seq ID No 257; 44-63 and 57-76 of Seq ID No 258; 185-196 of Seq ID No 260; 119-129 of Seq ID No 263; 182-195 of Seq ID No 266; 32-44 and 424-442 of Seq ID No 267; 247-256 of Seq ID No 268; 678-694, 785-805, 55-77 and 72-94 of Seq ID No 269; 210-226 of Seq ID No 281; 37-59 of Seq ID No 289; 13-29 of Seq ID No 296; 136-159 of Seq ID No 348; 205-222 of Seq ID No 349; 99-110 of Seq ID No 350; 160-176 of Seq ID No 351; 457-470 of Seq ID No 355; 221-237 of Seq ID No 356; 167-190 of Seq ID No 357; 96-120 of Seq ID No 361; 399-417, 503-519 and 544-563 of Seq ID No 364; 46-68, 159-183 and 184-198 of Seq ID No 371; 463-481 of Seq ID No 372; the immunogenic epitopes as specified in the column of "aa from" to "aa to" of Table 4; especially peptides comprising amino acid 110-129 and 168-184 of Seq ID No 219; 877-901, 333-354, 326-344 and 801-809 of Seq ID No 277; 1-54 of Seq ID No 347; 544-563, 31-51, 107-119, 399-417 and 503-519 of Seq ID No 364; 120-198 of Seq ID No 218; 20-35 of Seq ID No 219; 118-201 of Seq ID No 221; 48-132 of Seq ID No 242; 118-136 of Seq ID No 249; 162-178 of Seq ID No 253; 347-364 of Seq ID No 254; 699-715 of Seq ID No 255; 50-76 of Seq ID No 258; 785-819 and 44-128 of Seq ID No 269; 90-128 of Seq ID No 274; 314-384 of Seq ID No 289; 327-349 of Seq ID No 293; 242-314, 405-478 and 23-100 of Seq ID No 304; 129-210 of Seq ID No 305; 162-188 of Seq ID No 307; 750-772 of Seq ID No 310; 1-56 of Seq ID No 335; 322-337 of Seq ID No 337; 72-90 of Seq ID No 339; 374-395 of Seq ID No 345; 136-159 of Seq ID No 348; 141-164 of Seq ID No 358; 96-157 of Seq ID No 361; 1-82 of Seq ID No 363; 489-556 of Seq ID No 364; 159-183 and 49-133 of Seq ID No 371; The peptides comprising amino acid sequences of column "predicted immunogenic aa" and "location of identified immunogenic region (aa)" of Table 5, especially peptides comprising amino acid 4-26, 35-41, 53-61, 73-84, 103-108, 114-120, 140-146, 156-162, 192-208, 214-219, 227-233, 239-252, 260-268, 284-297, 1-48 and 113-133 of Seq ID No 475; 4-27, 38-44, 50-56, 59-64, 72-79, 83-89, 92-97, 108-116, 123-148, 152-167, 183-196, 200-220, 232-244, 255-261, 265-274, 282-302, 309-317, 1-79 and 231-302 of Seq ID No 476; 6-28, 66-72, 85-105, 115-121, 144-151, 160-170, 176-185, 223-230, 252-288, 296-

310, 319-333, 367-374, 458-464, 471-480, 483-488, 520-528, 530-549, 559-564, 593-601, 606-616, 636-643, 655-662, 676-682, 684-699, 719-726, 735-750, 757-764, 777-785, 799-810, 812-843, 846-853, 868-873, 880-889, 891-899, 909-929, 934-940, 963-969, 998-1004, 1007-1014, 1016-1022, 1030-1046, 1-80 and 808-821 of Seq ID No 477; 7-24, 35-41, 75-81, 91-114, 122-132, 137-144, 148-156, 183-192, 194-200, 212-228, 233-238, 251-258, 275-295, 326-332, 337-346, 1-79 and 305-321 of Seq ID No 478; 31-38, 42-52, 66-72, 86-92, 98-104, 115-122, 127-146, 154-164, 169-187, 198-212, 225-237, 255-269, 13-92 and 135-142 of Seq ID No 479; 4-36, 39-49, 63-69, 71-77, 81-88, 123-131, 133-139, 160-169, 174-180, 188-194, 210-217, 273-278, 289-300, 317-334, 336-341, 383-401, 425-438, 1-68, 212-270 and 402-446 of Seq ID No 480; 21-29, 31-42, 49-63, 72-79, 81-93, 112-132, 159-165, 188-195, 197-232, 262-267, 279-286, 294-301, 318-326, 348-366, 381-405, 409-426, 436-465, 471-480, 484-492, 497-505, 521-544, 554-561, 567-577, 581-589, 601-609, 611-622, 636-651, 653-667, 669-685, 700-708, 716-722, 729-744, 749-766, 780-786, 789-811, 814-864, 1-57 and 84-106 of Seq ID No 481; 6-24, 35-48, 57-63, 72-78, 87-92, 113-119, 123-137, 147-153, 173-181, 212-233 and 1-124 of Seq ID No 482; 13-34, 62-69, 78-83, 86-91, 98-104, 107-115, 146-159, 179-188, 195-205, 209-221, 226-233, 239-253, 276-282, 284-294, 297-308, 331-354, 375-382, 388-399, 421-433, 449-458, 464-469, 472-491, 508-513, 525-531, 534-550, 575-593, 601-618, 629-635, 654-661, 666-680, 706-721, 723-740, 771-805, 810-830, 845-851 and 1-84 of Seq ID No 483; 4-32, 45-64, 73-83, 86-92, 100-111, 125-147, 157-163, 170-175, 177-188, 226-232, 245-252, 258-274, 320-335, 348-359 and 1-71 of Seq ID No 484; 13-40, 43-71, 76-83, 87-101, 109-119, 125-156, 162-175, 182-219, 226-232, 240-262, 270-287, 306-318, 326-342, 344-408, 414-444, 449-456 and 1-51 of Seq ID No 485; 4-16, 18-34, 45-54, 99-108, 134-140, 203-212, 241-257, 266-274, 279-291, 308-315, 330-336, 355-370, 374-382, 402-410, 428-455, 466-472, 474-480, 531-554, 560-566, 572-580, 597-618, 632-660, 664-674, 676-685, 691-705, 708-735, 750-768, 1-87 and 342-480 of Seq ID No 486; **The serum reactive epitopes as specified in the column of "aa from" to "aa to" of Table 6, especially peptides comprising amino acid 115-132 and 1-26 of Seq ID No 475; 33-55 of Seq ID No 476; 1-25 of Seq ID No 478; 37-61 of Seq ID No 479; 1-24 of Seq ID No 480; 1-23 of Seq ID No 481; 46-60 of Seq ID No 482; 1-28, 23-50 and 45-71 of Seq ID No 483; 1-22 and 17-38 of Seq ID No 484; 1-22 and 17-38 of Seq ID No 485; 1-27, 22-47 and 422-447 of Seq ID No 486; The immunogenic epitopes as specified in the column of "aa from" to "aa to" of Table 7, especially peptides comprising amino acid 115-132 and 1-47 of Seq ID No 475; 1-55 of Seq ID No 476; 22-85 of Seq ID No 477; 307-320 and 1-44 of Seq ID No 478; 15-76 and 40-92 of Seq ID No 479; 1-59, 213-269 and 403-445 of Seq ID No 480; 1-56 and 85-105 of Seq ID No 481; 37-121 of Seq ID No 482; 1-71 of Seq ID No 483; 1-38 of Seq ID No 484; 1-38 of Seq ID No 485; 1-47 of Seq ID No 486.**

The present invention also provides a process for producing a *S. agalactiae* hyperimmune serum reactive antigen or a fragment thereof according to the present invention comprising expressing one or more of the nucleic acid molecules according to the present invention in a suitable expression system.

Moreover, the present invention provides a process for producing a cell, which expresses a *S. agalactiae* hyperimmune serum reactive antigen or a fragment thereof according to the present invention comprising transforming or transfecting a suitable host cell with the vector according to the present invention.

According to the present invention a pharmaceutical composition, especially a vaccine, comprising a hyperimmune serum-reactive antigen or a fragment thereof as defined in the present invention or a nucleic acid molecule as defined in the present invention is provided.

In a preferred embodiment the pharmaceutical composition further comprises an immunostimulatory substance, preferably selected from the group comprising polycationic polymers, especially polycationic peptides, immunostimulatory deoxynucleotides (ODNs), peptides containing at least two LysLeuLys motifs, especially KLKLSKLK, neuroactive compounds, especially human growth hormone, alum, Freund's complete or incomplete adjuvants or combinations thereof.

In a more preferred embodiment the immunostimulatory substance is a combination of either a polycationic polymer and immunostimulatory deoxynucleotides or of a peptide containing at least two

LysLeuLys motifs and immunostimulatory deoxynucleotides.

In a still more preferred embodiment the polycationic polymer is a polycationic peptide, especially polyarginine.

According to the present invention the use of a nucleic acid molecule according to the present invention or a hyperimmune serum-reactive antigen or fragment thereof according to the present invention for the manufacture of a pharmaceutical preparation, especially for the manufacture of a vaccine against *S. agalactiae* infection, is provided.

Also an antibody, or at least an effective part thereof, which binds at least to a selective part of the hyperimmune serum-reactive antigen or a fragment thereof according to the present invention, is provided herewith.

In a preferred embodiment the antibody is a monoclonal antibody.

In another preferred embodiment the effective part of the antibody comprises Fab fragments.

In a further preferred embodiment the antibody is a chimeric antibody.

In a still preferred embodiment the antibody is a humanized antibody.

The present invention also provides a hybridoma cell line, which produces an antibody according to the present invention.

Moreover, the present invention provides a method for producing an antibody according to the present invention, characterized by the following steps:

- initiating an immune response in a non-human animal by administering an hyperimmune serum-reactive antigen or a fragment thereof, as defined in the invention, to said animal,
- removing an antibody containing body fluid from said animal, and
- producing the antibody by subjecting said antibody containing body fluid to further purification steps.

Accordingly, the present invention also provides a method for producing an antibody according to the present invention, characterized by the following steps:

- initiating an immune response in a non-human animal by administering an hyperimmune serum-reactive antigen or a fragment thereof, as defined in the present invention, to said animal,
- removing the spleen or spleen cells from said animal,
- producing hybridoma cells of said spleen or spleen cells,
- selecting and cloning hybridoma cells specific for said hyperimmune serum-reactive antigens or a fragment thereof,
- producing the antibody by cultivation of said cloned hybridoma cells and optionally further purification steps.

The antibodies provided or produced according to the above methods may be used for the preparation of a medicament for treating or preventing *S. agalactiae* infections.

According to another aspect the present invention provides an antagonist, which binds to a hyperimmune serum-reactive antigen or a fragment thereof according to the present invention.

Such an antagonist capable of binding to a hyperimmune serum-reactive antigen or fragment thereof according to the present invention may be identified by a method comprising the following steps:

- 16 -

- a) contacting an isolated or immobilized hyperimmune serum-reactive antigen or a fragment thereof according to the present invention with a candidate antagonist under conditions to permit binding of said candidate antagonist to said hyperimmune serum-reactive antigen or fragment, in the presence of a component capable of providing a detectable signal in response to the binding of the candidate antagonist to said hyperimmune serum reactive antigen or fragment thereof; and
- b) detecting the presence or absence of a signal generated in response to the binding of the antagonist to the hyperimmune serum reactive antigen or the fragment thereof.

An antagonist capable of reducing or inhibiting the interaction activity of a hyperimmune serum-reactive antigen or a fragment thereof according to the present invention to its interaction partner may be identified by a method comprising the following steps:

- a) providing a hyperimmune serum reactive antigen or a hyperimmune fragment thereof according to the present invention,
- b) providing an interaction partner to said hyperimmune serum reactive antigen or a fragment thereof, especially an antibody according to the present invention,
- c) allowing interaction of said hyperimmune serum reactive antigen or fragment thereof to said interaction partner to form an interaction complex,
- d) providing a candidate antagonist,
- e) allowing a competition reaction to occur between the candidate antagonist and the interaction complex,
- f) determining whether the candidate antagonist inhibits or reduces the interaction activities of the hyperimmune serum reactive antigen or the fragment thereof with the interaction partner.

The hyperimmune serum reactive antigens or fragments thereof according to the present invention may be used for the isolation and/or purification and/or identification of an interaction partner of said hyperimmune serum reactive antigen or fragment thereof.

The present invention also provides a process for *in vitro* diagnosing a disease related to expression of a hyperimmune serum-reactive antigen or a fragment thereof according to the present invention comprising determining the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen or fragment thereof according to the present invention or the presence of the hyperimmune serum reactive antigen or fragment thereof according to the present invention.

The present invention also provides a process for *in vitro* diagnosis of a bacterial infection, especially a *S. agalactiae* infection, comprising analyzing for the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen or fragment thereof according to the present invention or the presence of the hyperimmune serum reactive antigen or fragment thereof according to the present invention.

Moreover, the present invention provides the use of a hyperimmune serum reactive antigen or fragment thereof according to the present invention for the generation of a peptide binding to said hyperimmune serum reactive antigen or fragment thereof, wherein the peptide is an anticaline.

The present invention also provides the use of a hyperimmune serum-reactive antigen or fragment thereof according to the present invention for the manufacture of a functional nucleic acid, wherein the functional nucleic acid is selected from the group comprising aptamers and spiegelmers.

The nucleic acid molecule according to the present invention may also be used for the manufacture of a functional ribonucleic acid, wherein the functional ribonucleic acid is selected from the group comprising ribozymes, antisense nucleic acids and siRNA.

The present invention advantageously provides an efficient, relevant and comprehensive set of isolated nucleic acid molecules and their encoded hyperimmune serum reactive antigens or fragments thereof identified from *S. agalactiae* using an antibody preparation from multiple human plasma pools and surface expression libraries derived from the genome of *S. agalactiae*. Thus, the present invention fulfils a widely felt demand for *S. agalactiae* antigens, vaccines, diagnostics and products useful in procedures for preparing antibodies and for identifying compounds effective against *S. agalactiae* infection.

An effective vaccine should be composed of proteins or polypeptides, which are expressed by all strains and are able to induce high affinity, abundant antibodies against cell surface components of *S. agalactiae*. The antibodies should be IgG1 and/or IgG3 for opsonization, and any IgG subtype and IgA for neutralisation of adherence and toxin action. A chemically defined vaccine must be definitely superior compared to a whole cell vaccine (attenuated or killed), since components of *S. agalactiae*, which cross-react with human tissues or inhibit opsonization can be eliminated, and the individual proteins inducing protective antibodies and/or a protective immune response can be selected.

The approach, which has been employed for the present invention, is based on the interaction of GBS proteins or peptides with the antibodies present in human sera. The antibodies produced against *S. agalactiae* by the human immune system and present in human sera are indicative of the *in vivo* expression of the antigenic proteins and their immunogenicity. In addition, the antigenic proteins as identified by the bacterial surface display expression libraries using pools of pre-selected sera, are processed in a second and third round of screening by individual selected or generated sera. Thus the present invention supplies an efficient, relevant, comprehensive set of GBS antigens as a pharmaceutical composition, especially a vaccine preventing infection by *S. agalactiae*.

In the antigen identification program for identifying a comprehensive set of antigens according to the present invention, at least two different bacterial surface expression libraries are screened with several serum pools or plasma fractions or other pooled antibody containing body fluids (antibody pools). The antibody pools are derived from a serum collection, which has been tested against antigenic compounds of *S. agalactiae*, such as whole cell extracts and culture supernatant proteins. Preferably, three distinct serum collections are used, obtained ad 1. from healthy pregnant women tested negative for cervical and anorectal carriage of GBS, ad 2. healthy pregnant women tested positive for cervical and/or anorectal carriage of GBS who's newborn remained GBS-free (although with antibiotic prevention), ad 3. from adults below <45 years of age without clinical disease. Sera have to react with multiple GBS-specific antigens in order to be considered hyperimmune and therefore relevant in the screening method applied for the present invention.

The expression libraries as used in the present invention should allow expression of all potential antigens, e.g. derived from all secreted and surface proteins of *S. agalactiae*. Bacterial surface display libraries will be represented by a recombinant library of a bacterial host displaying a (total) set of expressed peptide sequences of *S. agalactiae* on two selected outer membrane proteins (LamB and FhuA) at the bacterial host membrane {Georgiou, G., 1997}; {Etz, H. et al., 2001}. One of the advantages of using recombinant expression libraries is that the identified hyperimmune serum-reactive antigens may be instantly produced by expression of the coding sequences of the screened and selected clones expressing the hyperimmune serum-reactive antigens without further recombinant DNA technology or cloning steps necessary.

The comprehensive set of antigens identified by the described program according to the present invention is analysed further by one or more additional rounds of screening. Therefore individual antibody preparations or antibodies generated against selected peptides, which were identified as immunogenic are used. According to a preferred embodiment the individual antibody preparations for the second round of screening are derived from pregnant women and non-pregnant adults who show an antibody titer above a certain minimum level, for example an antibody titer being higher than 80

percentile, preferably higher than 90 percentile, especially higher than 95 percentile of the human (patient or healthy individual) sera tested. Using such high titer individual antibody preparations in the second screening round allows a very selective identification of the hyperimmune serum-reactive antigens and fragments thereof from *S. agalactiae*.

Following the comprehensive screening procedure, the selected antigenic proteins, expressed as recombinant proteins or *in vitro* translated products, in case it can not be expressed in prokaryotic expression systems, or the identified antigenic peptides (produced synthetically) are tested in a second screening by a series of ELISA and Western blotting assays for the assessment of their immunogenicity with a large human serum collection (minimum ~150 healthy and patients sera).

It is important that the individual antibody preparations (which may also be the selected serum) allow a selective identification of the most promising candidates of all the hyperimmune serum-reactive antigens from all the promising candidates from the first round. Therefore, preferably at least 10 individual antibody preparations (i.e. antibody preparations (e.g. sera) from at least 10 different individuals having suffered from an infection to the chosen pathogen) should be used in identifying these antigens in the second screening round. Of course, it is possible to use also less than 10 individual preparations, however, selectivity of the step may not be optimal with a low number of individual antibody preparations. On the other hand, if a given hyperimmune serum-reactive antigen (or an antigenic fragment thereof) is recognized by at least 10 individual antibody preparations, preferably at least 30, especially at least 50 individual antibody preparations, identification of the hyperimmune serum-reactive antigen is also selective enough for a proper identification. Hyperimmune serum-reactivity may of course be tested with as many individual preparations as possible (e.g. with more than 100 or even with more than 1,000).

Therefore, the relevant portion of the hyperimmune serum-reactive antibody preparations according to the method of the present invention should preferably be at least 10, more preferred at least 30, especially at least 50 individual antibody preparations. Alternatively (or in combination) hyperimmune serum-reactive antigens may preferably be also identified with at least 20%, preferably at least 30%, especially at least 40% of all individual antibody preparations used in the second screening round.

According to a preferred embodiment of the present invention, the sera from which the individual antibody preparations for the second round of screening are prepared (or which are used as antibody preparations), are selected by their titer against *S. agalactiae* (e.g. against a preparation of this pathogen, such as a lysate, cell wall components and recombinant proteins). Preferably, some are selected with a total IgA titer above 300 U, especially above 500 U, and/or an IgG titer above 5,000 U, especially above 10,000 U (U = units, calculated from the OD_{405nm} reading at a given dilution) when the whole organism (total lysate or whole cells) is used as antigen in the ELISA.

The antibodies produced against streptococci by the human immune system and present in human sera are indicative of the *in vivo* expression of the antigenic proteins and their immunogenicity. The recognition of linear epitopes recognized by serum antibodies can be based on sequences as short as 4-5 amino acids. Of course it does not necessarily mean that these short peptides are capable of inducing the given antibody *in vivo*. For that reason the defined epitopes, polypeptides and proteins are further to be tested in animals (mainly in mice) for their capacity to induce antibodies against the selected proteins *in vivo*.

The preferred antigens are located on the cell surface or secreted, and are therefore accessible extracellularly. Antibodies against cell wall proteins are expected to serve multiple purposes: to inhibit adhesion, to interfere with nutrient acquisition, to inhibit immune evasion and to promote phagocytosis [Hornef, M. et al., 2002]. Antibodies against secreted proteins are beneficial in neutralisation of their function as toxin or virulence component. It is also known that bacteria communicate with each other

through secreted proteins. Neutralizing antibodies against these proteins will interrupt growth-promoting cross-talk between or within streptococcal species. Bioinformatic analyses (signal sequences, cell wall localisation signals, transmembrane domains) proved to be very useful in assessing cell surface localisation or secretion. The experimental approach includes the isolation of antibodies with the corresponding epitopes and proteins from human serum, and the generation of immune sera in mice against (poly) peptides selected by the bacterial surface display screens. These sera are then used in a third round of screening as reagents in the following assays: cell surface staining of *S. agalactiae* grown under different conditions (FACS or microscopy), determination of neutralizing capacity (toxin, adherence), and promotion of opsonization and phagocytosis (*in vitro* phagocytosis assay).

For that purpose, bacterial *E. coli* clones are directly injected into mice and immune sera are taken and tested in the relevant *in vitro* assay for functional opsonic or neutralizing antibodies. Alternatively, specific antibodies may be purified from human or mouse sera using peptides or proteins as substrate.

Host defence against *S. agalactiae* relies mainly on opsonophagocytic killing mechanism. Inducing high affinity antibodies of the opsonic and neutralizing type by vaccination helps the innate immune system to eliminate bacteria and toxins. This makes the method according to the present invention an optimal tool for the identification of GBS antigenic proteins.

The skin and mucous membranes are formidable barriers against invasion by streptococci. However, once the skin or the mucous membranes are breached the first line of non-adaptive cellular defence begins its co-ordinate action through complement and phagocytes, especially the polymorphonuclear leukocytes (PMNs). These cells can be regarded as the cornerstones in eliminating invading bacteria. As *Streptococcus agalactiae* is a primarily extracellular pathogen, the major anti-streptococcal adaptive response comes from the humoral arm of the immune system, and is mediated through three major mechanisms: promotion of opsonization, toxin neutralisation, and inhibition of adherence. It is believed that opsonization is especially important, because of its requirement for an effective phagocytosis. For efficient opsonization the microbial surface has to be coated with antibodies and complement factors for recognition by PMNs through receptors to the Fc fragment of the IgG molecule or to activated C3b. After opsonization, streptococci are phagocytosed and killed. Antibodies bound to specific antigens on the cell surface of bacteria serve as ligands for the attachment to PMNs and to promote phagocytosis. The very same antibodies bound to the adhesins and other cell surface proteins are expected to neutralize adhesion and prevent colonization. The selection of antigens as provided by the present invention is thus well suited to identify those that will lead to protection against infection in an animal model or in humans.

According to the antigen identification method used herein, the present invention can surprisingly provide a set of comprehensive novel nucleic acids and novel hyperimmune serum reactive antigens and fragments thereof of *S. agalactiae*, among other things, as described below. According to one aspect, the invention particularly relates to the nucleotide sequences encoding hyperimmune serum reactive antigens which sequences are set forth in the Sequence listing **Seq ID No:** 1-217, 435-448 and 463-474 and the corresponding encoded amino acid sequences representing hyperimmune serum reactive antigens are set forth in the Sequence Listing **Seq ID No** 218-434, 449-462 and 475-486.

In a preferred embodiment of the present invention, a nucleic acid molecule is provided which exhibits 70% identity over their entire length to a nucleotide sequence set forth with **Seq ID No** 14, 90, 157-216.. Most highly preferred are nucleic acids that comprise a region that is at least 80% or at least 85% identical over their entire length to a nucleic acid molecule set forth with **Seq ID No** 14, 90, 157-216. In this regard, nucleic acid molecules at least 90%, 91%, 92%, 93%, 94%, 95%, or 96% identical over their entire length to the same are particularly preferred. Furthermore, those with at least 97% are highly preferred, those with at least 98% and at least 99% are particularly highly preferred, with at least 99% or 99.5% being the more preferred, with 100% identity being especially preferred. Moreover, preferred embodiments in this respect are nucleic acids which encode hyperimmune serum reactive antigens or fragments thereof

(polypeptides) which retain substantially the same biological function or activity as the mature polypeptide encoded by said nucleic acids set forth in the **Seq ID No 14, 90, 157-216**.

Identity, as known in the art and used herein, is the relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, identity also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. Identity can be readily calculated. While there exist a number of methods to measure identity between two polynucleotide or two polypeptide sequences, the term is well known to skilled artisans (e.g. *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987). Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity are codified in computer programs. Preferred computer program methods to determine identity between two sequences include, but are not limited to, GCG program package [Devereux, J. et al., 1984], BLASTP, BLASTN, and FASTA [Altschul, S. et al., 1990].

According to another aspect of the invention, nucleic acid molecules are provided which exhibit 96 % or more than 96 %, especially 100 % sequence identity to the nucleic acid sequence set forth with **Seq ID No 1, 3, 5-13, 15, 18-25, 27-31, 33-36, 39-68, 70-85, 92-100, 103-126, 128-145, 147, 149-156, 217, 435-448 and 463-474**.

According to a further aspect of the present invention, nucleic acid molecules having 98 % or more than 98%, especially 100 % sequence identity to a nucleic acid molecule are provided which are identical to the nucleic acid sequences set forth with **Seq ID No 32, 86, 91, 101, 127**.

The nucleic acid molecules according to the present invention can as a second alternative also be a nucleic acid molecule which is at least essentially complementary to the nucleic acid described as the first alternative above. As used herein complementary means that a nucleic acid strand is base pairing via Watson-Crick base pairing with a second nucleic acid strand. Essentially complementary as used herein means that the base pairing is not occurring for all of the bases of the respective strands but leaves a certain number or percentage of the bases unpaired or wrongly paired. The percentage of correctly pairing bases is preferably at least 70 %, more preferably 80 %, even more preferably 90 % and most preferably any percentage higher than 90 %. It is to be noted that a percentage of 70 % matching bases is considered as homology and the hybridization having this extent of matching base pairs is considered as stringent. Hybridization conditions for this kind of stringent hybridization may be taken from Current Protocols in Molecular Biology (John Wiley and Sons, Inc., 1987). More particularly, the hybridization conditions can be as follows:

- Hybridization performed e.g. in 5 x SSPE, 5 x Denhardt's reagent, 0.1% SDS, 100 g/mL sheared DNA at 68°C
- Moderate stringency wash in 0.2xSSC, 0.1% SDS at 42°C
- High stringency wash in 0.1xSSC, 0.1% SDS at 68°C

Genomic DNA with a GC content of 50% has an approximate T_m of 96°C. For 1% mismatch, the T_m is reduced by approximately 1°C.

In addition, any of the further hybridization conditions described herein are in principle applicable as well.

Of course, all nucleic acid sequence molecules which encode the same polypeptide molecule as those identified by the present invention are encompassed by any disclosure of a given coding sequence, since the degeneracy of the genetic code is directly applicable to unambiguously determine all possible nucleic acid molecules which encode a given polypeptide molecule, even if the number of such degenerated

nucleic acid molecules may be high. This is also applicable for fragments of a given polypeptide, as long as the fragments encode a polypeptide being suitable to be used in a vaccination connection, e.g. as an active or passive vaccine.

The nucleic acid molecule according to the present invention can as a third alternative also be a nucleic acid which comprises a stretch of at least 15 bases of the nucleic acid molecule according to the first and second alternative of the nucleic acid molecules according to the present invention as outlined above. Preferably, the bases form a contiguous stretch of bases. However, it is also within the scope of the present invention that the stretch consists of two or more moieties, which are separated by a number of bases.

The present nucleic acids may preferably consist of at least 20, even more preferred at least 30, especially at least 50 contiguous bases from the sequences disclosed herein. The suitable length may easily be optimized due to the planned area of use (e.g. as (PCR) primers, probes, capture molecules (e.g. on a (DNA) chip), etc.). Preferred nucleic acid molecules contain at least a contiguous 15 base portion of one or more of the predicted immunogenic amino acid sequences listed in tables 1 and 2, especially the sequences of table 2 with scores of more than 10, preferably more than 20, especially with a score of more than 25. Specifically preferred are nucleic acids containing a contiguous portion of a DNA sequence of any sequence in the sequence protocol of the present application which shows 1 or more, preferably more than 2, especially more than 5, non-identical nucleic acid residues compared to the published *Streptococcus agalactiae* strain NEM316 (ATCC 12403) genome ([Glaser, P. et al., 2002]; GenBank accession AL732656) and/or any other published *S. agalactiae* genome sequence or parts thereof, especially of the serotype V 2603 V/R (A909) strain [Tettelin, H. et al., 2002]; GenBank accession AE009948). Specifically preferred non-identical nucleic acid residues are residues, which lead to a non-identical amino acid residue. Preferably, the nucleic acid sequences encode polypeptides having at least 1, preferably at least 2, preferably at least 3 different amino acid residues compared to the published *S. agalactiae* counterparts mentioned above. Also such isolated polypeptides, being fragments of the proteins (or the whole protein) mentioned herein e.g. in the sequence listing, having at least 6, 7, or 8 amino acid residues and being encoded by these nucleic acids are preferred.

The nucleic acid molecule according to the present invention can as a fourth alternative also be a nucleic acid molecule which anneals under stringent hybridisation conditions to any of the nucleic acids of the present invention according to the above outlined first, second, and third alternative. Stringent hybridisation conditions are typically those described herein.

Finally, the nucleic acid molecule according to the present invention can as a fifth alternative also be a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to any of the nucleic acid molecules according to any nucleic acid molecule of the present invention according to the first, second, third, and fourth alternative as outlined above. This kind of nucleic acid molecule refers to the fact that preferably the nucleic acids according to the present invention code for the hyperimmune serum reactive antigens or fragments thereof according to the present invention. This kind of nucleic acid molecule is particularly useful in the detection of a nucleic acid molecule according to the present invention and thus the diagnosis of the respective microorganisms such as *S. agalactiae* and any disease or diseased condition where this kind of microorganisms is involved. Preferably, the hybridisation would occur or be preformed under stringent conditions as described in connection with the fourth alternative described above.

Nucleic acid molecule as used herein generally refers to any ribonucleic acid molecule or deoxyribonucleic acid molecule, which may be unmodified RNA or DNA or modified RNA or DNA. Thus, for instance, nucleic acid molecule as used herein refers to, among other, single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded RNA, and RNA that is a mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-

stranded or, more typically, double-stranded, or triple-stranded, or a mixture of single- and double-stranded regions. In addition, nucleic acid molecule as used herein refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The strands in such regions may be from the same molecule or from different molecules. The regions may include all of one or more of the molecules, but more typically involve only a region of some of the molecules. One of the molecules of a triple-helical region often is an oligonucleotide. As used herein, the term nucleic acid molecule includes DNAs or RNAs as described above that contain one or more modified bases. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are "nucleic acid molecule" as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritylated bases, to name just two examples, are nucleic acid molecule as the term is used herein. It will be appreciated that a great variety of modifications have been made to DNA and RNA that serve many useful purposes known to those of skill in the art. The term nucleic acid molecule as it is employed herein embraces such chemically, enzymatically or metabolically modified forms of nucleic acid molecule, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including simple and complex cells, *inter alia*. The term nucleic acid molecule also embraces short nucleic acid molecules often referred to as oligonucleotide(s). "Polynucleotide" and "nucleic acid" or "nucleic acid molecule" are often used interchangeably herein.

Nucleic acid molecules provided in the present invention also encompass numerous unique fragments, both longer and shorter than the nucleic acid molecule sequences set forth in the sequencing listing of the *S. agalactiae* coding regions, which can be generated by standard cloning methods. To be unique, a fragment must be of sufficient size to distinguish it from other known nucleic acid sequences, most readily determined by comparing any selected *S. agalactiae* fragment to the nucleotide sequences in computer databases such as GenBank.

Additionally, modifications can be made to the nucleic acid molecules and polypeptides that are encompassed by the present invention. For example, nucleotide substitutions can be made which do not affect the polypeptide encoded by the nucleic acid, and thus any nucleic acid molecule which encodes a hyperimmune serum reactive antigen or fragments thereof is encompassed by the present invention.

Furthermore, any of the nucleic acid molecules encoding hyperimmune serum reactive antigens or fragments thereof provided by the present invention can be functionally linked, using standard techniques such as standard cloning techniques, to any desired regulatory sequences, whether a *S. agalactiae* regulatory sequence or a heterologous regulatory sequence, heterologous leader sequence, heterologous marker sequence or a heterologous coding sequence to create a fusion protein.

Nucleic acid molecules of the present invention may be in the form of RNA, such as mRNA or cRNA, or in the form of DNA, including, for instance, cDNA and genomic DNA obtained by cloning or produced by chemical synthetic techniques or by a combination thereof. The DNA may be triple-stranded, double-stranded or single-stranded. Single-stranded DNA may be the coding strand, also known as the sense strand, or it may be the non-coding strand, also referred to as the anti-sense strand.

The present invention further relates to variants of the herein above described nucleic acid molecules which encode fragments, analogs and derivatives of the hyperimmune serum reactive antigens and fragments thereof having a deduced *S. agalactiae* amino acid sequence set forth in the Sequence Listing. A variant of the nucleic acid molecule may be a naturally occurring variant such as a naturally occurring allelic variant, or it may be a variant that is not known to occur naturally. Such non-naturally occurring variants of the nucleic acid molecule may be made by mutagenesis techniques, including those applied to nucleic acid molecules, cells or organisms.

Among variants in this regard are variants that differ from the aforementioned nucleic acid molecules by nucleotide substitutions, deletions or additions. The substitutions, deletions or additions may involve one

or more nucleotides. The variants may be altered in coding or non-coding regions or both. Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. Preferred are nucleic acid molecules encoding a variant, analog, derivative or fragment, or a variant, analogue or derivative of a fragment, which have a *S. agalactiae* sequence as set forth in the Sequence Listing, in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid(s) is substituted, deleted or added, in any combination. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the *S. agalactiae* polypeptides set forth in the Sequence Listing. Also especially preferred in this regard are conservative substitutions.

The peptides and fragments according to the present invention also include modified epitopes wherein preferably one or two of the amino acids of a given epitope are modified or replaced according to the rules disclosed in e.g. {Tourdot, S. et al., 2000}, as well as the nucleic acid sequences encoding such modified epitopes.

It is clear that also epitopes derived from the present epitopes by amino acid exchanges improving, conserving or at least not significantly impeding the T cell activating capability of the epitopes are covered by the epitopes according to the present invention. Therefore the present epitopes also cover epitopes, which do not contain the original sequence as derived from *S. agalactiae*, but trigger the same or preferably an improved T cell response. These epitopes are referred to as "heteroclitic"; they need to have a similar or preferably greater affinity to MHC/HLA molecules, and the need the ability to stimulate the T cell receptors (TCR) directed to the original epitope in a similar or preferably stronger manner.

Heteroclitic epitopes can be obtained by rational design i.e. taking into account the contribution of individual residues to binding to MHC/HLA as for instance described by {Rammensee, H. et al., 1999}, combined with a systematic exchange of residues potentially interacting with the TCR and testing the resulting sequences with T cells directed against the original epitope. Such a design is possible for a skilled man in the art without much experimentation.

Another possibility includes the screening of peptide libraries with T cells directed against the original epitope. A preferred way is the positional scanning of synthetic peptide libraries. Such approaches have been described in detail for instance by {Hemmer, B. et al., 1999} and the references given therein.

As an alternative to epitopes represented by the present derived amino acid sequences or heteroclitic epitopes, also substances mimicking these epitopes e.g. "peptidomimetics" or "retro-inverso-peptides" can be applied.

Another aspect of the design of improved epitopes is their formulation or modification with substances increasing their capacity to stimulate T cells. These include T helper cell epitopes, lipids or liposomes or preferred modifications as described in WO 01/78767.

Another way to increase the T cell stimulating capacity of epitopes is their formulation with immune stimulating substances for instance cytokines or chemokines like interleukin-2, -7, -12, -18, class I and II interferons (IFN), especially IFN-gamma, GM-CSF, TNF-alpha, flt3-ligand and others.

As discussed additionally herein regarding nucleic acid molecule assays of the invention, for instance, nucleic acid molecules of the invention as discussed above, may be used as a hybridization probe for RNA, cDNA and genomic DNA to isolate full-length cDNAs and genomic clones encoding polypeptides of the present invention and to isolate cDNA and genomic clones of other genes that have a high sequence similarity to the nucleic acid molecules of the present invention. Such probes generally will comprise at least 15 bases. Preferably, such probes will have at least 20, at least 25 or at least 30 bases, and may have at least 50 bases. Particularly preferred probes will have at least 30 bases, and will have 50 bases or less, such as 30, 35, 40, 45, or 50 bases.

For example, the coding region of a nucleic acid molecule of the present invention may be isolated by screening a relevant library using the known DNA sequence to synthesize an oligonucleotide probe. A labeled oligonucleotide having a sequence complementary to that of a gene of the present invention is then used to screen a library of cDNA, genomic DNA or mRNA to determine to which members of the library the probe hybridizes.

The nucleic acid molecules and polypeptides of the present invention may be employed as reagents and materials for development of treatments of and diagnostics for disease, particularly human disease, as further discussed herein relating to nucleic acid molecule assays, *inter alia*.

The nucleic acid molecules of the present invention that are oligonucleotides can be used in the processes herein as described, but preferably for PCR, to determine whether or not the *S. agalactiae* genes identified herein in whole or in part are present and/or transcribed in infected tissue such as blood. It is recognized that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained. For this and other purposes the arrays comprising at least one of the nucleic acids according to the present invention as described herein, may be used.

The nucleic acid molecules according to the present invention may be used for the detection of nucleic acid molecules and organisms or samples containing these nucleic acids. Preferably such detection is for diagnosis, more preferable for the diagnosis of a disease related or linked to the present or abundance of *S. agalactiae*.

Eukaryotes (herein also "individual(s)"), particularly mammals, and especially humans, infected with *S. agalactiae* may be identifiable by detecting any of the nucleic acid molecules according to the present invention detected at the DNA level by a variety of techniques. Preferred nucleic acid molecules candidates for distinguishing a *S. agalactiae* from other organisms can be obtained.

The invention provides a process for diagnosing disease, arising from infection with *S. agalactiae*, comprising determining from a sample isolated or derived from an individual an increased level of expression of a nucleic acid molecule having the sequence of a nucleic acid molecule set forth in the Sequence Listing. Expression of nucleic acid molecules can be measured using any one of the methods well known in the art for the quantitation of nucleic acid molecules, such as, for example, PCR, RT-PCR, Rnase protection, Northern blotting, other hybridisation methods and the arrays described herein.

Isolated as used herein means separated "by the hand of man" from its natural state; i.e., that, if it occurs in nature, it has been changed or removed from its original environment, or both. For example, a naturally occurring nucleic acid molecule or a polypeptide naturally present in a living organism in its natural state is not "isolated," but the same nucleic acid molecule or polypeptide separated from the coexisting materials of its natural state is "isolated", as the term is employed herein. As part of or following isolation, such nucleic acid molecules can be joined to other nucleic acid molecules, such as DNAs, for mutagenesis, to form fusion proteins, and for propagation or expression in a host, for instance. The isolated nucleic acid molecules, alone or joined to other nucleic acid molecules such as vectors, can be introduced into host cells, in culture or in whole organisms. Introduced into host cells in culture or in whole organisms, such DNAs still would be isolated, as the term is used herein, because they would not be in their naturally occurring form or environment. Similarly, the nucleic acid molecules and polypeptides may occur in a composition, such as a media formulations, solutions for introduction of nucleic acid molecules or polypeptides, for example, into cells, compositions or solutions for chemical or enzymatic reactions, for instance, which are not naturally occurring compositions, and, therein remain isolated nucleic acid molecules or polypeptides within the meaning of that term as it is employed herein.

The nucleic acids according to the present invention may be chemically synthesized. Alternatively, the

nucleic acids can be isolated from *S. agalactiae* by methods known to the one skilled in the art.

According to another aspect of the present invention, a comprehensive set of novel hyperimmune serum reactive antigens and fragments thereof are provided by using the herein described antigen identification method. In a preferred embodiment of the invention, a hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by any one of the nucleic acids molecules herein described and fragments thereof are provided. In another preferred embodiment of the invention a novel set of hyperimmune serum-reactive antigens which comprises amino acid sequences selected from a group consisting of the polypeptide sequences as represented in **Seq ID No 231, 307, 374-433** and fragments thereof are provided. In a further preferred embodiment of the invention hyperimmune serum-reactive antigens which comprise amino acid sequences selected from a group consisting of the polypeptide sequences as represented in **Seq ID No 218, 220, 222-230, 232, 235-242, 244-248, 250-253, 256-285, 287-302, 309-317, 320-343, 345-362, 364, 366-373, 434, 449-462 and 475-486** and fragments thereof are provided. In a still preferred embodiment of the invention hyperimmune serum-reactive antigens which comprise amino acid sequences selected from a group consisting of the polypeptide sequences as represented in **Seq ID No 249, 303, 308, 318, 344** and fragments thereof are provided.

The hyperimmune serum reactive antigens and fragments thereof as provided in the invention include any polypeptide set forth in the Sequence Listing as well as polypeptides which have at least 70% identity to a polypeptide set forth in the Sequence Listing, preferably at least 80% or 85% identity to a polypeptide set forth in the Sequence Listing, and more preferably at least 90% similarity (more preferably at least 90% identity) to a polypeptide set forth in the Sequence Listing and still more preferably at least 95%, 96%, 97%, 98%, 99% or 99.5% similarity (still more preferably at least 95%, 96%, 97%, 98%, 99%, or 99.5% identity) to a polypeptide set forth in the Sequence Listing and also include portions of such polypeptides with such portion of the polypeptide generally containing at least 4 amino acids and more preferably at least 8, still more preferably at least 30, still more preferably at least 50 amino acids, such as 4, 8, 10, 20, 30, 35, 40, 45 or 50 amino acids.

The invention also relates to fragments, analogs, and derivatives of these hyperimmune serum reactive antigens and fragments thereof. The terms "fragment", "derivative" and "analog" when referring to an antigen whose amino acid sequence is set forth in the Sequence Listing, means a polypeptide which retains essentially the same or a similar biological function or activity as such hyperimmune serum reactive antigen and fragment thereof.

The fragment, derivative or analog of a hyperimmune serum reactive antigen and fragment thereof may be 1) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code, or 2) one in which one or more of the amino acid residues includes a substituent group, or 3) one in which the mature hyperimmune serum reactive antigen or fragment thereof is fused with another compound, such as a compound to increase the half-life of the hyperimmune serum reactive antigen and fragment thereof (for example, polyethylene glycol), or 4) one in which the additional amino acids are fused to the mature hyperimmune serum reactive antigen or fragment thereof, such as a leader or secretory sequence or a sequence which is employed for purification of the mature hyperimmune serum reactive antigen or fragment thereof or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

The present invention also relates to antigens of different *S. agalactiae* isolates. Such homologues may easily be isolated based on the nucleic acid and amino acid sequences disclosed herein. There are 9 serotypes distinguished to date and the typing is based on serotype specific antisera. The presence of any antigen can accordingly be determined for every serotype. In addition it is possible to determine the variability of a particular antigen in the various serotypes as described for the *S. pyogenes* sic gene [Hoe,

N. et al., 2001}. The contribution of the various serotypes to the different GBS infections varies in the different age groups and geographical regions. It is an important aspect that the most valuable protective antigens are expected to be conserved among various clinical strains.

Among the particularly preferred embodiments of the invention in this regard are the hyperimmune serum reactive antigens set forth in the Sequence Listing, variants, analogs, derivatives and fragments thereof, and variants, analogs and derivatives of fragments. Additionally, fusion polypeptides comprising such hyperimmune serum reactive antigens, variants, analogs, derivatives and fragments thereof, and variants, analogs and derivatives of the fragments are also encompassed by the present invention. Such fusion polypeptides and proteins, as well as nucleic acid molecules encoding them, can readily be made using standard techniques, including standard recombinant techniques for producing and expression of a recombinant polynucleic acid encoding a fusion protein.

Among preferred variants are those that vary from a reference by conservative amino acid substitutions. Such substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe and Tyr.

Further particularly preferred in this regard are variants, analogs, derivatives and fragments, and variants, analogs and derivatives of the fragments, having the amino acid sequence of any polypeptide set forth in the Sequence Listing, in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid residues are substituted, deleted or added, in any combination. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the polypeptide of the present invention. Also especially preferred in this regard are conservative substitutions. Most highly preferred are polypeptides having an amino acid sequence set forth in the Sequence Listing without substitutions.

The hyperimmune serum reactive antigens and fragments thereof of the present invention are preferably provided in an isolated form, and preferably are purified to homogeneity.

Also among preferred embodiments of the present invention are polypeptides comprising fragments of the polypeptides having the amino acid sequence set forth in the Sequence Listing, and fragments of variants and derivatives of the polypeptides set forth in the Sequence Listing.

In this regard a fragment is a polypeptide having an amino acid sequence that entirely is the same as part but not all of the amino acid sequence of the afore mentioned hyperimmune serum reactive antigen and fragment thereof, and variants or derivative, analogs, fragments thereof. Such fragments may be "free-standing", i.e., not part of or fused to other amino acids or polypeptides, or they may be comprised within a larger polypeptide of which they form a part or region. Also preferred in this aspect of the invention are fragments characterised by structural or functional attributes of the polypeptide of the present invention, i.e. fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta-amphipathic regions, flexible regions, surface-forming regions, substrate binding regions, and high antigenic index regions of the polypeptide of the present invention, and combinations of such fragments. Preferred regions are those that mediate activities of the hyperimmune serum reactive antigens and fragments thereof of the present invention. Most highly preferred in this regard are fragments that have a chemical, biological or other activity of the hyperimmune serum reactive antigen and fragments thereof of the present invention, including those with a similar activity or an improved activity, or with a decreased undesirable activity. Particularly preferred are fragments comprising receptors or domains of enzymes that confer a function essential for

viability of *S. agalactiae* or the ability to cause disease in humans. Further preferred polypeptide fragments are those that comprise or contain antigenic or immunogenic determinants in an animal, especially in a human.

An antigenic fragment is defined as a fragment of the identified antigen, which is for itself antigenic or may be made antigenic when provided as a hapten. Therefore, also antigens or antigenic fragments showing one or (for longer fragments) only a few amino acid exchanges are enabled with the present invention, provided that the antigenic capacities of such fragments with amino acid exchanges are not severely deteriorated on the exchange(s), i.e., suited for eliciting an appropriate immune response in an individual vaccinated with this antigen and identified by individual antibody preparations from individual sera.

Preferred examples of such fragments of hyperimmune serum-reactive antigens selected from the group consisting of peptides comprising amino acid sequences of column "predicted immunogenic aa" and "location of identified immunogenic region" of Table 1A, **especially peptides comprising amino acid 4-20, 35-44, 65-70, 73-87, 92-98, 112-137, 152-161, 177-186, 193-200, 206-213, 229-255, 282-294, 308-313, 320-326, 349-355, 373-384, 388-406, 420-425 and 115-199 of Seq ID No 218; 5-24, 35-41, 44-70, 73-89, 103-109, 127-143, 155-161, 185-190, 192-207, 212-219, 246-262, 304-336, 372-382, 384-393, 398-407, 412-418, 438-444, 1-75, 76-161 and 164-239 of Seq ID No 219; 4-10, 16-58, 60-71, 77-92, 100-126, 132-146, 149-164, 166-172, 190-209, 214-220, 223-229, 241-256, 297-312, 314-319, 337-343, 351-359, 378-387, 398-418, 421-428, 430-437, 440-448, 462-471, 510-519, 525-536, 552-559, 561-568, 573-582, 596-602, 608-630, 637-649, 651-665, 681-702, 714-732, 739-745, 757-778, 790-805, 807-815, 821-829, 836-842, 846-873, 880-903, 908-914, 916-923, 931-940, 943-948, 956-970, 975-986, 996-1015, 1031-1040, 1051-1069, 1072-1095, 1114-1119, 1130-1148, 1150-1157, 1169-1176, 1229-1238 and 802-812 of Seq ID No 220; 5-12, 14-26, 35-47, 52-67, 72-78, 83-98, 121-141, 152-159, 163-183, 186-207, 209-257, 264-277, 282-299, 301-309, 312-318, 324-339, 358-368, 372-378, 387-397, 425-431 and 46-291 of Seq ID No 221; 29-38, 44-64, 70-76, 78-87, 94-100, 102-112, 119-134, 140-149, 163-173, 178-186, 188-194, 207-234, 247-262, 269-290 and 73-92 of Seq ID No 222; 10-28, 36-63, 77-87, 103-119, 127-136, 141-169, 171-183, 195-200, 207-232, 236-246, 251-265, 268-283, 287-297, 314-322, 335-343, 354-363, 384-390, 405-411, 419-436, 443-455, 467-473, 480-513, 518-529, 550-557, 565-585, 602-608, 616-625, 632-660, 665-677, 685-701, 726-736, 738-747, 752-761, 785-796, 801-813, 838-853, 866-871 and 757-774 of Seq ID No 223; 31-38, 61-66, 74-81, 90-115, 123-145, 154-167, 169-179, 182-193, 200-206, 238-244, 267-272 and 235-251 of Seq ID No 224; 19-25, 38-54, 56-64, 66-72, 74-92, 94-100, 116-129, 143-149, 156-183, 204-232, 253-266, 269-275, 294-307 and 241-313 of Seq ID No 225; 5-34, 50-56, 60-65, 74-85, 89-97, 108-119, 159-165, 181-199, 209-225, 230-240, 245-251, 257-262, 274-282, 300-305 and 64-75 of Seq ID No 226; 5-13, 16-21, 27-42, 45-52, 58-66, 74-87, 108-114, 119-131 and 39-51 of Seq ID No 227; 6-23, 46-54, 59-65, 78-84, 100-120, 128-133, 140-146, 159-165, 171-183, 190-204, 224-232, 240-248, 250-259, 274-280, 288-296, 306-315 and 267-274 of Seq ID No 228; 5-12, 15-24, 26-36, 42-65, 68-80, 82-104, 111-116, 125-144, 159-167, 184-189, 209-218, 235-243, 254-265, 269-283, 287-300, 306-316, 318-336, 338-352, 374-392 and 162-174 of Seq ID No 229; 30-42, 45-54 and 25-37 of Seq ID No 230; 10-30, 53-59, 86-95, 116-130, 132-147, 169-189, 195-201, 212-221, 247-256, 258-265, 278-283, 291-298, 310-316, 329-339, 341-352, 360-367, 388-396, 398-411, 416-432, 443-452, 460-466, 506-512, 515-521, 542-548 and 419-431 of Seq ID No 231; 4-27, 30-53, 60-67, 70-90, 92-151, 159-185, 189-195, 198-210, 215-239 and 173-189 of Seq ID No 232; 4-26, 41-54, 71-78, 116-127, 140-149, 151-158, 161-175, 190-196, 201-208, 220-226, 240-252, 266-281, 298-305, 308-318, 321-329, 344-353, 372-378, 384-405, 418-426, 429-442, 457-463, 494-505, 514-522 and 174-188 of Seq ID No 233; 17-25, 27-39, 61-67, 81-89, 99-110, 120-131, 133-139, 147-161, 167-172, 179-185, 192-198, 203-213, 226-238, 243-258, 261-267, 284-290, 296-307, 311-328, 340-352, 356-371 and 239-256 of Seq ID No 234; 8-30, 40-49, 67-80, 114-123, 126-142, 152-162, 188-194 and 57-70 of Seq ID No 235; 4-23, 28-34, 36-47, 50-61, 76-81, 89-94, 96-104, 112-119, 126-146, 155-181, 195-200, 208-214, 220-229, 244-260, 263-276, 282-288, 292-300, 317-323, 336-351, 353-359, 363-375, 382-399, 415-432, 444-455, 458-471, 476-481, 484-492, 499-517, 522-529, 535-541, 543-568, 572-584, 586-600, 607-617, 626-637, 656-675 and 282-297 of Seq ID No 236; 6-24, 30-35, 38-45, 63-91, 134-140, 146-160, 167-188, 214-220, 226-234, 244-250, 260-270, 286-301, 316-329, 340-371, 429-446, 448-459, 474-481, 485-491, 512-526, 537-544, 550-565, 573-583, 596-613, 621-630, 652-658 and 87-97 of Seq ID No 237; 8-20, 26-48, 56-67, 76-86, 94-109, 115-121, 123-**

129, 143-160, 178-186, 191-198, 201-208, 221-236, 238-244, 260-268 and 237-247 of **Seq ID No 238**; 4-40, 42-57, 73-87, 98-117, 126-135, 150-156, 166-174, 196-217, 231-236, 248-258, 276-284, 293-301, 307-313, 339-347, 359-365, 375-387, 395-402, 428-440, 445-456, 485-490, 497-505, 535-541, 547-555, 610-625, 648-656, 665-671 and 448-528 of **Seq ID No 239**; 10-18, 39-45, 51-61, 80-96, 98-106, 110-115, 158-172, 174-183, 191-200, 220-237, 249-255, 274-289, 308-324, 331-341, 372-381, 384-397, 405-414 and 322-338 of **Seq ID No 240**; 30-36, 38-56, 85-108, 134-147, 149-160, 163-183, 188-201, 206-211, 219-238, 247-254 and 5-13 of **Seq ID No 241**; 11-40, 98-103, 110-115, 133-145, 151-159, 172-179, 192-201, 204-212, 222-228, 235-245, 258-268, 283-296, 298-309, 322-329, 342-351, 354-362, 372-378, 385-393, 407-418, 495-516 and 1-148 of **Seq ID No 242**; 5-19, 21-36, 73-94, 112-119, 122-137, 139-145, 152-167, 184-190, 198-204, 208-224, 249-265, 267-281, 299-304, 309-317, 326-333, 356-364, 368-374, 381-389, 391-414, 419-425, 430-435 and 113-140 of **Seq ID No 243**; 45-54, 59-67, 78-91 and 15-23 of **Seq ID No 244**; 11-22, 33-47, 52-80, 88-112, 124-129 and 6-25 of **Seq ID No 245**; 26-41, 51-63, 80-89, 93-115, 150-163, 187-193, 220-237, 240-249, 286-294, 296-306, 316-329, 345-353, 361-370, 407-425, 428-437, 474-482, 484-494, 504-517, 533-541, 549-558, 595-613, 616-625, 660-668, 673-685, 711-726, 736-744, 749-761, 787-802, 812-820, 825-837, 863-878, 888-896, 901-913, 939-954, 964-972, 977-989, 1003-1008, 1016-1022, 1028-1034, 1041-1053, 1059-1074, 1101-1122, 420-511 and 581-704 of **Seq ID No 246**; 18-25, 27-55, 71-83, 89-95, 102-113, 120-146, 150-156, 174-185 and 159-175 of **Seq ID No 247**; 24-30, 38-56, 63-68, 87-93, 136-142, 153-164, 183-199, 213-219, 226-234, 244-261, 269-278, 283-289, 291-297, 320-328, 330-336, 340-346, 348-356, 358-366, 382-387, 401-408, 414-419, 449-455, 468-491, 504-512, 531-537, 554-560, 597-608, 621-627, 632-643, 650-662, 667-692, 703-716, 724-737, 743-758, 783-794, 800-818, 846-856 and 806-884 of **Seq ID No 248**; 4-14, 21-39, 86-92, 99-107, 121-131, 136-144, 147-154, 158-166, 176-185, 193-199, 207-222, 224-230 and 117-136 of **Seq ID No 249**; 65-76, 85-97, 103-109, 115-121, 125-146, 163-169, 196-205, 212-219, 228-237, 241-247, 254-262, 269-288, 294-303, 305-313, 328-367, 395-401, 405-412, 418-429, 437-447, 481-488, 506-513, 519-524, 530-541, 546-557 and 266-284 of **Seq ID No 250**; 5-14, 37-42, 49-71, 78-92, 97-112, 127-136, 147-154, 156-163, 186-198, 216-225, 233-243, 248-253, 295-307, 323-332, 359-366, 368-374, 380-398 and 194-223 of **Seq ID No 251**; 4-11, 33-39, 45-72, 100-113, 119-129, 136-144, 169-175, 177-185, 200-208, 210-219, 262-276, 278-297, 320-326, 336-344, 347-362, 381-394, 443-453 and 438-454 of **Seq ID No 252**; 4-29, 31-52, 55-61, 95-110, 138-158, 162-171, 179-187, 202-229, 239-248, 251-256, 262-267, 269-285, 304-310, 351-360, 362-368, 381-388, 415-428, 435-440, 448-458 and 161-178 of **Seq ID No 253**; 4-17, 19-28, 32-43, 47-59, 89-110, 112-126, 128-134, 140-148, 152-161, 169-184, 191-204, 230-235, 255-264, 328-338, 341-347, 401-409, 413-419, 433-441, 449-458, 463-468, 476-482, 486-492, 500-506, 529-545 and 305-381 of **Seq ID No 254**; 10-29, 38-45, 53-61, 134-145, 152-160, 163-170, 202-208, 219-229, 248-258, 266-275, 282-288, 315-320, 328-334, 377-385, 392-402, 418-424, 447-453, 460-471, 479-487, 491-497, 500-507, 531-537, 581-594, 615-623, 629-635, 644-652, 659-666, 668-678, 710-717, 719-728, 736-741, 747-760, 766-773, 784-789, 794-800, 805-817, 855-861, 866-887 and 698-715 of **Seq ID No 255**; 16-26, 29-37, 44-58, 62-68, 74-80, 88-95, 97-120, 125-144, 165-196 and 58-72 of **Seq ID No 256**; 14-21, 23-46, 49-60, 63-74, 78-92, 96-103, 117-129, 134-161, 169-211, 217-231, 239-248, 252-281, 292-299, 313-343 and 243-257 of **Seq ID No 257**; 11-27, 46-52, 67-72, 76-84, 91-112, 116-153, 160-175, 187-196, 202-211, 213-220 and 43-76 of **Seq ID No 258**; 5-29, 37-56, 78-86, 108-118, 152-161 and 120-130 of **Seq ID No 259**; 8-14, 19-41, 52-66, 75-82, 87-92, 106-121, 127-133, 136-143, 158-175, 180-187, 196-204, 221-228, 239-245, 259-265, 291-306, 318-323, 328-340, 352-358, 361-368, 375-381, 391-399, 411-418, 431-442, 446-455, 484-496, 498-510, 527-533, 541-549, 558-565, 575-585, 587-594, 644-655, 661-668, 671-677 and 184-196 of **Seq ID No 260**; 4-22, 29-38, 55-62, 75-81, 102-107, 110-134, 143-150, 161-167, 172-179, 191-215, 223-233, 241-247, 251-264, 266-272, 288-309, 340-352, 354-366, 394-402, 414-438 and 198-218 of **Seq ID No 261**; 24-44, 49-70, 80-91, 105-118, 128-136, 140-154 and 77-92 of **Seq ID No 262**; 5-22, 31-36, 41-47, 67-74, 83-90, 105-122, 135-143, 160-167 and 118-129 of **Seq ID No 263**; 4-25, 33-73, 81-93, 96-106, 114-120, 122-128, 130-172, 179-208, 210-241, 251-283, 296-301 and 92-100 of **Seq ID No 264**; 14-24, 29-38, 43-50, 52-72, 86-97, 101-107, 110-125, 127-141, 145-157, 168-175, 177-184, 186-195, 205-226, 238-250, 255-261, 284-290, 293-304, 307-314, 316-323, 325-356, 363-371, 383-390, 405-415, 423-432, 442-454, 466-485, 502-511, 519-527, 535-556, 558-565, 569-574, 612-634, 641-655, 672-686, 698-709, 715-722, 724-732, 743-753, 760-769, 783-792, 818-825, 830-839, 842-849, 884-896, 905-918, 926-940, 957-969, 979-1007, 1015-1021, 1049-1057 and 336-349 of **Seq ID No 265**; 6-16, 26-31, 33-39, 62-73, 75-85, 87-100, 113-123, 127-152, 157-164, 168-181, 191-198, 208-214, 219-226, 233-254, 259-266, 286-329 and 181-195 of **Seq ID No 266**; 4-13, 32-39, 53-76, 99-108, 110-116, 124-135, 137-146, 149-157, 162-174, 182-190, 207-231, 242-253, 255-264, 274-283, 291-323, 334-345, 351-360, 375-388, 418-425, 456-474, 486-492, 508-517,

520-536, 547-560, 562-577, 31-45 and 419-443 of **Seq ID No 267**; 15-26, 30-37, 42-49, 58-90, 93-99, 128-134, 147-154, 174-179, 190-197, 199-205, 221-230, 262-274, 277-287, 300-314, 327-333, 343-351, 359-377, 388-396, 408-413, 416-425, 431-446 and 246-256 of **Seq ID No 268**; 5-26, 34-42, 47-54, 61-67, 71-104, 107-115, 131-138, 144-153, 157-189, 196-202, 204-210, 228-245, 288-309, 316-329, 332-341, 379-386, 393-399, 404-412, 414-421, 457-468, 483-489, 500-506, 508-517, 523-534, 543-557, 565-580, 587-605, 609-617, 619-627, 631-636, 640-646, 662-668, 675-682, 705-710, 716-723, 727-732, 750-758, 784-789, 795-809, 869-874, 14-138, 166-286, 372-503, 674-696 and 754-859 of **Seq ID No 269**; 5-17, 32-38, 40-47, 80-89, 113-119, 125-137, 140-154, 157-163, 170-177, 185-199, 213-225, 228-236, 242-248, 277-290, 292-305, 323-333, 347-353, 364-370, 385-394, 399-406, 423-433, 441-451, 462-474, 477-487 and 116-124 of **Seq ID No 270**; 7-16, 18-30, 32-49, 53-61, 63-85, 95-101, 105-115, 119-134, 143-150, 159-178, 185-202, 212-229, 236-250, 254-265, 268-294 and 63-72 of **Seq ID No 271**; 4-12, 19-47, 73-81, 97-103, 153-169, 188-198, 207-213, 217-223, 236-242, 255-265, 270-278, 298-305, 309-317, 335-347, 354-363, 373-394, 419-424, 442-465, 486-492, 500-507, 542-549, 551-558, 560-572, 580-589, 607-614, 617-623, 647-653, 666-676, 694-704, 706-714, 748-754, 765-772, 786-792, 795-806 and 358-370 of **Seq ID No 272**; 18-28, 30-38, 40-46, 49-55, 69-78, 82-98, 104-134, 147-153, 180-190, 196-202, 218-236, 244-261, 266-273, 275-286, 290-295, 301-314, 378-387, 390-395, 427-434 and 290-305 of **Seq ID No 273**; 4-13, 20-31, 39-51, 54-61, 69-84, 87-105, 117-124 and 108-125 of **Seq ID No 274**; 24-34, 43-54, 56-66, 68-79 and 50-69 of **Seq ID No 275**; 5-43, 71-77, 102-131, 141-148, 150-156, 159-186, 191-207, 209-234, 255-268, 280-286, 293-299, 317-323, 350-357, 363-372, 391-397, 406-418, 428-435, 455-465, 484-497, 499-505, 525-531, 575-582, 593-607, 621-633, 638-649, 655-673, 684-698, 711-725, 736-741, 743-752, 759-769, 781-793, 813-831, 843-853, 894-905, 908-916, 929-946, 953-963, 970-978, 1001-1007, 1011-1033, 165-178 and 818-974 of **Seq ID No 276**; 16-44, 63-86, 98-108, 185-191, 222-237, 261-274, 282-294, 335-345, 349-362, 374-384, 409-420, 424-430, 440-447, 453-460, 465-473, 475-504, 522-534, 538-551, 554-560, 567-582, 598-607, 611-619, 627-640, 643-653, 655-661, 669-680, 684-690, 701-707, 715-731, 744-750, 756-763, 768-804, 829-837, 845-853, 855-879, 884-890, 910-928, 77-90, 144-212, 279-355, 434-536, 782-810 and 875-902 of **Seq ID No 277**; 4-22, 29-41, 45-51, 53-66, 70-77, 86-95, 98-104, 106-124, 129-135, 142-151, 153-161, 169-176, 228-251, 284-299, 331-337, 339-370, 380-387, 393-398, 406-411, 423-433, 440-452, 461-469, 488-498, 501-516, 523-530, 532-559, 562-567, 570-602, 612-628, 630-645, 649-659, 666-672, 677-696, 714-723, 727-747 and 212-227 of **Seq ID No 278**; 4-9, 17-31, 35-41, 56-61, 66-75, 81-87, 90-124, 133-138, 149-163, 173-192, 213-219, 221-262, 265-275, 277-282, 292-298, 301-307, 333-346, 353-363, 371-378, 419-430, 435-448, 456-469, 551-570, 583-599, 603-612 and 275-291 of **Seq ID No 279**; 28-34, 53-58, 72-81, 100-128, 145-154, 159-168, 172-189, 217-225, 227-249, 256-263, 299-309, 322-330, 361-379, 381-388, 392-401, 404-417, 425-436, 440-446, 451-464, 469-487, 502-511, 543-551, 559-564, 595-601, 606-612, 615-626, 633-642, 644-650, 664-670, 674-684, 692-701, 715-723, 726-734, 749-756, 763-771, 781-787, 810-843, 860-869, 882-889, 907-917, 931-936, 941-948, 951-958, 964-971, 976-993, 1039-1049, 1051-1065, 1092-1121, 1126-1132, 1145-1151, 1158-1173, 1181-1192, 1194-1208, 1218-1223, 1229-1243, 1249-1254, 1265-1279, 1287-1297, 1303-1320, 1334-1341, 1343-1358, 1372-1382, 1406-1417, 1419-1425, 1428-1434, 1441-1448, 1460-1473, 1494-1504, 1509-1514, 1529-1550, 654-669 and 1400-1483 of **Seq ID No 280**; 10-16, 20-25, 58-65, 97-109, 118-132, 134-146, 148-155, 186-195, 226-233, 244-262, 275-284, 295-310, 317-322, 330-339, 345-351, 366-375, 392-403, 408-415, 423-430, 435-444, 446-457, 467-479, 486-499, 503-510, 525-537, 540-585, 602-612, 614-623, 625-634, 639-645, 650-669, 700-707, 717-724, 727-739, 205-230 and 733-754 of **Seq ID No 281**; 5-22, 37-43, 72-81, 105-113, 128-133, 148-160, 188-194, 204-230, 238-245, 251-257 and 194-213 of **Seq ID No 282**; 16-21, 35-41, 56-72, 74-92, 103-109 and 62-68 of **Seq ID No 283**; 4-15, 17-82, 90-104, 107-159, 163-170, 188-221, 234-245, 252-265 and 220-235 of **Seq ID No 284**; 16-22, 36-46, 61-75, 92-107, 113-121, 139-145, 148-160 and 30-42 of **Seq ID No 285**; 4-12, 20-26, 43-49, 55-62, 66-78, 121-127, 135-141, 146-161, 164-170, 178-189, 196-205, 233-238, 269-279, 288-318, 325-332, 381-386, 400-407 and 328-346 of **Seq ID No 286**; 5-12, 31-49, 57-63, 69-79, 89-97, 99-114, 116-127, 134-142, 147-154, 160-173, 185-193, 199-204, 211-222, 229-236, 243-249, 256-274 and 58-68 of **Seq ID No 287**; 10-20, 28-34, 39-53, 68-79, 84-90, 99-106 and 73-79 of **Seq ID No 288**; 14-37, 45-50, 61-66, 77-82, 93-98, 109-114, 125-130, 141-146, 157-162, 173-178, 189-194, 205-210, 221-226, 237-242, 253-258, 269-274, 285-290, 301-306, 316-332, 349-359, 371-378, 385-406, 34-307 and 312-385 of **Seq ID No 289**; 4-10, 17-38, 50-85, 93-99, 109-116, 128-185, 189-197, 199-210, 223-256, 263-287, 289-312, 327-337, 371-386, 389-394, 406-419, 424-432, 438-450, 458-463, 475-502, 507-513, 519-526, 535-542, 550-567 and 361-376 of **Seq ID No 290**; 10-39, 42-93, 100-144, 155-176, 178-224, 230-244, 246-255, 273-282, 292-301, 308-325, 332-351, 356-361, 368-379, 386-393, 400-421 and 138-155 of **Seq ID No 291**; 5-11, 17-34, 40-45, 50-55, 72-80, 101-123, 145-151, 164-172,

182-187, 189-195, 208-218, 220-241, 243-252, 255-270, 325-331, 365-371, 391-398, 402-418, 422-428, 430-435, 443-452, 463-469, 476-484, 486-494, 503-509, 529-553, 560-565, 570-590, 608-614, 619-627, 654-661, 744-750, 772-780, 784-790, 806-816, 836-853, 876-885, 912-918, 926-933, 961-975, 980-987, 996-1006, 1016-1028, 1043-1053, 1057-1062, 994-1003 and 1033-1056 of **Seq ID No 292**; 17-45, 64-71, 73-81, 99-109, 186-192, 223-238, 262-275, 283-295, 336-346, 350-363, 375-385, 410-421, 425-431, 441-448, 454-463, 468-474, 476-512, 523-537, 539-552, 568-583, 599-608, 612-620, 628-641, 644-654, 656-662, 670-681, 685-695, 702-708, 716-723, 725-735, 757-764, 769-798, 800-806, 808-816, 826-840, 846-854, 856-862, 874-881, 885-902, 907-928, 274-350 and 443-513 of **Seq ID No 293**; 4-22, 29-41, 45-51, 53-61, 70-76, 85-92, 99-104, 111-122, 134-140, 142-154, 163-174, 224-232, 255-265, 273-279, 283-297, 330-335, 337-348, 356-367, 373-385, 391-396, 421-431, 442-455, 475-485, 493-505, 526-538, 544-561, 587-599, 605-620, 622-651, 662-670, 675-681, 687-692, 697-712, 714-735 and 252-262 of **Seq ID No 294**; 4-12, 15-35, 40-46, 50-59, 67-94, 110-128, 143-169, 182-188, 207-215, 218-228, 238-250 and 74-90 of **Seq ID No 295**; 9-18, 42-58, 78-85, 88-95, 97-106, 115-122, 128-134, 140-145, 154-181, 186-202, 204-223, 261-267, 269-278, 284-293, 300-336, 358-368 and 12-29 of **Seq ID No 296**; 7-34, 46-53, 62-72, 82-88, 100-105, 111-117, 132-137, 144-160, 166-180, 183-189, 209-221, 231-236, 246-253, 268-282, 286-293, 323-336, 364-372, 378-392, 422-433 and 388-405 of **Seq ID No 297**; 21-27, 34-50, 72-77, 80-95, 164-177, 192-198, 202-220, 226-236, 239-247, 270-279, 285-292, 315-320, 327-334, 348-355, 364-371, 388-397, 453-476, 488-497, 534-545, 556-576, 582-588, 601-607, 609-616, 642-662, 674-681, 687-697, 709-715, 721-727, 741-755 and 621-739 of **Seq ID No 298**; 4-14, 16-77, 79-109 and 25-99 of **Seq ID No 299**; 4-9, 17-23, 30-37, 44-55, 65-72, 77-93, 102-121, 123-132, 146-153 and 17-29 of **Seq ID No 300**; 4-18, 25-41, 52-60, 83-92, 104-112, 117-123, 149-155, 159-167, 170-192, 201-210, 220-227, 245-250 and 124-137 of **Seq ID No 301**; 8-25, 50-55, 89-95, 138-143, 148-153, 159-169, 173-179, 223-238, 262-268, 288-295, 297-308, 325-335, 403-409, 411-417, 432-446, 463-475, 492-501, 524-530, 542-548, 561-574, 576-593, 604-609, 612-622, 637-654, 665-672, 678-685, 720-725, 731-739, 762-767, 777-783, 820-838, 851-865, 901-908, 913-920, 958-970, 1000-1006, 1009-1015, 1020-1026, 1043-1052, 1055-1061, 1-128, 252-341, 771-793 and 1043-1058 of **Seq ID No 302**; 16-26, 33-46 and 64-76 of **Seq ID No 303**; 4-27, 69-77, 79-101, 117-123, 126-142, 155-161, 171-186, 200-206, 213-231, 233-244, 267-273, 313-329, 335-344, 347-370, 374-379, 399-408, 422-443, 445-453, 461-468, 476-482, 518-534, 544-553, 556-567, 578-595, 601-620, 626-636, 646-658, 666-681, 715-721, 762-768, 778-785, 789-803, 809-819, 22-108, 153-318, 391-527 and 638-757 of **Seq ID No 304**; 6-21, 32-43, 62-92, 104-123, 135-141, 145-152, 199-216, 218-226, 237-247, 260-269, 274-283, 297-303, 1-72 and 127-211 of **Seq ID No 305**; 6-26, 50-56, 83-89, 108-114, 123-131, 172-181, 194-200, 221-238, 241-247, 251-259, 263-271, 284-292, 304-319, 321-335, 353-358, 384-391, 408-417, 424-430, 442-448, 459-466, 487-500, 514-528, 541-556, 572-578, 595-601, 605-613, 620-631, 635-648, 660-670, 673-679, 686-693, 702-708, 716-725, 730-735, 749-755, 770-777, 805-811, 831-837, 843-851, 854-860, 863-869, 895-901, 904-914, 922-929, 933-938, 947-952, 956-963, 1000-1005, 1008-1014, 1021-1030, 1097-1103, 1120-1130, 1132-1140, 1-213, 269-592 and 992-1120 of **Seq ID No 306**; 9-16, 33-39, 47-59, 65-79, 81-95, 103-108, 115-123, 138-148, 163-171, 176-185, 191-196, 205-211, 213-221, 224-256, 261-276, 294-302, 357-363, 384-390, 95-111 and 161-189 of **Seq ID No 307**; 21-27, 35-45, 70-76, 92-105, 129-143, 145-155, 161-166, 170-191, 204-211, 214-231, 234-246, 249-255, 259-275 and 1-18 of **Seq ID No 308**; 21-35, 45-53, 56-64, 69-97 and 1-16 of **Seq ID No 309**; 25-33, 41-47, 61-68, 86-101, 106-114, 116-129, 134-142, 144-156, 163-176, 181-190, 228-251, 255-261, 276-292, 295-305, 334-357, 368-380, 395-410, 424-429, 454-460, 469-482, 510-516, 518-527, 531-546, 558-570, 579-606, 628-636, 638-645, 651-656, 668-674, 691-698, 717-734, 742-754, 765-770, 792-797, 827-835, 847-859, 874-881, 903-909, 926-933, 942-961, 964-977, 989-1004, 1010-1028, 1031-1047, 1057-1075, 1081-1095, 1108-1117, 1138-1144, 1182-1189, 1193-1206, 1220-1229, 1239-1246, 1257-1267, 1271-1279, 1284-1301, 1312-1320, 1329-1335, 1341-1347, 1358-1371, 1399-1404, 1417-1426, 1458-1463, 1468-1476, 1478-1485, 1493-1506, 1535-1541, 1559-1574, 1583-1590, 1595-1601, 1603-1611, 1622-1628, 1634-1644, 1671-1685, 1689-1696, 1715-1720, 1734-1746, 1766-1775, 1801-1806, 1838-1844, 1858-1871, 1910-1917, 1948-1955, 1960-1974, 2000-2015, 2019-2036, 2041-2063, 748-847 and 1381-1391 of **Seq ID No 310**; 5-12, 18-24, 27-53, 56-63, 96-113, 119-124, 131-136, 157-163, 203-209, 215-223, 233-246, 264-273, 311-316, 380-389, 393-399, 425-433, 445-450, 457-462, 464-470, 475-482, 507-513, 527-535, 542-548, 550-565, 591-602, 607-613, 627-642, 644-664, 673-712, 714-732, 739-764, 769-782, 812-818, 826-838, 848-854, 860-871, 892-906, 930-938, 940-954, 957-973, 990-998, 1002-1021, 1024-1033, 1037-1042, 1050-1060, 1077-1083, 1085-1092, 1100-1129, 1144-1161, 1169-1175, 1178-1189, 1192-1198, 1201-1207, 1211-1221, 1229-1239, 1250-1270, 1278-1292, 1294-1300, 1314-1335, 1344-1352, 1360-1374, 1394-1405, 1407-1414, 1416-1424, 1432-1452, 1456-1462, 1474-1497, 1500-1510, 1516-1522, 1534-1542, 1550-1559, 1584-1603, 1608-1627, 187-

273 and 306-441 of **Seq ID No 311**; 70-80, 90-97, 118-125, 128-140, 142-148, 154-162, 189-202, 214-222, 224-232, 254-260, 275-313, 317-332, 355-360, 392-398, 425-432, 448-456, 464-470, 476-482, 491-505, 521-528, 533-546, 560-567, 592-597, 605-614, 618-626, 637-644, 646-653, 660-666, 677-691 and 207-227 of **Seq ID No 312**; 5-19, 26-34, 37-55, 57-66, 69-83, 86-102, 115-134, 138-143, 154-172, 178-195, 209-246, 251-257, 290-302, 306-311 and 256-266 of **Seq ID No 313**; 10-20, 22-28, 35-57, 72-79, 87-103, 108-128, 130-144, 158-171, 190-198, 225-242, 274-291, 301-315, 317-324, 374-385 and 353-365 of **Seq ID No 314**; 4-9, 17-30, 34-54, 59-66, 73-94, 118-130, 135-150, 158-171, 189-198, 219-239, 269-275, 283-301, 89-106 and 176-193 of **Seq ID No 315**; 14-20, 22-74, 77-86, 89-99, 104-109, 126-135, 154-165, 181-195, 197-212, 216-224, 264-275 and 107-118 of **Seq ID No 316**; 4-18, 21-38, 63-72, 101-109, 156-162, 165-179, 183-192, 195-210, 212-218, 230-239, 241-256, 278-290, 299-311, 313-322, 332-341, 348-366, 386-401, 420-426, 435-450, 455-460, 468-479, 491-498, 510-518, 532-538, 545-552, 557-563, 567-573, 586-595, 599-609, 620-626, 628-636, 652-657, 665-681 and 1-198 of **Seq ID No 317**; 4-10, 16-38, 51-68, 73-79, 94-115, 120-125, 132-178, 201-208, 216-223, 238-266, 269-295, 297-304, 337-342, 347-356, 374-401, 403-422, 440-447, 478-504, 510-516, 519-530, 537-544 and 191-206 of **Seq ID No 318**; 12-40, 42-48, 66-71, 77-86, 95-102, 113-120, 129-137, 141-148, 155-174, 208-214, 218-225, 234-240, 256-267, 275-283, 300-306, 313-321, 343-350, 359-367, 370-383, 398-405, 432-439, 443-461, 492-508, 516-526, 528-535 and 370-478 of **Seq ID No 319**; 6-14, 20-37, 56-62, 90-95, 97-113, 118-125, 140-145, 161-170, 183-202, 237-244, 275-284, 286-305, 309-316, 333-359, 373-401, 405-412 and 176-187 of **Seq ID No 320**; 33-44, 50-55, 59-80, 86-101, 129-139, 147-153, 157-163, 171-176, 189-201, 203-224, 239-245, 257-262, 281-287, 290-297, 304-320, 322-331, 334-350, 372-390, 396-401, 71-88 and 353-372 of **Seq ID No 321**; 5-11, 15-24, 26-33, 40-47, 75-88, 95-103, 105-112 and 17-30 of **Seq ID No 322**; 5-11, 16-39, 46-54, 62-82, 100-107, 111-124, 126-150, 154-165, 167-183, 204-238, 245-295, 301-313, 316-335 and 8-16 of **Seq ID No 323**; 4-19, 34-48, 69-74, 79-107, 115-127, 129-135, 143-153, 160-169, 171-182 and 142-153 of **Seq ID No 324**; 4-30, 65-74, 82-106, 110-120, 124-132, 135-140, 146-175, 179-184, 190-196, 217-223, 228-233, 250-267, 275-292, 303-315, 322-332 and 174-186 of **Seq ID No 325**; 9-16, 29-41, 47-57, 68-84, 87-109, 113-119, 162-180, 186-193, 195-201, 203-208, 218-230, 234-243, 265-271, 281-292, 305-312, 323-332, 341-347, 349-363, 368-374, 383-390, 396-410, 434-440, 446-452, 455-464, 466-473, 515-522, 529-542, 565-570, 589-600, 602-613, 618-623, 637-644, 1019-1027, 1238-1244, 1258-1264, 1268-1276, 1281-1292, 1296-1302 and 883-936 of **Seq ID No 326**; 10-17, 23-32, 39-44, 54-72, 75-81, 88-111, 138-154, 160-167, 178-185, 201-210, 236-252, 327-334, 336-342, 366-376, 388-400, 410-430, 472-482, 493-526, 552-558, 586-592, 598-603, 612-621, 630-635, 641-660 and 384-393 of **Seq ID No 327**; 4-22, 24-39, 50-59, 73-84, 100-105, 111-117, 130-138, 155-161, 173-178, 182-189, 205-215, 266-284, 308-313, 321-328, 330-337, 346-363, 368-374, 388-395, 397-405, 426-434, 453-459, 482-492, 501-507, 509-515, 518-523, 527-544, 559-590, 598-612, 614-629, 646-659, 663-684, 686-694, 698-721 and 445-461 of **Seq ID No 328**; 14-22, 27-33 and 3-17 of **Seq ID No 329**; 29-41, 66-73, 81-87, 90-108, 140-146, 150-159, 165-184, 186-196, 216-226, 230-238, 247-253, 261-269 and 126-140 of **Seq ID No 330**; 5-12, 16-25, 27-33, 36-45, 60-68, 83-88, 103-126 and 86-101 of **Seq ID No 331**; 14-23, 36-47, 56-66, 84-89, 94-105, 111-127, 140-153, 160-174, 176-183, 189-203, 219-225, 231-237, 250-257 and 194-227 of **Seq ID No 332**; 4-25, 54-60, 64-71, 73-82, 89-106, 117-124, 157-169, 183-188, 199-210, 221-232, 236-244, 255-264 and 58-98 of **Seq ID No 333**; 13-19, 26-36, 41-53, 55-71, 77-84, 86-108, 114-135, 157-172, 177-183, 187-194, 208-213, 218-226, 110-125 and 156-170 of **Seq ID No 334**; 5-24, 63-69, 77-85, 94-112, 120-137, 140-146, 152-159, 166-172, 179-187, 193-199, 206-212, 222-228, 234-240, 244-252, 257-264, 270-289, 298-309, 316-328, 337-348, 363-375, 1-56 and 340-352 of **Seq ID No 335**; 18-39, 42-71, 78-120, 124-144, 152-173, 179-189, 199-209, 213-222, 228-258, 269-304, 329-361, 364-372, 374-389, 396-441 and 313-327 of **Seq ID No 336**; 19-25, 91-98, 108-120, 156-162, 168-174, 191-204, 211-216, 232-266, 272-278, 286-308, 316-321, 327-333, 344-355, 358-364, 384-391, 395-428, 464-476, 487-495, 497-511, 544-561, 563-573, 575-582, 588-594, 10-25 and 322-338 of **Seq ID No 337**; 14-26, 32-49, 51-57, 59-72, 80-91, 102-112, 119-125, 147-161, 164-173, 175-183, 188-213, 217-222, 246-254, 260-276, 282-303, 308-318, 321-328, 333-350, 352-359, 371-378, 392-401, 407-414, 416-443, 448-463, 471-484, 490-497, 501-514, 519-527, 539-551, 557-570, 578-590, 592-598, 600-610, 618-629, 633-647, 654-667, 676-689, 702-709, 718-726, 728-737, 741-760, 764-780, 786-795, 808-826, 836-842, 845-852, 865-874, 881-887, 931-945, 949-957, 968-974, 979-986, 1003-1009, 1023-1029 and 90-103 of **Seq ID No 338**; 11-16, 37-56, 60-66, 69-77, 80-88, 93-106, 117-139, 166-171 and 72-90 of **Seq ID No 339**; 59-84, 123-133, 145-150, 161-167, 178-189 and 115-128 of **Seq ID No 340**; 15-33, 39-46, 52-64, 74-87, 108-124, 127-144, 150-156, 173-179, 184-194, 201-208, 219-236, 243-269, 272-295, 302-309, 343-349, 356-361, 370-379, 405-411, 414-423, 430-451, 457-464, 466-475, 477-483, 496-502, 507-522, 541-548, 557-563, 571-577, 579-585, 590-605, 626-642, 650-662,

671-691, 704-710, 751-769, 775-781, 786-791, 794-829, 851-858, 868-878, 884-904, 913-919, 931-939 and 132-142 of **Seq ID No 341**; 33-58, 64-71, 74-80, 83-88, 96-120, 122-139, 146-157, 167-177, 207-213, 220-225, 236-242, 264-279, 300-305, 326-336, 340-347, 350-360, 97-115 and 199-211 of **Seq ID No 342**; 4-26, 43-57, 70-99, 102-117, 121-133, 142-148, 151-168, 170-183, 192-220, 235-249, 258-279 and 30-41 of **Seq ID No 343**; 34-42, 48-58, 70-94, 110-130, 154-160, 164-172, 178-183, 195-203, 211-222, 229-250, 256-261, 274-284, 286-292, 312-323 and 222-233 of **Seq ID No 344**; 4-9, 15-36, 38-45, 49-74, 78-88, 100-112, 136-191, 211-220, 226-233, 239-246, 254-274, 287-307, 316-322, 342-353, 356-366, 373-378, 384-393, 405-431, 449-457, 459-468, 487-511, 515-524, 529-541, 544-552, 562-568, 571-576 and 208-280 of **Seq ID No 345**; 10-27, 31-37, 39-54, 71-108, 124-143 and 2-107 of **Seq ID No 346**; 16-27, 38-57, 64-70, 90-102, 104-113, 116-137, 160-166 and 1-80 of **Seq ID No 347**; 13-21, 31-36, 56-67, 127-136, 153-171, 173-180, 184-200, 214-222, 225-231, 239-263, 267-273 and 135-159 of **Seq ID No 348**; 12-27, 31-51, 68-74, 77-87, 94-101, 108-114, 117-123, 127-134, 138-168, 173-196, 201-207, 212-217, 227-237, 247-257, 264-280 and 205-223 of **Seq ID No 349**; 17-22, 25-54, 70-76, 92-100 and 98-110 of **Seq ID No 350**; 7-29, 40-50, 60-67, 87-96, 105-111, 119-164, 172-199, 206-212, 220-227, 237-259, 272-279, 282-293, 295-309, 313-319, 321-328, 345-363, 376-386 and 159-176 of **Seq ID No 351**; 4-19, 24-30, 36-43, 50-68, 71-89, 93-106, 141-152, 154-172, 179-197, 199-215, 229-239, 246-252, 255-263, 281-298, 319-325, 329-356, 358-368, 374-390, 397-409, 420-429, 432-444, 450-456, 459-475, 483-494, 496-502, 520-528, 532-556 and 362-377 of **Seq ID No 352**; 18-25, 40-62, 77-85, 91-97, 105-116, 123-133, 139-184, 189-197 and 122-140 of **Seq ID No 353**; 4-49, 52-58, 62-70, 79-105, 109-133, 142-150, 163-168, 206-214, 220-228, 233-240, 243-254, 274-281, 303-311, 327-338, 357-373, 378-396, 403-413, 420-436, 441-453, 461-467, 475-481, 484-498, 506-512, 514-521, 523-529, 562-579, 589-595, 598-603, 615-648, 714-722, 728-742, 749-758, 777-792, 795-807 and 643-658 of **Seq ID No 354**; 8-27, 37-48, 51-56, 72-79, 87-106, 120-138, 140-147, 167-176, 187-197, 205-216, 222-229, 234-239, 243-249, 277-288, 292-315, 334-343, 347-353, 363-391, 398-404, 430-447, 461-467, 478-492, 498-507 and 456-470 of **Seq ID No 355**; 5-12, 18-24, 59-69, 80-93, 95-109, 119-125, 130-137, 139-147, 158-163, 168-176, 182-202, 206-215, 222-239, 241-249, 267-277, 291-298, 311-318, 321-327, 338-344, 348-355, 373-386, 393-406, 411-417, 434-443, 446-465, 473-484, 514-521, 532-553, 584-594 and 221-237 of **Seq ID No 356**; 4-14, 27-34, 50-58, 63-72, 79-106, 109-114, 121-142, 146-154, 161-167, 169-175, 178-201, 223-238, 249-254, 259-264, 278-292, 294-312, 319-330 and 167-191 of **Seq ID No 357**; 7-28, 36-42, 50-61, 63-80, 122-152, 161-174, 176-191 and 140-190 of **Seq ID No 358**; 20-57, 59-65, 70-78, 86-102, 119-133, 142-161, 163-173, 177-188, 192-202, 204-220, 222-236, 240-253, 279-319, 326-331, 337-383, 390-399, 406-412, 420-427, 431-438 and 381-395 of **Seq ID No 359**; 13-18, 28-34, 37-43, 50-59, 75-81, 83-97, 105-121, 139-147, 200-206, 209-227, 231-247, 260-271, 318-327, 366-381, 388-394, 399-406 and 182-201 of **Seq ID No 360**; 6-29, 37-43, 51-56, 70-77, 82-102, 110-119, 127-143, 178-190, 201-209, 216-243, 261-269, 281-292, 305-313, 327-339, 341-354, 356-373, 391-397, 423-429, 438-445, 450-478 and 21-314 of **Seq ID No 361**; 4-12, 15-21, 32-41, 59-76, 80-89, 96-104 and 90-103 of **Seq ID No 362**; 9-28, 30-41, 44-54, 69-74, 77-82, 90-97, 104-123, 125-135, 149-155, 164-173, 177-184, 217-226, 230-235, 238-244, 258-272, 282-297, 300-305, 309-315, 317-322, 327-336, 348-362, 368-374, 380-387, 400-411, 414-424, 451-458, 460-466, 483-494, 497-503, 506-511, 521-528, 540-553, 569-587, 598-606, 628-642, 661-681, 688-700, 718-733, 740-749, 752-764, 769-783, 823-834, 848-854, 862-872, 878-884, 886-898, 915-920, 938-951, 954-961, 963-972, 982-989, 996-1003, 1010-1016, 1021-1032, 1038-1044, 1047-1057, 1060-1070, 1079-1088, 1094-1102, 1117-1127, 1129-1135, 1142-1153, 1158-1204, 1212-1229, 1234-1263, 1269-1277, 1308-1313, 1327-1338, 1344-1376, 1400-1415, 1436-1443, 1448-1458, 1497-1504, 1511-1522, 1544-1566, 3-82 and 509-576 of **Seq ID No 363**; 8-36, 40-64, 71-79, 88-94, 102-109, 118-127, 138-148, 151-159, 163-174, 192-198, 200-206, 220-233, 268-273, 290-301, 304-309, 316-323, 331-349, 378-391, 414-420, 427-437, 455-475, 494-510, 541-547, 549-555, 616-640, 1-60, 55-139, 212-308, 386-458 and 458-624 of **Seq ID No 364**; 16-31, 35-42, 70-77, 91-101, 120-130, 132-140, 143-153, 185-190, 195-202, 215-222, 228-238, 241-251, 257-264, 268-277, 288-302, 312-324, 326-333, 341-348, 364-382, 415-429, 438-454, 458-466, 491-499, 501-521 and 273-281 of **Seq ID No 365**; 8-14, 32-57, 74-149, 155-177, 179-212, 221-266, 271-296, 304-324, 329-346, 349-359, 368-401, 413-419, 426-454, 465-478, 493-510 and 466-490 of **Seq ID No 366**; 22-28, 33-51, 64-89, 96-119, 126-132, 138-146, 152-159, 161-169, 172-179, 193-198, 205-211, 221-231, 235-254, 273-280, 297-303, 312-320, 328-346, 351-373, 378-384, 391-398, 448-454, 460-468, 470-481, 516-558, 574-593, 597-602, 613-623, 626-646, 649-656, 668-673, 675-683, 696-708, 715-722, 724-739, 745-751, 759-777, 780-804, 816-822 and 102-113 of **Seq ID No 367**; 12-28, 41-91, 98-107, 112-120, 125-131, 151-193, 215-221, 240-250, 263-280 and 128-138 of **Seq ID No 368**; 16-24, 32-38, 46-62, 68-81, 90-105, 127-133, 144-150, 160-166, 178-184, 186-202, 210-219, 232-240, 252-258, 264-273, 293-324, 337-344, 349-357, 360-369,

385-398, 410-416, 419-427, 441-449, 458-476, 508-515, 523-539, 544-549, 562-569, 571-579, 96-109 and 127-139 of Seq ID No 369; 19-25, 28-34, 56-61, 85-97, 110-116 and 39-53 of Seq ID No 370; 4-37, 41-50, 62-72, 91-97, 99-109, 114-125, 136-141, 149-158, 160-166, 201-215 and 27-225 of Seq ID No 371; 15-31, 44-51, 96-105, 122-130, 149-157, 162-168, 178-183, 185-192, 198-204, 206-213, 221-234, 239-245, 248-255, 257-266, 289-335, 349-357, 415-422, 425-441, 448-454, 462-468 and 463-481 of Seq ID No 372; 5-31, 39-55, 63-72, 76-99, 106-155, 160-177, 179-199, 207-217, 223-240, 245-255, 261-267, 294-316, 321-343, 354-378, 382-452, 477-488, 529-536, 555-569, 584-591, 593-612, 620-627, 632-640, 647-654, 671-680, 698-704, 723-730, 732-750, 769-775, 781-788, 822-852 and 505-525 of Seq ID No 373; 3-18 of Seq ID No 374; 4-14 and 12-24 of Seq ID No 375; 4-11, 22-30 and 12-25 of Seq ID No 376; 5-12 and 4-18 of Seq ID No 377; 4-28 and 7-14 of Seq ID No 378; 6-16 and 8-16 of Seq ID No 379; 4-15, 18-33 and 24-36 of Seq ID No 380; 4-10, 16-21 and 20-31 of Seq ID No 381; 6-19 of Seq ID No 382; 11-18 and 3-10 of Seq ID No 383; 13-24 and 3-15 of Seq ID No 384; 15-27 and 7-16 of Seq ID No 385; 11-16 and 1-15 of Seq ID No 386; 4-16 and 9-21 of Seq ID No 387; 4-24, 40-48, 54-67 and 22-39 of Seq ID No 388; 6-30, 34-55, 62-68, 78-106 and 68-74 of Seq ID No 389; 3-14 of Seq ID No 390; 9-19 and 6-21 of Seq ID No 391; 4-17 and 1-9 of Seq ID No 392; 5-30 and 1-8 of Seq ID No 393; 4-16, 23-46, 51-56 and 45-55 of Seq ID No 394; 7-16 of Seq ID No 395; 2-14 of Seq ID No 396; 4-36, 43-65 and 50-62 of Seq ID No 397; 10-30 and 14-21 of Seq ID No 398; 9-17 and 1-10 of Seq ID No 399; 4-12 and 3-16 of Seq ID No 400; 4-15 and 5-23 of Seq ID No 401; 10-21 of Seq ID No 402; 6-16 of Seq ID No 403; 4-29, 31-38 and 2-14 of Seq ID No 404; 4-35 and 33-42 of Seq ID No 405; 2-17 of Seq ID No 406; 9-18, 30-35 and 15-33 of Seq ID No 407; 4-9 and 6-12 of Seq ID No 408; 3-17 of Seq ID No 409; 12-21, 37-44, 52-61, 72-80 and 38-48 of Seq ID No 410; 4-10, 29-44, 54-61, 69-78 and 13-27 of Seq ID No 411; 13-23, 36-53 and 2-15 of Seq ID No 412; 4-25, 28-46, 56-72, 81-99, 120-132, 134-142, 154-160 and 129-141 of Seq ID No 413; 4-15, 24-33, 35-41, 64-86 and 21-33 of Seq ID No 414; 9-15 and 4-13 of Seq ID No 415; 4-11, 13-19, 34-48 and 15-32 of Seq ID No 416; 4-21 and 11-31 of Seq ID No 417; 23-57 and 38-50 of Seq ID No 418; 4-32 and 3-13 of Seq ID No 419; 4-10, 13-25, 32-42, 56-68, 72-84 and 26-38 of Seq ID No 420; 4-20, 31-48, 52-58, 65-71, 80-93, 99-108, 114-123 and 37-49 of Seq ID No 421; 6-12, 14-20 and 3-25 of Seq ID No 422; 14-25, 27-38 and 5-14 of Seq ID No 423; 4-41, 57-105, 109-118, 123-136, 144-152 and 86-99 of Seq ID No 424; 6-19 of Seq ID No 425; 2-19 of Seq ID No 426; 14-47 and 1-14 of Seq ID No 427; 4-21, 29-44 and 2-18 of Seq ID No 428; 23-29 and 10-28 of Seq ID No 429; 6-16, 22-36 and 11-22 of Seq ID No 430; 4-19, 30-44 and 18-27 of Seq ID No 431; 5-15, 37-45, 58-65 and 38-47 of Seq ID No 432; 4-15, 23-34 and 4-15 of Seq ID No 433; 30-36, 44-54, 79-85, 101-114, 138-152, 154-164, 170-175, 179-200, 213-220, 223-240, 243-255, 258-264, 268-284 and 10-28 of Seq ID No 434; the peptides comprising amino acid sequences of column "Identical region" of the Table 1B, especially peptides comprising amino acid 210-226 and 738-753 of Seq ID No 449; 326-344, 326-348, 338-354, 371-392, 801-809 and 877-901 of Seq ID No 450; 893-906 of Seq ID No 451; 51-69 of Seq ID No 452; 110-125 of Seq ID No 453; 291-305 of Seq ID No 454; 210-226 and 738-753 of Seq ID No 455; 326-344, 326-348, 338-354, 371-392, 801-809 and 877-901 of Seq ID No 456; 893-906 of Seq ID No 457; 51-69 of Seq ID No 458; 110-125 of Seq ID No 459; 291-305 of Seq ID No 460; 32-44 of Seq ID No 461; 399-410 of Seq ID No 462; the serum reactive epitopes as specified in the column of "aa from" to "aa to" of Table 2, especially peptides comprising amino acid 120-143, 138-161 and 156-179 of Seq ID No 218; 110-129 and 168-184 of Seq ID No 219; 74-90 of Seq ID No 222; 759-773 of Seq ID No 223; 237-260 of Seq ID No 224; 265-284 of Seq ID No 225; 65-74 of Seq ID No 226; 41-50 of Seq ID No 227; 163-174 of Seq ID No 229; 26-37 of Seq ID No 230; 174-189 of Seq ID No 232; 240-256 of Seq ID No 234; 285-297 of Seq ID No 236; 238-247 of Seq ID No 238; 491-519 of Seq ID No 239; 114-140 of Seq ID No 243; 267-284 of Seq ID No 250; 439-453 of Seq ID No 252; 162-178 of Seq ID No 253; 347-364 of Seq ID No 254; 699-715 of Seq ID No 255; 60-71 of Seq ID No 256; 244-257 of Seq ID No 257; 44-63 and 57-76 of Seq ID No 258; 185-196 of Seq ID No 260; 119-129 of Seq ID No 263; 182-195 of Seq ID No 266; 32-44 and 424-442 of Seq ID No 267; 247-256 of Seq ID No 268; 678-694, 785-805, 55-77 and 72-94 of Seq ID No 269; 210-226 of Seq ID No 281; 37-59 of Seq ID No 289; 13-29 of Seq ID No 296; 136-159 of Seq ID No 348; 205-222 of Seq ID No 349; 99-110 of Seq ID No 350; 160-176 of Seq ID No 351; 457-470 of Seq ID No 355; 221-237 of Seq ID No 356; 167-190 of Seq ID No 357; 96-120 of Seq ID No 361; 399-417, 503-519 and 544-563 of Seq ID No 364; 46-68, 159-183 and 184-198 of Seq ID No 371; 463-481 of Seq ID No 372; the immunogenic epitopes as specified in the column of "aa from" to "aa to" of Table 4; especially peptides comprising amino acid 110-129 and 168-184 of Seq ID No 219; 877-901, 333-354, 326-344 and 801-809 of Seq ID No 277; 1-54 of

Seq ID No 347; 544-563, 31-51, 107-119, 399-417 and 503-519 of Seq ID No 364; 120-198 of Seq ID No 218; 20-35 of Seq ID No 219; 118-201 of Seq ID No 221; 48-132 of Seq ID No 242; 118-136 of Seq ID No 249; 162-178 of Seq ID No 253; 347-364 of Seq ID No 254; 699-715 of Seq ID No 255; 50-76 of Seq ID No 258; 785-819 and 44-128 of Seq ID No 269; 90-128 of Seq ID No 274; 314-384 of Seq ID No 289; 327-349 of Seq ID No 293; 242-314, 405-478 and 23-100 of Seq ID No 304; 129-210 of Seq ID No 305; 162-188 of Seq ID No 307; 750-772 of Seq ID No 310; 1-56 of Seq ID No 335; 322-337 of Seq ID No 337; 72-90 of Seq ID No 339; 374-395 of Seq ID No 345; 136-159 of Seq ID No 348; 141-164 of Seq ID No 358; 96-157 of Seq ID No 361; 1-82 of Seq ID No 363; 489-556 of Seq ID No 364; 159-183 and 49-133 of Seq ID No 371; **The peptides comprising amino acid sequences of column "predicted immunogenic aa" and "location of identified immunogenic region (aa)" of Table 5, especially peptides comprising amino acid 4-26, 35-41, 53-61, 73-84, 103-108, 114-120, 140-146, 156-162, 192-208, 214-219, 227-233, 239-252, 260-268, 284-297, 1-48 and 113-133 of Seq ID No 475; 4-27, 38-44, 50-56, 59-64, 72-79, 83-89, 92-97, 108-116, 123-148, 152-167, 183-196, 200-220, 232-244, 255-261, 265-274, 282-302, 309-317, 1-79 and 231-302 of Seq ID No 476; 6-28, 66-72, 85-105, 115-121, 144-151, 160-170, 176-185, 223-230, 252-288, 296-310, 319-333, 367-374, 458-464, 471-480, 483-488, 520-528, 530-549, 559-564, 593-601, 606-616, 636-643, 655-662, 676-682, 684-699, 719-726, 735-750, 757-764, 777-785, 799-810, 812-843, 846-853, 868-873, 880-889, 891-899, 909-929, 934-940, 963-969, 998-1004, 1007-1014, 1016-1022, 1030-1046, 1-80 and 808-821 of Seq ID No 477; 7-24, 35-41, 75-81, 91-114, 122-132, 137-144, 148-156, 183-192, 194-200, 212-228, 233-238, 251-258, 275-295, 326-332, 337-346, 1-79 and 305-321 of Seq ID No 478; 31-38, 42-52, 66-72, 86-92, 98-104, 115-122, 127-146, 154-164, 169-187, 198-212, 225-237, 255-269, 13-92 and 135-142 of Seq ID No 479; 4-36, 39-49, 63-69, 71-77, 81-88, 123-131, 133-139, 160-169, 174-180, 188-194, 210-217, 273-278, 289-300, 317-334, 336-341, 383-401, 425-438, 1-68, 212-270 and 402-446 of Seq ID No 480; 21-29, 31-42, 49-63, 72-79, 81-93, 112-132, 159-165, 188-195, 197-232, 262-267, 279-286, 294-301, 318-326, 348-366, 381-405, 409-426, 436-465, 471-480, 484-492, 497-505, 521-544, 554-561, 567-577, 581-589, 601-609, 611-622, 636-651, 653-667, 669-685, 700-708, 716-722, 729-744, 749-766, 780-786, 789-811, 814-864, 1-57 and 84-106 of Seq ID No 481; 6-24, 35-48, 57-63, 72-78, 87-92, 113-119, 123-137, 147-153, 173-181, 212-233 and 1-124 of Seq ID No 482; 13-34, 62-69, 78-83, 86-91, 98-104, 107-115, 146-159, 179-188, 195-205, 209-221, 226-233, 239-253, 276-282, 284-294, 297-308, 331-354, 375-382, 388-399, 421-433, 449-458, 464-469, 472-491, 508-513, 525-531, 534-550, 575-593, 601-618, 629-635, 654-661, 666-680, 706-721, 723-740, 771-805, 810-830, 845-851 and 1-84 of Seq ID No 483; 4-32, 45-64, 73-83, 86-92, 100-111, 125-147, 157-163, 170-175, 177-188, 226-232, 245-252, 258-274, 320-335, 348-359 and 1-71 of Seq ID No 484; 13-40, 43-71, 76-83, 87-101, 109-119, 125-156, 162-175, 182-219, 226-232, 240-262, 270-287, 306-318, 326-342, 344-408, 414-444, 449-456 and 1-51 of Seq ID No 485; 4-16, 18-34, 45-54, 99-108, 134-140, 203-212, 241-257, 266-274, 279-291, 308-315, 330-336, 355-370, 374-382, 402-410, 428-455, 466-472, 474-480, 531-554, 560-566, 572-580, 597-618, 632-660, 664-674, 676-685, 691-705, 708-735, 750-768, 1-87 and 342-480 of Seq ID No 486; **The serum reactive epitopes as specified in the column of "aa from" to "aa to" of Table 6, especially peptides comprising amino acid 115-132 and 1-26 of Seq ID No 475; 33-55 of Seq ID No 476; 1-25 of Seq ID No 478; 37-61 of Seq ID No 479; 1-24 of Seq ID No 480; 1-23 of Seq ID No 481; 46-60 of Seq ID No 482; 1-28, 23-50 and 45-71 of Seq ID No 483; 1-22 and 17-38 of Seq ID No 484; 1-22 and 17-38 of Seq ID No 485; 1-27, 22-47 and 422-447 of Seq ID No 486; **The immunogenic epitopes as specified in the column of "aa from" to "aa to" of Table 7, especially peptides comprising amino acid 115-132 and 1-47 of Seq ID No 475; 1-55 of Seq ID No 476; 22-85 of Seq ID No 477; 307-320 and 1-44 of Seq ID No 478; 15-76 and 40-92 of Seq ID No 479; 1-59, 213-269 and 403-445 of Seq ID No 480; 1-56 and 85-105 of Seq ID No 481; 37-121 of Seq ID No 482; 1-71 of Seq ID No 483; 1-38 of Seq ID No 484; 1-38 of Seq ID No 485; 1-47 of Seq ID No 486 and fragments comprising at least 6, preferably more than 8, especially more than 10 aa and preferably not more than 70, 50, 40, 20, 15 or 11 aa of said sequences. All these fragments individually and each independently form a preferred selected aspect of the present invention.******

All linear hyperimmune serum reactive fragments of a particular antigen may be identified by analysing the entire sequence of the protein antigen by a set of peptides overlapping by 1 amino acid with a length of at least 10 amino acids. Subsequently, non-linear epitopes can be identified by analysis of the protein antigen with hyperimmune sera using the expressed full-length protein or domain polypeptides thereof. Assuming that a distinct domain of a protein is sufficient to form the 3D structure independent from the

native protein, the analysis of the respective recombinant or synthetically produced domain polypeptide with hyperimmune serum would allow the identification of conformational epitopes within the individual domains of multi-domain proteins. For those antigens where a domain possesses linear as well as conformational epitopes, competition experiments with peptides corresponding to the linear epitopes may be used to confirm the presence of conformational epitopes.

It will be appreciated that the invention also relates to, among others, nucleic acid molecules encoding the aforementioned fragments, nucleic acid molecules that hybridise to nucleic acid molecules encoding the fragments, particularly those that hybridise under stringent conditions, and nucleic acid molecules, such as PCR primers, for amplifying nucleic acid molecules that encode the fragments. In these regards, preferred nucleic acid molecules are those that correspond to the preferred fragments, as discussed above.

The present invention also relates to vectors, which comprise a nucleic acid molecule or nucleic acid molecules of the present invention, host cells which are genetically engineered with vectors of the invention and the production of hyperimmune serum reactive antigens and fragments thereof by recombinant techniques.

A great variety of expression vectors can be used to express a hyperimmune serum reactive antigen or fragment thereof according to the present invention. Generally, any vector suitable to maintain, propagate or express nucleic acids to express a polypeptide in a host may be used for expression in this regard. In accordance with this aspect of the invention the vector may be, for example, a plasmid vector, a single or double-stranded phage vector, a single or double-stranded RNA or DNA viral vector. Starting plasmids disclosed herein are either commercially available, publicly available, or can be constructed from available plasmids by routine application of well-known, published procedures. Preferred among vectors, in certain respects, are those for expression of nucleic acid molecules and hyperimmune serum reactive antigens or fragments thereof of the present invention. Nucleic acid constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Alternatively, the hyperimmune serum reactive antigens and fragments thereof of the invention can be synthetically produced by conventional peptide synthesizers. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA construct of the present invention.

Host cells can be genetically engineered to incorporate nucleic acid molecules and express nucleic acid molecules of the present invention. Representative examples of appropriate hosts include bacterial cells, such as streptococci, staphylococci, *E. coli*, *Streptomyces* and *Bacillus subtilis* cells; fungal cells, such as yeast cells and *Aspergillus* cells; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS, HeLa, C127, 3T3, BHK, 293 and Bowes melanoma cells; and plant cells.

The invention also provides a process for producing a *S. agalactiae* hyperimmune serum reactive antigen and a fragment thereof comprising expressing from the host cell a hyperimmune serum reactive antigen or fragment thereof encoded by the nucleic acid molecules provided by the present invention. The invention further provides a process for producing a cell, which expresses a *S. agalactiae* hyperimmune serum reactive antigen or a fragment thereof comprising transforming or transfecting a suitable host cell with the vector according to the present invention such that the transformed or transfected cell expresses the polypeptide encoded by the nucleic acid contained in the vector.

The polypeptide may be expressed in a modified form, such as a fusion protein, and may include not only secretion signals but also additional heterologous functional regions. Thus, for instance, a region of additional amino acids, particularly charged amino acids, may be added to the N- or C-terminus of the polypeptide to improve stability and persistence in the host cell, during purification or during

subsequent handling and storage. Also, regions may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to polypeptides to engender secretion or excretion, to improve stability or to facilitate purification, among others, are familiar and routine techniques in the art. A preferred fusion protein comprises a heterologous region from immunoglobulin that is useful to solubilize or purify polypeptides. For example, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another protein or part thereof. In drug discovery, for example, proteins have been fused with antibody Fc portions for the purpose of high-throughout screening assays to identify antagonists. See for example, {Bennett, D. et al., 1995} and {Johanson, K. et al., 1995}.

The *S. agalactiae* hyperimmune serum reactive antigen or a fragment thereof can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, hydroxylapatite chromatography and lectin chromatography.

The hyperimmune serum reactive antigens and fragments thereof according to the present invention can be produced by chemical synthesis as well as by biotechnological means. The latter comprise the transfection or transformation of a host cell with a vector containing a nucleic acid according to the present invention and the cultivation of the transfected or transformed host cell under conditions, which are known to the ones skilled in the art. The production method may also comprise a purification step in order to purify or isolate the polypeptide to be manufactured. In a preferred embodiment the vector is a vector according to the present invention.

The hyperimmune serum reactive antigens and fragments thereof according to the present invention may be used for the detection of the organism or organisms in a sample containing these organisms or polypeptides derived thereof. Preferably such detection is for diagnosis, more preferable for the diagnosis of a disease, most preferably for the diagnosis of a diseases related or linked to the presence or abundance of Gram-positive bacteria, especially bacteria selected from the group comprising streptococci, staphylococci and lactococci. More preferably, the microorganisms are selected from the group comprising *Streptococcus pneumoniae*, *Streptococcus pyogenes* and *Streptococcus mutans*, especially the microorganism is *Streptococcus pyogenes*.

The present invention also relates to diagnostic assays such as quantitative and diagnostic assays for detecting levels of the hyperimmune serum reactive antigens and fragments thereof of the present invention in cells and tissues, including determination of normal and abnormal levels. Thus, for instance, a diagnostic assay in accordance with the invention for detecting over-expression of the polypeptide compared to normal control tissue samples may be used to detect the presence of an infection, for example, and to identify the infecting organism. Assay techniques that can be used to determine levels of a polypeptide, in a sample derived from a host are well known to those of skill in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western Blot analysis and ELISA assays. Among these, ELISAs frequently are preferred. An ELISA assay initially comprises preparing an antibody specific to the polypeptide, preferably a monoclonal antibody. In addition, a reporter antibody generally is prepared which binds to the monoclonal antibody. The reporter antibody is attached to a detectable reagent such as radioactive, fluorescent or enzymatic reagent, such as horseradish peroxidase enzyme.

The hyperimmune serum reactive antigens and fragments thereof according to the present invention may also be used for the purpose of or in connection with an array. More particularly, at least one of the hyperimmune serum reactive antigens and fragments thereof according to the present invention may be immobilized on a support. Said support typically comprises a variety of hyperimmune serum reactive

antigens and fragments thereof whereby the variety may be created by using one or several of the hyperimmune serum reactive antigens and fragments thereof according to the present invention and/or hyperimmune serum reactive antigens and fragments thereof being different. The characterizing feature of such array as well as of any array in general is the fact that at a distinct or predefined region or position on said support or a surface thereof, a distinct polypeptide is immobilized. Because of this any activity at a distinct position or region of an array can be correlated with a specific polypeptide. The number of different hyperimmune serum reactive antigens and fragments thereof immobilized on a support may range from as little as 10 to several 1000 different hyperimmune serum reactive antigens and fragments thereof. The density of hyperimmune serum reactive antigens and fragments thereof per cm² is in a preferred embodiment as little as 10 peptides/polypeptides per cm² to at least 400 different peptides/polypeptides per cm² and more particularly at least 1000 different hyperimmune serum reactive antigens and fragments thereof per cm².

The manufacture of such arrays is known to the one skilled in the art and, for example, described in US patent 5,744,309. The array preferably comprises a planar, porous or non-porous solid support having at least a first surface. The hyperimmune serum reactive antigens and fragments thereof as disclosed herein, are immobilized on said surface. Preferred support materials are, among others, glass or cellulose. It is also within the present invention that the array is used for any of the diagnostic applications described herein. Apart from the hyperimmune serum reactive antigens and fragments thereof according to the present invention also the nucleic acid molecules according to the present invention may be used for the generation of an array as described above. This applies as well to an array made of antibodies, preferably monoclonal antibodies as, among others, described herein.

In a further aspect the present invention relates to an antibody directed to any of the hyperimmune serum reactive antigens and fragments thereof, derivatives or fragments thereof according to the present invention. The present invention includes, for example, monoclonal and polyclonal antibodies, chimeric, single chain, and humanized antibodies, as well as Fab fragments, or the product of a Fab expression library. It is within the present invention that the antibody may be chimeric, i. e. that different parts thereof stem from different species or at least the respective sequences are taken from different species.

Antibodies generated against the hyperimmune serum reactive antigens and fragments thereof corresponding to a sequence of the present invention can be obtained by direct injection of the hyperimmune serum reactive antigens and fragments thereof into an animal or by administering the hyperimmune serum reactive antigens and fragments thereof to an animal, preferably a non-human. The antibody so obtained will then bind the hyperimmune serum reactive antigens and fragments thereof itself. In this manner, even a sequence encoding only a fragment of a hyperimmune serum reactive antigen and fragments thereof can be used to generate antibodies binding the whole native hyperimmune serum reactive antigen and fragments thereof. Such antibodies can then be used to isolate the hyperimmune serum reactive antigens and fragments thereof from tissue expressing those hyperimmune serum reactive antigens and fragments thereof.

For preparation of monoclonal antibodies, any technique known in the art, which provides antibodies produced by continuous cell line cultures can be used (as described originally in {Kohler, G. et al., 1975}).

Techniques described for the production of single chain antibodies (U.S. Patent No. 4,946,778) can be adapted to produce single chain antibodies to immunogenic hyperimmune serum reactive antigens and fragments thereof according to this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies to immunogenic hyperimmune serum reactive antigens and fragments thereof according to this invention.

Alternatively, phage display technology or ribosomal display could be utilized to select antibody genes with binding activities towards the hyperimmune serum reactive antigens and fragments thereof either

from repertoires of PCR amplified v-genes of lymphocytes from humans screened for possessing respective target antigens or from naïve libraries {McCafferty, J. et al., 1990}; {Marks, J. et al., 1992}. The affinity of these antibodies can also be improved by chain shuffling {Clackson, T. et al., 1991}.

If two antigen binding domains are present, each domain may be directed against a different epitope – termed 'bispecific' antibodies.

The above-described antibodies may be employed to isolate or to identify clones expressing the hyperimmune serum reactive antigens and fragments thereof or purify the hyperimmune serum reactive antigens and fragments thereof of the present invention by attachment of the antibody to a solid support for isolation and/or purification by affinity chromatography.

Thus, among others, antibodies against the hyperimmune serum reactive antigens and fragments thereof of the present invention may be employed to inhibit and/or treat infections, particularly bacterial infections and especially infections arising from *S. agalactiae*.

Hyperimmune serum reactive antigens and fragments thereof include antigenically, epitopically or immunologically equivalent derivatives, which form a particular aspect of this invention. The term "antigenically equivalent derivative" as used herein encompasses a hyperimmune serum reactive antigen and fragments thereof or its equivalent which will be specifically recognized by certain antibodies which, when raised to the protein or hyperimmune serum reactive antigen and fragments thereof according to the present invention, interfere with the interaction between pathogen and mammalian host. The term "immunologically equivalent derivative" as used herein encompasses a peptide or its equivalent which when used in a suitable formulation to raise antibodies in a vertebrate, the antibodies act to interfere with the interaction between pathogen and mammalian host.

The hyperimmune serum reactive antigens and fragments thereof, such as an antigenically or immunologically equivalent derivative or a fusion protein thereof can be used as an antigen to immunize a mouse or other animal such as a rat or chicken. The fusion protein may provide stability to the hyperimmune serum reactive antigens and fragments thereof. The antigen may be associated, for example by conjugation, with an immunogenic carrier protein, for example bovine serum albumin (BSA) or keyhole limpet haemocyanin (KLH). Alternatively, an antigenic peptide comprising multiple copies of the protein or hyperimmune serum reactive antigen and fragments thereof, or an antigenically or immunologically equivalent hyperimmune serum reactive antigen and fragments thereof, may be sufficiently antigenic to improve immunogenicity so as to obviate the use of a carrier.

Preferably the antibody or derivative thereof is modified to make it less immunogenic in the individual. For example, if the individual is human the antibody may most preferably be "humanized", wherein the complementarity determining region(s) of the hybridoma-derived antibody has been transplanted into a human monoclonal antibody, for example as described in {Jones, P. et al., 1986} or {Tempest, P. et al., 1991}.

The use of a polynucleotide of the invention in genetic immunization will preferably employ a suitable delivery method such as direct injection of plasmid DNA into muscle, delivery of DNA complexed with specific protein carriers, coprecipitation of DNA with calcium phosphate, encapsulation of DNA in various forms of liposomes, particle bombardment {Tang, D. et al., 1992}, {Eisenbraun, M. et al., 1993} and *in vivo* infection using cloned retroviral vectors {Seeger, C. et al., 1984}.

In a further aspect the present invention relates to a peptide binding to any of the hyperimmune serum reactive antigens and fragments thereof according to the present invention, and a method for the manufacture of such peptides whereby the method is characterized by the use of the hyperimmune serum reactive antigens and fragments thereof according to the present invention and the basic steps are

known to the one skilled in the art.

Such peptides may be generated by using methods according to the state of the art such as phage display or ribosome display. In case of phage display, basically a library of peptides is generated, in form of phages, and this kind of library is contacted with the target molecule, in the present case a hyperimmune serum reactive antigen and fragments thereof according to the present invention. Those peptides binding to the target molecule are subsequently removed, preferably as a complex with the target molecule, from the respective reaction. It is known to the one skilled in the art that the binding characteristics, at least to a certain extent, depend on the particularly realized experimental set-up such as the salt concentration and the like. After separating those peptides binding to the target molecule with a higher affinity or a bigger force, from the non-binding members of the library, and optionally also after removal of the target molecule from the complex of target molecule and peptide, the respective peptide(s) may subsequently be characterised. Prior to the characterisation optionally an amplification step is realized such as, e. g. by propagating the peptide encoding phages. The characterisation preferably comprises the sequencing of the target binding peptides. Basically, the peptides are not limited in their lengths, however, preferably peptides having a lengths from about 8 to 20 amino acids are preferably obtained in the respective methods. The size of the libraries may be about 10^2 to 10^{18} , preferably 10^8 to 10^{15} different peptides, however, is not limited thereto.

A particular form of target binding hyperimmune serum reactive antigens and fragments thereof are the so-called "anticalines" which are, among others, described in German patent application DE 197 42 706.

In a further aspect the present invention relates to functional nucleic acids interacting with any of the hyperimmune serum reactive antigens and fragments thereof according to the present invention, and a method for the manufacture of such functional nucleic acids whereby the method is characterized by the use of the hyperimmune serum reactive antigens and fragments thereof according to the present invention and the basic steps are known to the one skilled in the art. The functional nucleic acids are preferably aptamers and spiegelmers.

Aptamers are D-nucleic acids, which are either single stranded or double stranded and which specifically interact with a target molecule. The manufacture or selection of aptamers is, e.g. described in European patent EP 0 533 838. Basically the following steps are realized. First, a mixture of nucleic acids, i. e. potential aptamers, is provided whereby each nucleic acid typically comprises a segment of several, preferably at least eight subsequent randomised nucleotides. This mixture is subsequently contacted with the target molecule whereby the nucleic acid(s) bind to the target molecule, such as based on an increased affinity towards the target or with a bigger force thereto, compared to the candidate mixture. The binding nucleic acid(s) are/is subsequently separated from the remainder of the mixture. Optionally, the thus obtained nucleic acid(s) is amplified using, e.g. polymerase chain reaction. These steps may be repeated several times giving at the end a mixture having an increased ratio of nucleic acids specifically binding to the target from which the final binding nucleic acid is then optionally selected. These specifically binding nucleic acid(s) are referred to as aptamers. It is obvious that at any stage of the method for the generation or identification of the aptamers samples of the mixture of individual nucleic acids may be taken to determine the sequence thereof using standard techniques. It is within the present invention that the aptamers may be stabilized such as, e. g., by introducing defined chemical groups which are known to the one skilled in the art of generating aptamers. Such modification may for example reside in the introduction of an amino group at the 2'-position of the sugar moiety of the nucleotides. Aptamers are currently used as therapeutical agents. However, it is also within the present invention that the thus selected or generated aptamers may be used for target validation and/or as lead substance for the development of medicaments, preferably of medicaments based on small molecules. This is actually done by a competition assay whereby the specific interaction between the target molecule and the aptamer is inhibited by a candidate drug whereby upon replacement of the aptamer from the complex of target and aptamer it may be assumed that the respective drug candidate allows a specific inhibition of the

interaction between target and aptamer, and if the interaction is specific, said candidate drug will, at least in principle, be suitable to block the target and thus decrease its biological availability or activity in a respective system comprising such target. The thus obtained small molecule may then be subject to further derivatisation and modification to optimise its physical, chemical, biological and/or medical characteristics such as toxicity, specificity, biodegradability and bioavailability.

Spiegelmers and their generation or manufacture is based on a similar principle. The manufacture of Spiegelmers is described in international patent application WO 98/08856. Spiegelmers are L-nucleic acids, which means that they are composed of L-nucleotides rather than D-nucleotides as aptamers are. Spiegelmers are characterized by the fact that they have a very high stability in biological systems and, comparable to aptamers, specifically interact with the target molecule against which they are directed. In the process of generating Spiegelmers, a heterogeneous population of D-nucleic acids is created and this population is contacted with the optical antipode of the target molecule, in the present case for example with the D-enantiomer of the naturally occurring L-enantiomer of the hyperimmune serum reactive antigens and fragments thereof according to the present invention. Subsequently, those D-nucleic acids are separated which do not interact with the optical antipode of the target molecule. But those D-nucleic acids interacting with the optical antipode of the target molecule are separated, optionally identified and/or sequenced and subsequently the corresponding L-nucleic acids are synthesized based on the nucleic acid sequence information obtained from the D-nucleic acids. These L-nucleic acids which are identical in terms of sequence with the aforementioned D-nucleic acids interacting with the optical antipode of the target molecule, will specifically interact with the naturally occurring target molecule rather than with the optical antipode thereof. Similar to the method for the generation of aptamers it is also possible to repeat the various steps several times and thus to enrich those nucleic acids specifically interacting with the optical antipode of the target molecule.

In a further aspect the present invention relates to functional nucleic acids interacting with any of the nucleic acid molecules according to the present invention, and a method for the manufacture of such functional nucleic acids whereby the method is characterized by the use of the nucleic acid molecules and their respective sequences according to the present invention and the basic steps are known to the one skilled in the art. The functional nucleic acids are preferably ribozymes, antisense oligonucleotides and siRNA.

Ribozymes are catalytically active nucleic acids, which preferably consist of RNA, which basically comprises two moieties. The first moiety shows a catalytic activity whereas the second moiety is responsible for the specific interaction with the target nucleic acid, in the present case the nucleic acid coding for the hyperimmune serum reactive antigens and fragments thereof according to the present invention. Upon interaction between the target nucleic acid and the second moiety of the ribozyme, typically by hybridisation and Watson-Crick base pairing of essentially complementary stretches of bases on the two hybridising strands, the catalytically active moiety may become active which means that it catalyses, either intramolecularly or intermolecularly, the target nucleic acid in case the catalytic activity of the ribozyme is a phosphodiesterase activity. Subsequently, there may be a further degradation of the target nucleic acid, which in the end results in the degradation of the target nucleic acid as well as the protein derived from the said target nucleic acid. Ribozymes, their use and design principles are known to the one skilled in the art, and, for example described in {Doherty, E. et al., 2001} and {Lewin, A. et al., 2001}.

The activity and design of antisense oligonucleotides for the manufacture of a medicament and as a diagnostic agent, respectively, is based on a similar mode of action. Basically, antisense oligonucleotides hybridise based on base complementarity, with a target RNA, preferably with a mRNA, thereby activating RNase H. RNase H is activated by both phosphodiester and phosphorothioate-coupled DNA. Phosphodiester-coupled DNA, however, is rapidly degraded by cellular nucleases with the exception of phosphorothioate-coupled DNA. These resistant, non-naturally occurring DNA derivatives do not inhibit

RNase H upon hybridisation with RNA. In other words, antisense polynucleotides are only effective as DNA RNA hybrid complexes. Examples for this kind of antisense oligonucleotides are described, among others, in US-patent US 5,849,902 and US 5,989,912. In other words, based on the nucleic acid sequence of the target molecule which in the present case are the nucleic acid molecules for the hyperimmune serum reactive antigens and fragments thereof according to the present invention, either from the target protein from which a respective nucleic acid sequence may in principle be deduced, or by knowing the nucleic acid sequence as such, particularly the mRNA, suitable antisense oligonucleotides may be designed based on the principle of base complementarity.

Particularly preferred are antisense-oligonucleotides, which have a short stretch of phosphorothioate DNA (3 to 9 bases). A minimum of 3 DNA bases is required for activation of bacterial RNase H and a minimum of 5 bases is required for mammalian RNase H activation. In these chimeric oligonucleotides there is a central region that forms a substrate for RNase H that is flanked by hybridising "arms" comprised of modified nucleotides that do not form substrates for RNase H. The hybridising arms of the chimeric oligonucleotides may be modified such as by 2'-O-methyl or 2'-fluoro. Alternative approaches used methylphosphonate or phosphoramidate linkages in said arms. Further embodiments of the antisense oligonucleotide useful in the practice of the present invention are P-methoxyoligonucleotides, partial P-methoxyoligodeoxyribonucleotides or P-methoxyoligonucleotides.

Of particular relevance and usefulness for the present invention are those antisense oligonucleotides as more particularly described in the above two mentioned US patents. These oligonucleotides contain no naturally occurring 5'→3'-linked nucleotides. Rather the oligonucleotides have two types of nucleotides: 2'-deoxyphosphorothioate, which activate RNase H, and 2'-modified nucleotides, which do not. The linkages between the 2'-modified nucleotides can be phosphodiester, phosphorothioate or P-ethoxyphosphodiester. Activation of RNase H is accomplished by a contiguous RNase H-activating region, which contains between 3 and 5 2'-deoxyphosphorothioate nucleotides to activate bacterial RNase H and between 5 and 10 2'-deoxyphosphorothioate nucleotides to activate eucaryotic and, particularly, mammalian RNase H. Protection from degradation is accomplished by making the 5' and 3' terminal bases highly nuclease resistant and, optionally, by placing a 3' terminal blocking group.

More particularly, the antisense oligonucleotide comprises a 5' terminus and a 3' terminus; and from position 11 to 59 5'→3'-linked nucleotides independently selected from the group consisting of 2'-modified phosphodiester nucleotides and 2'-modified P-alkoxyphosphotriester nucleotides; and wherein the 5'-terminal nucleoside is attached to an RNase H-activating region of between three and ten contiguous phosphorothioate-linked deoxyribonucleotides, and wherein the 3'-terminus of said oligonucleotide is selected from the group consisting of an inverted deoxyribonucleotide, a contiguous stretch of one to three phosphorothioate 2'-modified ribonucleotides, a biotin group and a P-alkoxyphosphotriester nucleotide.

Also an antisense oligonucleotide may be used wherein not the 5' terminal nucleoside is attached to an RNase H-activating region but the 3' terminal nucleoside as specified above. Also, the 5' terminus is selected from the particular group rather than the 3' terminus of said oligonucleotide.

The nucleic acids as well as the hyperimmune serum reactive antigens and fragments thereof according to the present invention may be used as or for the manufacture of pharmaceutical compositions, especially vaccines. Preferably such pharmaceutical composition, preferably vaccine is for the prevention or treatment of diseases caused by, related to or associated with *S. agalactiae*. In so far another aspect of the invention relates to a method for inducing an immunological response in an individual, particularly a mammal, which comprises inoculating the individual with the hyperimmune serum reactive antigens and fragments thereof of the invention, or a fragment or variant thereof, adequate to produce antibodies to protect said individual from infection, particularly *streptococcal* infection and most particularly *S. agalactiae* infections.

Yet another aspect of the invention relates to a method of inducing an immunological response in an individual which comprises, through gene therapy or otherwise, delivering a nucleic acid functionally encoding hyperimmune serum reactive antigens and fragments thereof, or a fragment or a variant thereof, for expressing the hyperimmune serum reactive antigens and fragments thereof, or a fragment or a variant thereof *in vivo* in order to induce an immunological response to produce antibodies or a cell mediated T cell response, either cytokine-producing T cells or cytotoxic T cells, to protect said individual from disease, whether that disease is already established within the individual or not. One-way of administering the gene is by accelerating it into the desired cells as a coating on particles or otherwise.

A further aspect of the invention relates to an immunological composition which, when introduced into a host capable of having induced within it an immunological response, induces an immunological response in such host, wherein the composition comprises recombinant DNA which codes for and expresses an antigen of the hyperimmune serum reactive antigens and fragments thereof of the present invention. The immunological response may be used therapeutically or prophylactically and may take the form of antibody immunity or cellular immunity such as that arising from CTL or CD4+ T cells.

The hyperimmune serum reactive antigens and fragments thereof of the invention or a fragment thereof may be fused with a co-protein which may not by itself produce antibodies, but is capable of stabilizing the first protein and producing a fused protein which will have immunogenic and protective properties. This fused recombinant protein preferably further comprises an antigenic co-protein, such as Glutathione-S-transferase (GST) or beta-galactosidase, relatively large co-proteins which solubilise the protein and facilitate production and purification thereof. Moreover, the co-protein may act as an adjuvant in the sense of providing a generalized stimulation of the immune system. The co-protein may be attached to either the amino or carboxy terminus of the first protein.

Also, provided by this invention are methods using the described nucleic acid molecule or particular fragments thereof in such genetic immunization experiments in animal models of infection with *S. agalactiae*. Such fragments will be particularly useful for identifying protein epitopes able to provoke a prophylactic or therapeutic immune response. This approach can allow for the subsequent preparation of monoclonal antibodies of particular value from the requisite organ of the animal successfully resisting or clearing infection for the development of prophylactic agents or therapeutic treatments of *S. agalactiae* infection in mammals, particularly humans.

The hyperimmune serum reactive antigens and fragments thereof may be used as an antigen for vaccination of a host to produce specific antibodies which protect against invasion of bacteria, for example by blocking adherence of bacteria to damaged tissue. Examples of tissue damage include wounds in skin or connective tissue and mucosal tissues caused e.g. by viral infection (esp. respiratory, such as the flu) mechanical, chemical or thermal damage or by implantation of indwelling devices, or wounds in the mucous membranes, such as the mouth, mammary glands, urethra or vagina.

The present invention also includes a vaccine formulation, which comprises the immunogenic recombinant protein together with a suitable carrier. Since the protein may be broken down in the stomach, it is preferably administered parenterally, including, for example, administration that is subcutaneous, intramuscular, intravenous, intradermal intranasal or transdermal. Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteriostats and solutes which render the formulation isotonic with the bodily fluid, preferably the blood, of the individual; and aqueous and non-aqueous sterile suspensions which may include suspending agents or thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampoules and vials, and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use. The vaccine formulation may also include adjuvant systems for enhancing the immunogenicity of the

formulation, such as oil-in-water systems and other systems known in the art. The dosage will depend on the specific activity of the vaccine and can be readily determined by routine experimentation.

According to another aspect, the present invention relates to a pharmaceutical composition comprising such a hyperimmune serum-reactive antigen or a fragment thereof as provided in the present invention for *S. agalactiae*. Such a pharmaceutical composition may comprise one preferably at least two or more hyperimmune serum reactive antigens or fragments thereof against *S. agalactiae*. Optionally, such *S. agalactiae* hyperimmune serum reactive antigens or fragments thereof may also be combined with antigens against other pathogens in a combination pharmaceutical composition. Preferably, said pharmaceutical composition is a vaccine for preventing or treating an infection caused by *S. agalactiae* and/or other pathogens against which the antigens have been included in the vaccine.

According to a further aspect, the present invention relates to a pharmaceutical composition comprising a nucleic acid molecule encoding a hyperimmune serum-reactive antigen or a fragment thereof as identified above for *S. agalactiae*. Such a pharmaceutical composition may comprise one or more nucleic acid molecules encoding hyperimmune serum reactive antigens or fragments thereof against *S. agalactiae*. Optionally, such *S. agalactiae* nucleic acid molecules encoding hyperimmune serum reactive antigens or fragments thereof may also be combined with nucleic acid molecules encoding antigens against other pathogens in a combination pharmaceutical composition. Preferably, said pharmaceutical composition is a vaccine for preventing or treating an infection caused by *S. agalactiae* and/or other pathogens against which the antigens have been included in the vaccine.

The pharmaceutical composition may contain any suitable auxiliary substances, such as buffer substances, stabilisers or further active ingredients, especially ingredients known in connection of pharmaceutical composition and/or vaccine production.

A preferable carrier/or excipient for the hyperimmune serum-reactive antigens, fragments thereof or a coding nucleic acid molecule thereof according to the present invention is an immunostimulatory compound for further stimulating the immune response to the given hyperimmune serum-reactive antigen, fragment thereof or a coding nucleic acid molecule thereof. Preferably the immunostimulatory compound in the pharmaceutical preparation according to the present invention is selected from the group of polycationic substances, especially polycationic peptides, immunostimulatory nucleic acids molecules, preferably immunostimulatory deoxynucleotides, alum, Freund's complete adjuvants, Freund's incomplete adjuvants, neuroactive compounds, especially human growth hormone, or combinations thereof.

It is also within the scope of the present invention that the pharmaceutical composition, especially vaccine, comprises apart from the hyperimmune serum reactive antigens, fragments thereof and/or coding nucleic acid molecules thereof according to the present invention other compounds which are biologically or pharmaceutically active. Preferably, the vaccine composition comprises at least one polycationic peptide. The polycationic compound(s) to be used according to the present invention may be any polycationic compound, which shows the characteristic effects according to the WO 97/30721. Preferred polycationic compounds are selected from basic polypeptides, organic polycations, basic polyamino acids or mixtures thereof. These polyamino acids should have a chain length of at least 4 amino acid residues (WO 97/30721). Especially preferred are substances like polylysine, polyarginine and polypeptides containing more than 20 %, especially more than 50 % of basic amino acids in a range of more than 8, especially more than 20, amino acid residues or mixtures thereof. Other preferred polycations and their pharmaceutical compositions are described in WO 97/30721 (e.g. polyethyleneimine) and WO 99/38528. Preferably these polypeptides contain between 20 and 500 amino acid residues, especially between 30 and 200 residues.

These polycationic compounds may be produced chemically or recombinantly or may be derived from

natural sources.

Cationic (poly)peptides may also be anti-microbial with properties as reviewed in {Ganz, T., 1999}. These (poly)peptides may be of prokaryotic or animal or plant origin or may be produced chemically or recombinantly (WO 02/13857). Peptides may also belong to the class of defensins (WO 02/13857). Sequences of such peptides can be, for example, found in the Antimicrobial Sequences Database under the following internet address:

<http://www.bbcm.univ.trieste.it/~tossi/pag2.html>

Such host defence peptides or defensives are also a preferred form of the polycationic polymer according to the present invention. Generally, a compound allowing as an end product activation (or down-regulation) of the adaptive immune system, preferably mediated by APCs (including dendritic cells) is used as polycationic polymer.

Especially preferred for use as polycationic substances in the present invention are cathelicidin derived antimicrobial peptides or derivatives thereof (International patent application WO 02/13857, incorporated herein by reference), especially antimicrobial peptides derived from mammalian cathelicidin, preferably from human, bovine or mouse.

Polycationic compounds derived from natural sources include HIV-REV or HIV-TAT (derived cationic peptides, antennapedia peptides, chitosan or other derivatives of chitin) or other peptides derived from these peptides or proteins by biochemical or recombinant production. Other preferred polycationic compounds are cathelin or related or derived substances from cathelin. For example, mouse cathelin is a peptide which has the amino acid sequence NH₂-RLAGLLRKGGEKIGEKLLKKIGOKIKNFFQKLVPQPE-COOH. Related or derived cathelin substances contain the whole or parts of the cathelin sequence with at least 15-20 amino acid residues. Derivations may include the substitution or modification of the natural amino acids by amino acids which are not among the 20 standard amino acids. Moreover, further cationic residues may be introduced into such cathelin molecules. These cathelin molecules are preferred to be combined with the antigen. These cathelin molecules surprisingly have turned out to be also effective as an adjuvant for an antigen without the addition of further adjuvants. It is therefore possible to use such cathelin molecules as efficient adjuvants in vaccine formulations with or without further immunactivating substances.

Another preferred polycationic substance to be used according to the present invention is a synthetic peptide containing at least 2 KKK-motifs separated by a linker of 3 to 7 hydrophobic amino acids (International patent application WO 02/32451, incorporated herein by reference).

The pharmaceutical composition of the present invention may further comprise immunostimulatory nucleic acid(s). Immunostimulatory nucleic acids are e. g. neutral or artificial CpG containing nucleic acids, short stretches of nucleic acids derived from non-vertebrates or in form of short oligonucleotides (ODNs) containing non-methylated cytosine-guanine di-nucleotides (CpG) in a certain base context (e.g. described in WO 96/02555). Alternatively, also nucleic acids based on inosine and cytidine as e.g. described in the WO 01/93903, or deoxynucleic acids containing deoxy-inosine and/or deoxyuridine residues (described in WO 01/93905 and PCT/EP 02/05448, incorporated herein by reference) may preferably be used as immunostimulatory nucleic acids for the present invention. Preferably, the mixtures of different immunostimulatory nucleic acids may be used according to the present invention.

It is also within the present invention that any of the aforementioned polycationic compounds is combined with any of the immunostimulatory nucleic acids as aforementioned. Preferably, such combinations are according to the ones as described in WO 01/93905, WO 02/32451, WO 01/54720, WO

01/93903, WO 02/13857 and PCT/EP 02/05448 and the Austrian patent application A 1924/2001, incorporated herein by reference.

In addition or alternatively such vaccine composition may comprise apart from the hyperimmune serum reactive antigens and fragments thereof, and the coding nucleic acid molecules thereof according to the present invention a neuroactive compound. Preferably, the neuroactive compound is human growth factor as, e.g. described in WO 01/24822. Also preferably, the neuroactive compound is combined with any of the polycationic compounds and/or immunostimulatory nucleic acids as afore-mentioned.

In a further aspect the present invention is related to a pharmaceutical composition. Such pharmaceutical composition is, for example, the vaccine described herein. Also a pharmaceutical composition is a pharmaceutical composition which comprises any of the following compounds or combinations thereof: the nucleic acid molecules according to the present invention, the hyperimmune serum reactive antigens and fragments thereof according to the present invention, the vector according to the present invention, the cells according to the present invention, the antibody according to the present invention, the functional nucleic acids according to the present invention and the binding peptides such as the anticalines according to the present invention, any agonists and antagonists screened as described herein. In connection therewith any of these compounds may be employed in combination with a non-sterile or sterile carrier or carriers for use with cells, tissues or organisms, such as a pharmaceutical carrier suitable for administration to a subject. Such compositions comprise, for instance, a media additive or a therapeutically effective amount of a hyperimmune serum reactive antigen and fragments thereof of the invention and a pharmaceutically acceptable carrier or excipient. Such carriers may include, but are not limited to, saline, buffered saline, dextrose, water, glycerol, ethanol and combinations thereof. The formulation should suit the mode of administration.

The pharmaceutical compositions may be administered in any effective, convenient manner including, for instance, administration by topical, oral, anal, vaginal, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal, intratracheal or intradermal routes among others.

In therapy or as a prophylactic, the active agent may be administered to an individual as an injectable composition, for example as a sterile aqueous dispersion, preferably isotonic.

Alternatively the composition may be formulated for topical application, for example in the form of ointments, creams, lotions, eye ointments, eye drops, ear drops, mouthwash, impregnated dressings and sutures and aerosols, and may contain appropriate conventional additives, including, for example, preservatives, solvents to assist drug penetration, and emollients in ointments and creams. Such topical formulations may also contain compatible conventional carriers, for example cream or ointment bases, and ethanol or oleyl alcohol for lotions. Such carriers may constitute from about 1 % to about 98 % by weight of the formulation; more usually they will constitute up to about 80 % by weight of the formulation.

In addition to the therapy described above, the compositions of this invention may be used generally as a wound treatment agent to prevent adhesion of bacteria to matrix proteins exposed in wound tissue and for prophylactic use in dental treatment as an alternative to, or in conjunction with, antibiotic prophylaxis.

A vaccine composition is conveniently in injectable form. Conventional adjuvants may be employed to enhance the immune response. A suitable unit dose for vaccination is 0.05-5 μ g antigen / per kg of body weight, and such dose is preferably administered 1-3 times and with an interval of 1-3 weeks.

With the indicated dose range, no adverse toxicological effects should be observed with the compounds of the invention, which would preclude their administration to suitable individuals.

In a further embodiment the present invention relates to diagnostic and pharmaceutical packs and kits comprising one or more containers filled with one or more of the ingredients of the aforementioned compositions of the invention. The ingredient(s) can be present in a useful amount, dosage, formulation or combination. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, reflecting approval by the agency of the manufacture, use or sale of the product for human administration.

In connection with the present invention any disease related use as disclosed herein such as, e. g. use of the pharmaceutical composition or vaccine, is particularly a disease or diseased condition which is caused by, linked or associated with Streptococci, more preferably, *S. pyogenes* and *pneumoniae*. In connection therewith it is to be noted that *S. agalactiae* comprises several strains including those disclosed herein. A disease related, caused or associated with the bacterial infection to be prevented and/or treated according to the present invention includes besides others bacterial pharyngitis, otitis media, pneumonia, bacteremia, meningitis, peritonitis, wound infection and sepsis in humans.

In a still further embodiment the present invention is related to a screening method using any of the hyperimmune serum reactive antigens or nucleic acids according to the present invention. Screening methods as such are known to the one skilled in the art and can be designed such that an agonist or an antagonist is screened. Preferably an antagonist is screened which in the present case inhibits or prevents the binding of any hyperimmune serum reactive antigen and fragment thereof according to the present invention to an interaction partner. Such interaction partner can be a naturally occurring interaction partner or a non-naturally occurring interaction partner.

The invention also provides a method of screening compounds to identify those, which enhance (agonist) or block (antagonist) the function of hyperimmune serum reactive antigens and fragments thereof or nucleic acid molecules of the present invention, such as its interaction with a binding molecule. The method of screening may involve high-throughput.

For example, to screen for agonists or antagonists, the interaction partner of the nucleic acid molecule and nucleic acid, respectively, according to the present invention, maybe a synthetic reaction mix, a cellular compartment, such as a membrane, cell envelope or cell wall, or a preparation of any thereof, may be prepared from a cell that expresses a molecule that binds to the hyperimmune serum reactive antigens and fragments thereof of the present invention. The preparation is incubated with labelled hyperimmune serum reactive antigens and fragments thereof in the absence or the presence of a candidate molecule, which may be an agonist or antagonist. The ability of the candidate molecule to bind the binding molecule is reflected in decreased binding of the labelled ligand. Molecules which bind gratuitously, i. e., without inducing the functional effects of the hyperimmune serum reactive antigens and fragments thereof, are most likely to be good antagonists. Molecules that bind well and elicit functional effects that are the same as or closely related to the hyperimmune serum reactive antigens and fragments thereof are good agonists.

The functional effects of potential agonists and antagonists may be measured, for instance, by determining the activity of a reporter system following interaction of the candidate molecule with a cell or appropriate cell preparation, and comparing the effect with that of the hyperimmune serum reactive antigens and fragments thereof of the present invention or molecules that elicit the same effects as the hyperimmune serum reactive antigens and fragments thereof. Reporter systems that may be useful in this regard include but are not limited to colorimetric labelled substrate converted into product, a reporter gene that is responsive to changes in the functional activity of the hyperimmune serum reactive antigens and fragments thereof, and binding assays known in the art.

Another example of an assay for antagonists is a competitive assay that combines the hyperimmune serum reactive antigens and fragments thereof of the present invention and a potential antagonist with membrane-bound binding molecules, recombinant binding molecules, natural substrates or ligands, or substrate or ligand mimetics, under appropriate conditions for a competitive inhibition assay. The hyperimmune serum reactive antigens and fragments thereof can be labelled such as by radioactivity or a colorimetric compound, such that the molecule number of hyperimmune serum reactive antigens and fragments thereof bound to a binding molecule or converted to product can be determined accurately to assess the effectiveness of the potential antagonist.

Potential antagonists include small organic molecules, peptides, polypeptides and antibodies that bind to a hyperimmune serum reactive antigen and fragments thereof of the invention and thereby inhibit or extinguish its activity. Potential antagonists also may be small organic molecules, a peptide, a polypeptide such as a closely related protein or antibody that binds to the same sites on a binding molecule without inducing functional activity of the hyperimmune serum reactive antigens and fragments thereof of the invention.

Potential antagonists include a small molecule, which binds to and occupies the binding site of the hyperimmune serum reactive antigens and fragments thereof thereby preventing binding to cellular binding molecules, such that normal biological activity is prevented. Examples of small molecules include but are not limited to small organic molecules, peptides or peptide-like molecules.

Other potential antagonists include antisense molecules (see {Okano, H. et al., 1991}; OLIGODEOXYNUCLEOTIDES AS ANTISENSE INHIBITORS OF GENE EXPRESSION; CRC Press, Boca Raton, FL (1988), for a description of these molecules).

Preferred potential antagonists include derivatives of the hyperimmune serum reactive antigens and fragments thereof of the invention.

As used herein the activity of a hyperimmune serum reactive antigen and fragment thereof according to the present invention is its capability to bind to any of its interaction partner or the extent of such capability to bind to its or any interaction partner.

In a particular aspect, the invention provides the use of the hyperimmune serum reactive antigens and fragments thereof, nucleic acid molecules or inhibitors of the invention to interfere with the initial physical interaction between a pathogen and mammalian host responsible for sequelae of infection. In particular the molecules of the invention may be used: i) in the prevention of adhesion of *S. agalactiae* to mammalian extracellular matrix proteins at mucosal surfaces and on in-dwelling devices or to extracellular matrix proteins in wounds; ii) to block bacterial adhesion between mammalian extracellular matrix proteins and bacterial proteins which mediate tissue damage or invasion iii) or lead to evasion of immune defense; iv) to block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques, e.g. through inhibiting nutrient acquisition.

Each of the DNA coding sequences provided herein may be used in the discovery and development of antibacterial compounds. The encoded protein upon expression can be used as a target for the screening of antibacterial drugs. Additionally, the DNA sequences encoding the amino terminal regions of the encoded protein or Shine-Delgarno or other translation facilitating sequences of the respective mRNA can be used to construct antisense sequences to control the expression of the coding sequence of interest.

The antagonists and agonists may be employed, for instance, to inhibit diseases arising from infection with *Streptococcus*, especially *S. agalactiae*, such as sepsis.

In a still further aspect the present invention is related to an affinity device such affinity device comprises as least a support material and any of the hyperimmune serum reactive antigens and fragments thereof according to the present invention, which is attached to the support material. Because of the specificity of the hyperimmune serum reactive antigens and fragments thereof according to the present invention for their target cells or target molecules or their interaction partners, the hyperimmune serum reactive antigens and fragments thereof allow a selective removal of their interaction partner(s) from any kind of sample applied to the support material provided that the conditions for binding are met. The sample may be a biological or medical sample, including but not limited to, fermentation broth, cell debris, cell preparation, tissue preparation, organ preparation, blood, urine, lymph liquid, liquor and the like.

The hyperimmune serum reactive antigens and fragments thereof may be attached to the matrix in a covalent or non-covalent manner. Suitable support material is known to the one skilled in the art and can be selected from the group comprising cellulose, silicon, glass, aluminium, paramagnetic beads, starch and dextrane.

The present invention is further illustrated by the following figures, examples and the sequence listing, from which further features, embodiments and advantages may be taken. It is to be understood that the present examples are given by way of illustration only and not by way of limitation of the disclosure.

In connection with the present invention

Figure 1 shows the characterization of human antibody sources for *S. agalactiae*.

Figure 2 shows the characterization of the small fragment genomic library, LSAg-70, from *Streptococcus agalactiae* ATCC 12403.

Figure 3 shows the selection of bacterial cells by MACS using biotinylated human IgGs.

Figure 4 shows the serotypes of the applied strains and an example for the gene distribution analysis with one of the identified antigens.

Figure 5 shows examples for induction of epitope-specific antibodies in mice by immunization with *E. coli* lysates.

Figure 6 shows examples for cell surface staining with epitope-specific antisera by flow cytometry.

Figure 7 shows the determination of bactericidal activity of antibodies induced by selected epitopes in an *in vitro* assay.

Table 1A shows the summary of all screens performed with genomic *S. agalactiae* libraries and human serum. Table 1B shows antigenic proteins identified by sequence identity within antigenic regions of the proteins listed in Table 1A.

Table 2 shows the summary of epitope serology analysis with human sera.

Table 3 shows the summary of the gene distribution analysis for the identified antigens in 46 *S. agalactiae* strains.

Table 4 shows the summary of mouse immunogenicity experiments.

Table 5 shows the summary of all screens performed with genomic *S. agalactiae* libraries and human serum.

Table 6 shows the summary of epitope serology analysis with human sera.

Table 7 shows the summary of mouse immunogenicity experiments.

The figures to which it might be referred to in the specification are described in the following in more details.

Figure 1 shows the characterization of human sera and cervical secretions for anti-*S. agalactiae* antibodies as measured by immune assays. Total anti-*S. agalactiae* IgG and IgA antibody levels were measured by standard ELISA using total bacterial lysates or culture supernatant fractions prepared from *S. agalactiae* serotype III strain ATCC 12403 as coating antigens. **(A)** Results of representative experiments are shown with healthy adult sera with total bacterial lysate proteins. Data are expressed as ELISA units calculated from absorbance at 405nm at a serum dilution in the linear range of detection (2.000X for IgA, 10,000 for IgG). Selected sera (out of 52) included in the healthy adult non-pregnant serum pool (NSag8-IgG,-IgA) are indicated by bold numbers. **(B)** Immunoblot analysis was performed on high titer sera selected by ELISA in order to ensure multiple immune reactivity with protein antigens. Results of a representative experiment using total bacterial lysate prepared from *S. agalactiae* serotype III ATCC 12403 strain and selected patients' sera at 5.000X dilution are shown. Blots were developed with anti-human IgG secondary antibody reagent. Low titer sera were included as negative controls. Mw: molecular weight markers. **(C)** shows selection of cervical secretions from noncolonized pregnant women by immunoblot analysis. Antibodies extracted from cervical wicks were quantitated for IgA content. 2 µg IgA from each preparations were tested for immunoreactivity using total bacterial lysate in a multi-well blotting apparatus. Blots were developed with anti-human IgA secondary antibodies. IgA preparation showing reactivity with GBS proteins (indicated by arrows) were selected and pooled.

Figure 2 (A) shows the fragment size distribution of the *Streptococcus agalactiae* ATCC 12403 small fragment genomic library, LSAg-70. After sequencing 576 randomly selected clones, sequences were trimmed (464) to eliminate vector residues and the numbers of clones with various genomic fragment sizes were plotted. **(B)** shows the graphic illustration of the distribution of the same set of randomly sequenced clones of LSAg-70 over the *S. agalactiae* ATCC 12403 chromosome. Rectangles indicate matching sequences to annotated ORFs and diamonds represent fully matched clones to non-coding chromosomal sequences in +/- or +/- orientation. Circles position all clones with chimeric sequences. Numeric distances in base pairs are indicated over the circular genome for orientation. Partitioning of various clone sets within the library is given in numbers and percentage at the bottom of the figure.

Figure 3 (A) shows the MACS selection with biotinylated human IgGs. The LSAg-70 library in pMAL9.1 was screened with 15-20 µg biotinylated IgG (PSag11-IgG, purified from human serum). As negative control, no serum was added to the library cells for screening. Number of cells selected after the 1st, 2nd and 3rd elution are shown for each selection round (upper, middle and lower panel, respectively). **(B)** shows the reactivity of specific clones (1-26) selected by bacterial surface display as analysed by immunoblot analysis with the human serum IgG pool (PSag11-IgG, 4 µg/µl) used for selection by MACS at a dilution of 1:3,000. As a loading control the same blot was also analysed with antibodies directed against the platform protein LamB at a dilution of 1:5,000 of hyperimmune rabbit serum. M, Molecular weight marker; L, Extract from a clone expressing LamB without foreign peptide insert.

Figure 4 (A) shows the representation of different serotypes of *S. agalactiae* clinical isolates analysed for the gene distribution study. A number of the strains were not typable and may represent additional serotypes. **(B)** shows the PCR analysis for the gene distribution of gbs0061 with the respective oligonucleotides and 46 *S. agalactiae* strains. The predicted size of the PCR fragments is 814 bp. 1-46, *S. agalactiae* strains, clinical isolates as shown under A; -, no genomic DNA added; +, genomic DNA from *S.*

agalactiae ATCC 12403, which served as template for library construction.

Figure 5 shows the measurement of epitope-specific mouse serum IgG antibody levels induced by total bacterial lysates of Lamb or FhuA expressing *E. coli* clones with *S. agalactiae*-derived epitopes. **(A)** shows representative peptide ELISA experiments with three sets of mouse sera (5 mice in each group, 1-5) generated by gbs0428, gbs0628 and gbs632 epitopes, respectively. Sera were tested at two different dilutions: black bars: 100X; grey bars; 1000X. Biotin-labeled synthetic peptides corresponding to the respective epitopes were used in the peptide ELISA. Sera induced with *E. coli* lysate without *S. agalactiae* derived epitopes are indicated as FhuA or LamB. **(B)** shows a typical immunoblotting experiment using lysates prepared from individual *E. coli* clones selected for mouse injections. Sera were depleted by *E. coli* lysate not carrying epitope to remove antibodies against *E. coli* proteins. Examples are shown for gbs0918, gbs0428, gbs0628 and gbs632 epitopes. Negative controls (-) are *E. coli* clones with empty platform proteins. Location of platform proteins LamB and FhuA is indicated by arrows.

Figure 6 shows the detection of specific antibody binding on the cell surface of *Streptococcus agalactiae* by flow cytometry. In **Figure 6A** preimmune mouse sera and polyclonal sera raised against *S. agalactiae* serotype III lysate were incubated with *S. agalactiae* strain serotype III and analysed by flow cytometry. Control shows the level of non-specific binding of the secondary antibody to the surface of *S. agalactiae* cells. The histograms in **figure 6B** indicates the increased fluorescence due to specific binding of anti-gbs0031, anti-gbs1925 and anti-gbs0012 antibodies in comparison to the control sera generated against *E. coli* lysate containing only the 'empty' platform protein FhuA.

Figure 7 shows the bactericidal activity of epitope specific antibodies as determined in *in vitro* killing assay. The killing activity of immune sera is measured parallel with and calculated relative to the appropriate control sera. Data are expressed as percentage of killing, that is the reduction on bacterial cfu numbers as a consequence of the presence of specific antibodies. Hyperimmune polyclonal mouse sera generated with *S. agalactiae* lysate and sera from non-immunized mice served as positive and negative controls for the assay, respectively. Immune sera generated with (A) gbs0012, gbs0016, gbs0031, gbs0428, gbs1306 and gbs2018 epitopes and with (B) gbs0233, gbs0419, gbs0942, gbs0975, gbs1038, gbs1144 and gbs2093 epitopes were tested for bactericidal activity and data are expressed relative to appropriate controls, such as sera induced with Lamb or FhuA expressing *E. coli* clones without *S. agalactiae*-derived epitopes. *S. agalactiae* serotype III cells were incubated with mouse phagocytic cells for 60 min, and surviving bacteria were quantified by counting cfus after plating on blood agar.

Table 1: Immunogenic proteins identified by bacterial surface display.

(A) Columns A, 300bp library of *S. agalactiae* ATCC 12403 in fhuA with NSag8-IgA (826), **B**, 300bp library in fhuA with PSag10-IgA (768), **C**, 300bp library in fhuA with PSag10-IgG (711), **D**, 300bp library in fhuA with PSag11-IgG (640), **E**, 70bp library in lamB with NSag8-IgA (1057), **F**, 70bp library in lamB with NSag8-IgG (869), **G**, 70bp library in lamB with PSag10-IgA (904), **H**, 70bp library in lamB with PSag10-IgA-adsorbed (493), **I**, 70bp library in lamB with PSag10-IgG (910), **J**, 70bp library in lamB with PSag11-IgA (631), **K**, 70bp library in lamB with PSag11-IgG (926), **L**, 70bp library in lamB with PSag18-IgA (691), **M**, 70bp library in lamB with PSag-sIgA (628); *, prediction of antigenic sequences longer than 5 amino acids was performed with the program ANTIGENIC (Kolaskar and Tongaonkar, 1990). **Table 1B** lists the immunogenic proteins identified by amino acid sequence identity with peptides identified by bacterial surface display. Antigenic peptides, which have been identified by bacterial surface-display possess identical counterparts in the listed proteins from *S. agalactiae*. The peptides have been shown to react with multiple human sera (see Table 2). Sera directed against these peptides can therefore recognize multiple proteins.

Table 2: Epitope serology with human sera.

Immune reactivity of individual synthetic peptides representing selected epitopes with human sera is shown. Extent of reactivity is expressed as +, ++ or +++, and summed from individual reactivities of

peptides with individual sera (13 patient and 9 healthy adult, 22 total). A total score for each peptide was calculated based on ELISA units as the sum of all reactivities. Scores were 2-8 for +, 9-16 for ++ and 17-26 for +++. ELISA units were calculated from OD_{405nm} readings and the serum dilution after correction for background. Location of synthetic peptides within the antigenic ORFs according to the genome annotation of ATCC 12403 strain is given in columns **aa from** and **aa to** indicating the first and last amino acid residues, respectively. Peptide names: gbs0012.1 present in annotated ORF: gbs0012.

Table 3: Gene distribution in *S. agalactiae* strains.

Fourty six *S. agalactiae* strains as shown in Figure 4A were tested by PCR with oligonucleotides specific for the genes encoding relevant antigens. The PCR fragment of one selected PCR reaction was sequenced in order to confirm the amplification of the correct DNA fragment. *, number of amino acid substitutions in a serotype IA strain as derived from sequencing as compared to *S. agalactiae* ATCC 12403. #, alternative strain used for sequencing, because gene was not present in the serotype IA strain.

Table 4: Immunogenicity of antigenic epitopes.

S. agalactiae antigens were tested for immunogenicity by immunization with *E. coli* clones harboring plasmids encoding the platform proteins LamB or FhuA fused to *S. agalactiae* peptides. The presence of epitope-specific antibodies were detected and measured by peptide ELISA and/or immunoblotting using the corresponding *E. coli* clone lysate, which served as immunogen. Results are expressed as + to +++++, and calculated for peptide ELISA as the sum of the reactivity of individual mouse sera based on ELISA units (as indicated on Fig. 5A) and for immunoblotting (IB) as the strength of reactivity of pooled (5 individual) mouse sera with the epitope containing platform protein (as indicated on Fig. 5B). Location of synthetic peptides within the antigenic ORFs according to the genome annotation of ATCC 12403 strain is given in columns **aa from** and **aa to** indicating the first and last amino acid residues, respectively.

Table 5: Immunogenic proteins identified by bacterial surface display.

(A) 300bp library of *S. agalactiae* ATCC 12403 in fhuA with IC8-IgA (826), B, 300bp library in fhuA with P10-IgA (768), C, 300bp library in fhuA with P10-IgG (711), D, 300bp library in fhuA with P11-IgG (640), E, 70bp library in lamB with IC8-IgA (1057), F, 70bp library in lamB with IC8-IgG (869), G, 70bp library in lamB with P10-IgA (904), H, 70bp library in lamB with P10-IgA-adsorbed (493), I, 70bp library in lamB with P10-IgG (910), J, 70bp library in lamB with P11-IgA (631), K, 70bp library in lamB with P11-IgG (926), *, prediction of antigenic sequences longer than 5 amino acids was performed with the program ANTIGENIC (Kolaskar and Tongaonkar, 1990).

Table 6: Epitope serology with human sera.

Immune reactivity of individual synthetic peptides representing selected epitopes with human sera is shown. Extent of reactivity is expressed as +, ++ or +++, and summed from individual reactivities of peptides with individual sera (13 patient and 9 healthy adult, 22 total). A total score for each peptide was calculated based on ELISA units as the sum of all reactivities. Scores were 2-8 for +, 9-16 for ++ and 17-30 for +++. ELISA units were calculated from OD_{405nm} readings and the serum dilution after correction for background. Location of synthetic peptides within the antigenic ORFs according to the genome annotation of ATCC 12403 strain is given in columns **aa from** and **aa to** indicating the first and last amino acid residues, respectively. Peptide names: gbs0233.1 present in annotated ORF: gbs0233.

Table 7: Immunogenicity of antigenic epitopes in mice.

S. agalactiae antigens were tested for immunogenicity by immunization with *E. coli* clones harboring plasmids encoding the platform proteins LamB or FhuA fused to *S. agalactiae* peptides. The presence of epitope-specific antibodies were detected and measured by peptide ELISA. Results are expressed as + to +++++, and calculated for peptide ELISA as the sum of the reactivity of individual mouse sera based on ELISA units (as indicated on Fig. 5). Location of epitopes within the antigenic ORFs according to the genome annotation of ATCC 12403 strain is given in columns **aa from** and **aa to** indicating the first and last amino acid residues, respectively.

EXAMPLES

Example 1: Characterization and selection of human serum sources based on anti-*S. agalactiae* antibodies, preparation of antibody screening reagents

Experimental procedures

Enzyme linked immune assay (ELISA).

ELISA plates (Maxisorb, Millipore) were coated with 5-10 µg/ml total protein diluted in coating buffer (0.1M sodium carbonate pH 9.2). Three dilutions of sera (2,000X, 10,000X, 50,000X) were made in PBS-BSA. Highly specific Horse Radish Peroxidase (HRP)-conjugated anti-human IgG or anti-human IgA secondary antibodies (Southern Biotech) were used according to the manufacturers' recommendations (dilution: 1,000x). Antigen-antibody complexes were quantified by measuring the conversion of the substrate (ABTS) to colored product based on OD_{405nm} readings by automatic ELIAS reader (TECAN SUNRISE).

Preparation of bacterial antigen extracts

Total bacterial lysate: Bacteria were grown overnight in THB (Todd-Hewitt Broth) and lysed by repeated freeze-thaw cycles: incubation on dry ice/ethanol-mixture until frozen (1 min), then thawed at 37°C (5 min); repeated 3 times. This was followed by sonication and collection of supernatant by centrifugation (3,500 rpm, 15 min, 4°C).

Culture supernatant: After removal of bacteria by centrifugation, the supernatant of overnight grown bacterial cultures was precipitated with ice-cold ethanol by mixing 1 part supernatant with 3 parts absolute ethanol and incubated overnight at -20°C. Precipitates were collected by centrifugation (2,600 g, for 15 min). Dry pellets were dissolved either in PBS for ELISA, or in urea and SDS-sample buffer for SDS-PAGE and immunoblotting. The protein concentration of samples was determined by Bradford assay.

Immunoblotting

Total bacterial lysate and culture supernatant samples were prepared from *in vitro* grown *S. agalactiae* serotype III strain. 10 to 25µg total protein/lane was separated by SDS-PAGE using the BioRad Mini-Protean Cell electrophoresis system and proteins transferred to nitrocellulose membrane (ECL, Amersham Pharmacia). After overnight blocking in 5% milk, human sera were added at 2,000x dilution, and HRPO labeled anti-human IgG was used for detection.

Extraction of antibodies from cervical wicks

Cervical secretions were collected by absorbent cylindrical wicks (Polyfiltronics) which were introduced into the cervical canal during speculum examination and thereafter kept frozen until extraction. Extraction was done according to Hordnes *et al*, 1998 (provider of the samples). Briefly, wicks were mixed with PBS containing protease inhibitors, vortexed and fluid was drained from the tubes containing the wicks. The concentrations of total IgA and IgG antibodies in extracts were determined.

Purification of antibodies for genomic screening. Five sera from both the patient and the healthy group were selected based on the overall anti-GBS titers for serum or cervical secretion pools used in the screening procedure. Antibodies against *E. coli* proteins were removed by incubating the heat-inactivated sera with whole cell *E. coli* cells (DH5alpha, transformed with pHIE11, grown under the same condition as used for bacterial surface display). Highly enriched preparations of IgGs from the pooled, depleted sera were generated by protein G affinity chromatography, according to the manufacturer's instructions (UltraLink Immobilized Protein G, Pierce). IgA antibodies were purified also by affinity chromatography using biotin-labeled anti-human IgA (Southern Biotech) immobilized on Streptavidin-agarose (GIBCO BRL). The efficiency of depletion and purification was checked by SDS-PAGE, Western blotting, ELISA and protein concentration measurements.

Results

The antibodies produced against *S. agalactiae* by the human immune system and present in human sera are indicative of the *in vivo* expression of the antigenic proteins and their immunogenicity. These molecules are essential for the identification of individual antigens in the approach as described in the present invention, which is based on the interaction of the specific anti-GBS antibodies and the corresponding *S. agalactiae* peptides or proteins. To gain access to relevant antibody repertoires, human sera were collected from

- I. healthy pregnant women tested negative for cervical and anorectal carriage of GBS
- II. healthy pregnant women tested positive for cervical and/or anorectal carriage of GBS who's newborn remained GBS-free (although with antibiotic prevention).
- III. adults below <45 years of age without clinical disease.
- IV. naïve individuals, young children between 5 and 10 months of age, after they already lost maternal antibodies and have not acquired GBS-specific ones due to the lack of GBS disease.

In addition cervical secretions were also collected from the first two groups of donors. The extrem value of these antibody sources is mainly the secretory IgA component, which is directly implicated as protective effector molecule on mucosal surfaces.

It is important to screen with antibodies from at least two different populations, pregnant women and nonpregnant adults, since GBS disease affects elderly and immunocompromised adults, as well. Within the pregnant study group, there are again two different patient categories, women who are GBS colonized and those who are noncolonized, to be included in the antigen screen.

Antibodies in serum and other body fluids, such as mucosal secretions induced in individuals exposed to the pathogens are crucial for antigen identification. The exposure to GBS results in asymptomatic colonization, current or past acute or chronic infection. *S. agalactiae* colonization and infections are common, and antibodies are present as a consequence of natural immunization from previous encounters. It is likely that sera from high titer noncolonized individuals contain functional antibodies, which are able to eliminate carriage. At the same time certain antibodies might be induced against GBS components only if the antigen persist. For that reason sera from colonized individuals were also included. It has been shown that colonization is associated with capsular polysaccharide (CPS)-specific antibody responses. However, it is not clear whether sufficient level of antibodies to CPS's would prevent GBS colonization, since there are colonized women with both high and low levels of anti-CPS antibody, and the same is true for noncolonized pregnant women.

However, there are reports that effector function and avidity of antibodies produced during pregnancy might be altered. It is important to recognize that most healthy adults are protected from invasive GBS disease and are less susceptible than newborns and the elderly. Antibodies from these individuals seem to be especially valuable for identification of the corresponding antigens. It is known that anti-GBS antibody levels increase with age.

GBS is a mucosal pathogen and should induce IgA response; for that reason it was important to perform IgA-based screens, as well as IgG-based screens. The fact that some *S. agalactiae* strains express high affinity IgA-binding receptor also points to the importance of IgA in host response. Recently it was reported that not only IgG, but also IgA serum antibodies can be recognized by the FcRIII receptors of PMNs and promote opsonization [Phillips-Quagliata, J. et al., 2000]; [Shibuya, A. et al., 2000]. The primary role of IgA antibodies is neutralization, mainly at the mucosal surface. The level of serum IgA reflects the quality, quantity and specificity of the dimeric secretory IgA. For that reason the serum collection was not only analyzed for anti-streptococcal IgG, but also for IgA levels. In the ELISA assays highly specific secondary reagents were used to detect antibodies from the high affinity types, such as

IgG and IgA, but avoided IgM. Production of IgM antibodies occurs during the primary adaptive humoral response, and results in low affinity antibodies, while IgG and IgA antibodies had already undergone affinity maturation, and are more valuable in fighting or preventing disease.

127 serum samples and 97 cervical secretions from pregnant women and 50 sera from healthy adults were characterized for anti-*S. agalactiae* antibodies by a series of immune assays. Primary characterization was done by ELISA using two different antigen preparations, such as total bacterial extract and culture supernatant proteins prepared from *S. agalactiae* serotype III ATCC 12403 strain. A representative experiment is shown in Fig. 1A using sera from the healthy adult population. Antibody titers were compared at given dilutions where the response was linear. Sera were ranked based on the IgG and IgA reactivity against the two complex antigenic mixtures (including serotype specific type III capsule), and the highest ones were selected for further testing by immunoblotting. This analysis confirmed a high antibody reactivity of the pre-selected sera against multiple GBS proteins, especially when compared to not selected, low-titer sera (Fig 1B). However, ELISA ranking of sera did not always correlated with immunoblot signals suggesting that anti-capsular antibodies were abundant and dominated the ELISA reactivities against total bacterial extracts. Thus the final selection of sera to be included in antibody-pools was based mainly on multiple immunogenic bands in immunoblotting experiments. This extensive antibody characterization approach has led to the unambiguous identification of anti-GBS hyperimmune sera.

The 97 cervical secretions were determined for IgA content, and same amount (2µg) was tested for anti-GBS reactivity by immunoblotting. Positively selected sera (as it is shown in Fig. 1C) were divided into colonized and noncolonized IgA pools and used separately in bacterial surface display experiments.

5 sera from both donor groups were selected and pooled for antigen identification by bacterial surface display. Selected sera included in the four pregnant women pools (PSAg10-IgG,-IgA, PSAg11-IgG, PSAg18-IgG and PSAg-sIgA) and one healthy adult (non-pregnant) pool (NSAg8-IgG,-IgA). IgG and IgA antibodies were purified from pooled sera by affinity chromatography and depleted of *E. coli* -reactive antibodies to avoid background in the bacterial surface display screen.

Example 2: Generation of highly random, frame-selected, small-fragment, genomic DNA libraries of *Streptococcus agalactiae*

Experimental procedures

Preparation of streptococcal genomic DNA. 50 ml Todd-Hewitt Broth medium was inoculated with *S. agalactiae* ATCC 12403 bacteria from a frozen stab and grown with aeration and shaking for 18 h at 37°C. The culture was then harvested, centrifuged with 1,600x g for 15 min and the supernatant was removed. Bacterial pellets were washed 3 x with PBS and carefully re-suspended in 0.5 ml of Lysozyme solution (100 mg/ml). 0.1 ml of 10 mg/ml heat treated RNase A and 20 U of RNase T1 were added, mixed carefully and the solution was incubated for 1 h at 37°C. Following the addition of 0.2 ml of 20 % SDS solution and 0.1 ml of Proteinase K (10 mg/ml) the tube was incubated overnight at 55°C. 1/3 volume of saturated NaCl was then added and the solution was incubated for 20 min at 4°C. The extract was pelleted in a microfuge (13,000 rpm) and the supernatant transferred into a new tube. The solution was extracted with PhOH/CHCl₃/IAA (25:24:1) and with CHCl₃/IAA (24:1). DNA was precipitated at room temperature by adding 0.6x volume of Isopropanol, spooled from the solution with a sterile Pasteur pipette and transferred into tubes containing 80% ice-cold ethanol. DNA was recovered by centrifuging the precipitates with 10-12,000x g, then dried on air and dissolved in ddH₂O.

Preparation of small genomic DNA fragments. Genomic DNA fragments were mechanically sheared into fragments ranging in size between 150 and 300 bp using a cup-horn sonicator (Bandelin Sonoplus UV

2200 sonicator equipped with a BB5 cup horn, 10 sec. pulses at 100 % power output) or into fragments of size between 50 and 70 bp by mild DNase I treatment (Novagen). It was observed that sonication yielded a much tighter fragment size distribution when breaking the DNA into fragments of the 150-300 bp size range. However, despite extensive exposure of the DNA to ultrasonic wave-induced hydromechanical shearing force, subsequent decrease in fragment size could not be efficiently and reproducibly achieved. Therefore, fragments of 50 to 70 bp in size were obtained by mild DNase I treatment using Novagen's shotgun cleavage kit. A 1:20 dilution of DNase I provided with the kit was prepared and the digestion was performed in the presence of MnCl₂ in a 60 µl volume at 20°C for 5 min to ensure double-stranded cleavage by the enzyme. Reactions were stopped with 2 µl of 0.5 M EDTA and the fragmentation efficiency was evaluated on a 2% TAE-agarose gel. This treatment resulted in total fragmentation of genomic DNA into near 50-70 bp fragments. Fragments were then blunt-ended twice using T4 DNA Polymerase in the presence of 100 µM each of dNTPs to ensure efficient flushing of the ends. Fragments were used immediately in ligation reactions or frozen at -20°C for subsequent use.

Description of the vectors. The vector pMAL4.31 was constructed on a pASK-IBA backbone [Skerra, A., 1994] with the beta-lactamase (*bla*) gene exchanged with the Kanamycin resistance gene. In addition the *bla* gene was cloned into the multiple cloning site. The sequence encoding mature beta-lactamase is preceded by the leader peptide sequence of *ompA* to allow efficient secretion across the cytoplasmic membrane. Furthermore a sequence encoding the first 12 amino acids (spacer sequence) of mature beta-lactamase follows the *ompA* leader peptide sequence to avoid fusion of sequences immediately after the leader peptidase cleavage site, since e.g. clusters of positive charged amino acids in this region would decrease or abolish translocation across the cytoplasmic membrane [Kajava, A. et al., 2000]. A *SmaI* restriction site serves for library insertion. An upstream *FseI* site and a downstream *NotI* site, which were used for recovery of the selected fragment, flank the *SmaI* site. The three restriction sites are inserted after the sequence encoding the 12 amino acid spacer sequence in such a way that the *bla* gene is transcribed in the -1 reading frame resulting in a stop codon 15 bp after the *NotI* site. A +1 bp insertion restores the *bla* ORF so that beta-lactamase protein is produced with a consequent gain of Ampicillin resistance.

The vector pMAL9.1 was constructed by cloning the *lamB* gene into the multiple cloning site of pEH1 [Hashemzadeh-Bonehi, L. et al., 1998]. Subsequently, a sequence was inserted in *lamB* after amino acid 154, containing the restriction sites *FseI*, *SmaI* and *NotI*. The reading frame for this insertion was constructed in such a way that transfer of frame-selected DNA fragments excised by digestion with *FseI* and *NotI* from plasmid pMAL4.31 yields a continuous reading frame of *lamB* and the respective insert.

The vector pHIE11 was constructed by cloning the *fhuA* gene into the multiple cloning site of pEH1. Thereafter, a sequence was inserted in *fhuA* after amino acid 405, containing the restriction site *FseI*, *XbaI* and *NotI*. The reading frame for this insertion was chosen in a way that transfer of frame-selected DNA fragments excised by digestion with *FseI* and *NotI* from plasmid pMAL4.31 yields a continuous reading frame of *fhuA* and the respective insert.

Cloning and evaluation of the library for frame selection. Genomic *S. agalactiae* DNA fragments were ligated into the *SmaI* site of the vector pMAL4.31. Recombinant DNA was electroporated into DH10B electrocompetent *E. coli* cells (GIBCO BRL) and transformants plated on LB-agar supplemented with Kanamycin (50 µg/ml) and Ampicillin (50 µg/ml). Plates were incubated over night at 37°C and colonies collected for large scale DNA extraction. A representative plate was stored and saved for collecting colonies for colony PCR analysis and large-scale sequencing. A simple colony PCR assay was used to initially determine the rough fragment size distribution as well as insertion efficiency. From sequencing data the precise fragment size was evaluated, junction intactness at the insertion site as well as the frame selection accuracy (*3n+1 rule*).

Cloning and evaluation of the library for bacterial surface display. Genomic DNA fragments were excised from the pMAL4.31 vector, containing the *S. agalactiae* library with the restriction enzymes *FseI* and *NotI*. The

entire population of fragments was then transferred into plasmids pMAL9.1 (LamB) or pHIE11 (FhuA), which have been digested with *FseI* and *NotI*. Using these two restriction enzymes, which recognise an 8 bp GC rich sequence, the reading frame that was selected in the pMAL4.31 vector is maintained in each of the platform vectors. The plasmid library was then transformed into *E. coli* DH5alpha cells by electroporation. Cells were plated onto large LB-agar plates supplemented with 50 µg/ml Kanamycin and grown over night at 37°C at a density yielding clearly visible single colonies. Cells were then scraped off the surface of these plates, washed with fresh LB medium and stored in aliquots for library screening at -80°C.

Results

Libraries for frame selection. Two libraries (LSAg-70 and LSAg-300) were generated in the pMAL4.31 vector with sizes of approximately 70 and 300 bp, respectively. For each library, ligation and subsequent transformation of approximately 1 µg of pMAL4.31 plasmid DNA and 50 ng of fragmented genomic *S. agalactiae* DNA yielded 4×10^5 to 2×10^6 clones after frame selection. To assess the randomness of the libraries, approximately 576 randomly chosen clones of LSAg-70 were sequenced. The bioinformatic analysis showed that of these clones only very few were present more than once. Furthermore, it was shown that approximately 80% of the clones fell in the size range between 25 and 100 bp with an average size of approximately 40 bp (Figure 2). Almost all sequences followed the 3n+1 rule, showing that all clones were properly frame selected.

Bacterial surface display libraries. The display of peptides on the surface of *E. coli* required the transfer of the inserts from the LSAg-70 and LSAg-300 libraries from the frame selection vector pMAL4.31 to the display plasmids pMAL9.1 (LamB) or pHIE11 (FhuA). Genomic DNA fragments were excised by *FseI* and *NotI* restriction and ligation of 5ng inserts with 0.1µg plasmid DNA and subsequent transformation into DH5alpha cells resulted in $2\text{--}5 \times 10^6$ clones. The clones were scraped off the LB plates and frozen without further amplification.

Example 3: Identification of highly immunogenic peptide sequences from *S. agalactiae* using bacterial surface displayed genomic libraries and human serum

Experimental procedures

MACS screening. Approximately 2.5×10^8 cells from a given library were grown in 5 ml LB-medium supplemented with 50 µg/ml Kanamycin for 2 h at 37°C. Expression was induced by the addition of 1 mM IPTG for 30 min. Cells were washed twice with fresh LB medium and approximately 2×10^7 cells re-suspended in 100 µl LB medium and transferred to an Eppendorf tube.

10 to 20 µg of biotinylated, human IgGs purified from serum was added to the cells and the suspension incubated overnight at 4°C with gentle shaking. 900 µl of LB medium was added, the suspension mixed and subsequently centrifuged for 10 min at 6,000 rpm at 4°C (For IgA screens, 10 µg of purified IgAs were used and these captured with biotinylated anti-human-IgG secondary antibodies). Cells were washed once with 1 ml LB and then re-suspended in 100 µl LB medium. 10 µl of MACS microbeads coupled to streptavidin (Miltenyi Biotech, Germany) were added and the incubation continued for 20 min at 4°C. Thereafter 900 µl of LB medium was added and the MACS microbead cell suspension was loaded onto the equilibrated MS column (Miltenyi Biotech, Germany) which was fixed to the magnet. (The MS columns were equilibrated by washing once with 1 ml 70% EtOH and twice with 2 ml LB medium.)

The column was then washed three times with 3 ml LB medium. After removal of the magnet, cells were eluted by washing with 2 ml LB medium. After washing the column with 3 ml LB medium, the 2 ml eluate was loaded a second time on the same column and the washing and elution process repeated. The loading, washing and elution process was performed a third time, resulting in a final eluate of 2 ml.

A second and third round of screening was performed as follows. The cells from the final eluate were collected by centrifugation and re-suspended in 1 ml LB medium supplemented with 50 µg/ml Kanamycin. The culture was incubated at 37°C for 90 min and then induced with 1 mM IPTG for 30 min. Cells were subsequently collected, washed once with 1 ml LB medium and suspended in 10 µl LB medium. 10 to 20 µg of human, biotinylated IgGs were added again and the suspension incubated over night at 4°C with gentle shaking. All further steps were exactly the same as in the first selection round. Cells selected after two rounds of selection were plated onto LB-agar plates supplemented with 50 µg/ml Kanamycin and grown over night at 37°C.

Evaluation of selected clones by sequencing and Western blot analysis. Selected clones were grown overnight at 37°C in 3 ml LB medium supplemented with 50 µg/ml Kanamycin to prepare plasmid DNA using standard procedures. Sequencing was performed at MWG (Germany) or in collaboration with TIGR (U.S.A.).

For Western blot analysis approximately 10 to 20 µg of total cellular protein was separated by 10% SDS-PAGE and blotted onto HybondC membrane (Amersham Pharmacia Biotech, England). The LamB or FhuA fusion proteins were detected using human serum as the primary antibody at a dilution of approximately 1:3,000 to 1:5,000 and anti-human IgG or IgA antibodies coupled to HRP at a dilution of 1:5,000 as secondary antibodies. Detection was performed using the ECL detection kit (Amersham Pharmacia Biotech, England). Alternatively, rabbit anti-FhuA or rabbit anti-LamB polyclonal immune sera were used as primary antibodies in combination with the respective secondary antibodies coupled to HRP for the detection of the fusion proteins.

Results

Screening of bacterial surface display libraries by magnetic activated cell sorting (MACS) using biotinylated Igs. The libraries LSag-70 in pMAL9.1 and LSag-300 in pHIE11 were screened with pools of biotinylated, human IgGs and IgAs prepared from sera of healthy adults (NSag8-IgG,-IgA) or P10,11,18 (see Example 1: *Preparation of antibodies from human serum*). The selection procedure was performed as described under Experimental procedures. Figure 3A shows a representative example of a screen with the LSag-70 library and PSag11-IgGs. As can be seen from the colony count after the first selection cycle from MACS screening, the total number of cells recovered at the end is drastically reduced from 2×10^7 cells to approximately 2×10^4 cells, but the selection without antibodies added showed a similar reduction in cell numbers (Figure 3A). Therefore a second and third round of selection was performed. At the end of round three, approximately 10^4 cells was recovered with PSag11-IgGs, while only 2×10^3 cells were recovered when no IgGs from human serum were added, clearly showing that selection was dependent on *S. agalactiae* specific antibodies. To evaluate the performance of the screen, 26 selected clones were picked randomly and subjected to immunoblot analysis with screening IgG pool (Figure 3B). This analysis revealed that more than 80% of the selected clones showed reactivity with antibodies present in the relevant serum whereas the control strain expressing LamB without a *S. agalactiae* specific insert did not react with the same serum. In general, the rate of reactivity was observed to lie within the range of 35 to 90%. Colony PCR analysis showed that all selected clones contained an insert in the expected size range.

Subsequent sequencing of a larger number of randomly picked clones (600 to 1200 per screen) led to the identification of the gene and the corresponding peptide or protein sequence that was specifically recognized by the human serum antibodies used for screening. The frequency with which a specific clone is selected reflects at least in part the abundance and/or affinity of the specific antibodies in the serum used for selection and recognizing the epitope presented by this clone. In that regard it is striking that clones derived from some ORFs (e.g. gbs1087, gbs1306, gbs2018) were picked more than 100 times, indicating their highly immunogenic property. Table 1 and Table 5 summarizes the data obtained for all

13 performed screens. All clones that are presented in Table 1 and Table 5 have been verified by immunoblot analysis using whole cellular extracts from single clones to show the indicated reactivity with the pool of human serum used in the respective screen. As can be seen from Table 1 and Table 5, distinct regions of the identified ORF are identified as immunogenic, since variably sized fragments of the proteins are displayed on the surface by the platform proteins.

It is further worth noticing that most of the genes identified by the bacterial surface display screen encode proteins that are either attached to the surface of *S. agalactiae* and/or are secreted. This is in accordance with the expected role of surface attached or secreted proteins in virulence of *S. agalactiae*.

Example 4: Assessment of the reactivity of highly immunogenic peptide sequences with individual human sera.

Experimental procedures

Peptide synthesis

Peptides were synthesized in small scale (4 mg resin; up to 288 in parallel) using standard F-moc chemistry on a Rink amide resin (PepChem, Tübingen, Germany) using a SyroII synthesizer (MultisynTech, Witten, Germany). After the sequence was assembled, peptides were elongated with Fmoc-epsilon-amino-hexanoic acid (as a linker) and biotin (Sigma, St. Louis, MO; activated like a normal amino acid). Peptides were cleaved off the resin with 93% TFA, 5% triethylsilane, and 2% water for one hour. Peptides were dried under vacuum and freeze dried three times from acetonitrile/water (1:1). The presence of the correct mass was verified by mass spectrometry on a Reflex III MALDI-TOF (Bruker, Bremen Germany). The peptides were used without further purification.

Enzyme linked immune assay (ELISA).

Biotin-labeled peptides (at the N-terminus) were coated on Streptavidin ELISA plates (EXICON) at 10 µg/ml concentration according to the manufacturer's instructions. Highly specific Horse Radish Peroxidase (HRP)-conjugated anti-human IgG secondary antibodies (Southern Biotech) were used according to the manufacturers' recommendations (dilution: 1,000x). Sera were tested at two serum dilutions, 200X and 1,000X. Following manual coating, peptide plates were processed and analyzed by the Gemini 160 ELISA robot (TECAN) with a built-in ELISA reader (GENIOS, TECAN).

Results

Following the bioinformatic analysis of selected clones, corresponding peptides were designed and synthesized. In case of epitopes with more than 26 amino acid residues, overlapping peptides were made. All peptides were synthesized with a N-terminal biotin-tag and used as coating reagents on Streptavidin-coated ELISA plates.

The analysis was performed with peptides that were selected based on their reactivity with the individual sera, which were included in the serum pools used for preparations of IgG and IgA screening reagents for bacterial surface display. A summary for serum reactivity of 74 peptides representing 55 different *S. agalactiae* antigenic proteins from the genomic screen analysed with 22 human sera (from 13 patient and 9 healthy exposed high titer individuals) used for the antigen identification is shown in Table 2 and Table 6. The peptides were compared by the score calculated for each peptide based on the number of positive sera and the extent of reactivity. Peptides range from highly and widely reactive to weakly positive ones.

Example 5: Gene distribution studies with highly immunogenic proteins identified from *S. agalactiae*.***Experimental procedures***

Gene distribution of GBS antigens by PCR. An ideal vaccine antigen would be an antigen that is present in all, or the vast majority of strains of the target organism to which the vaccine is directed. In order to establish whether the genes encoding the identified *Streptococcus agalactiae* antigens occur ubiquitously in *S. agalactiae* strains, PCR was performed on a series of independent *S. agalactiae* isolates with primers specific for the gene of interest. *S. agalactiae* isolates were obtained covering the serotypes most frequently present in patients as shown in Figure 4A. Oligonucleotide sequences as primers were designed for all identified ORFs yielding products of approximately 1,000 bp, if possible covering all identified immunogenic epitopes. Genomic DNA of all *S. agalactiae* strains was prepared as described under Example 2. PCR was performed in a reaction volume of 25 µl using Taq polymerase (1U), 200 nM dNTPs, 10 pMol of each oligonucleotide and the kit according to the manufacturers instructions (Invitrogen, The Netherlands). As standard, 30 cycles (1x: 5min. 95°C, 30x: 30sec. 95°C, 30sec. 56°C, 30sec. 72°C, 1x 4min. 72°C) were performed, unless conditions had to be adapted for individual primer pairs.

Results

Identified genes encoding immunogenic proteins were tested by PCR for their presence in 46 different strains of *S. agalactiae* (Figure 4A). As an example, figure 4B shows the PCR reaction for GBS0061 with all indicated 46 strains. As clearly visible, the gene is present in all strains analysed. The PCR fragment from a type IA strain was sequenced and showed that all 657 bp were identical as compared to the *S. agalactiae* ATCC 12403 strain, indicating a high level of conservation between the two isolates.

From a total of 117 genes analysed, more than 100 were present in all or almost all strains tested, while only 5 genes were absent in more than 10% of the tested 46 strains (Table 3). In addition, only few genes (e.g. GBS0016, GBS1087, GBS1528 and GBS2018) showed variation in size but were present in all or most strain isolates. Sequencing of the generated PCR fragment from one strain and subsequent comparison to the type III strain ATCC 12403 confirmed the amplification of the correct DNA fragment and revealed a degree of sequence divergence as indicated in Table 3. Importantly, many of the identified antigens are well conserved in all strains in sequence and size and are therefore novel vaccine candidates to prevent infections by GBS.

Example 6: Characterization of immune sera obtained from mice immunized with highly immunogenic proteins/peptides from *S. agalactiae* displayed on the surface of *E. coli*.***Experimental procedures******Generation of immune sera from mice***

E. coli clones harboring plasmids encoding the platform protein fused to a *S. agalactiae* peptide, were grown in LB medium supplemented with 50µg/ml Kanamycin at 37°C. Overnight cultures were diluted 1:10, grown until an OD₆₀₀ of 0.5 and induced with 0.2 mM IPTG for 2 hours. Pelleted bacterial cells were suspended in PBS buffer and disrupted by sonication on ice, generating a crude cell extract. According to the OD₆₀₀ measurement, an aliquot corresponding to 5x10⁷ cells was injected into NMRI mice i.v., followed by a boost after 2 weeks. Serum was taken 1 week after the second injection. Epitope specific antibody levels were measured by peptide ELISA.

In vitro expression of antigens

Expression of antigens by *in vitro* grown *S. agalactiae* serotype III was tested by immunoblotting. Different growth media and culture conditions were tested to detect the presence of antigens in total lysates and bacterial culture supernatants. Expression was considered confirmed when a specific band corresponding to the predicted molecular weight and electrophoretic mobility was detected.

Cell surface staining

Flow cytometric analysis was carried out as follows. Bacteria were grown under culture conditions, which resulted in expression of the antigen as shown by the immunoblot analysis. Cells were washed twice in Hanks Balanced Salt Solution (HBSS) and the cell density was adjusted to approximately 1×10^6 CFU in 100 μ l HBSS, 0.5% BSA. After incubation for 30 to 60 min at 4°C with mouse antisera diluted 50 to 100-fold, unbound antibodies were washed away by centrifugation in excess HBSS, 0.5% BSA. Secondary goat anti-mouse antibody (F(ab')₂ fragment specific) labeled with fluorescein (FITC) was incubated with the cells at 4°C for 30 to 60 min. After washing, cells were fixed with 2% paraformaldehyde. Bound antibodies were detected using a Becton Dickinson FACScan flow cytometer and data further analyzed with the computer program CELLQuest. Negative control sera included mouse pre-immune serum and mouse polyclonal serum generated with lysates prepared from IPTG induced *E. coli* cells transformed with plasmids encoding the genes *lamB* or *fhuA* without *S. agalactiae* genomic insert.

Bactericidal (killing) assay

Murine macrophage cells (RAW246.7 or P388.D1) and bacteria were incubated and the loss of viable bacteria after 60 min was determined by colony counting. In brief, bacteria were washed twice in Hanks Balanced Salt Solution (HBSS) and the cell density was adjusted to approximately 1×10^5 CFU in 50 μ l HBSS. Bacteria were incubated with mouse sera (up to 25%) and guinea pig complement (up to 5%) in a total volume of 100 μ l for 60min at 4°C. Pre-opsonized bacteria were mixed with macrophages (murine cell line RAW264.7 or P388.D1; 2×10^6 cells per 100 μ l) at a 1:20 ratio and were incubated at 37°C on a rotating shaker at 500 rpm. An aliquot of each sample was diluted in sterile water and incubated for 5 min at room temperature to lyse macrophages. Serial dilutions were then plated onto Todd-Hewitt Broth agar plates. The plates were incubated overnight at 37°C, and the colonies were counted with the Counterstat flash colony counter (IUL Instruments). Control sera included mouse pre-immune serum and mouse polyclonal serum generated with lysates prepared from IPTG induced *E. coli* transformed with plasmids harboring the genes *lamB* or *fhuA* without *S. agalactiae* genomic insert.

Results

Immunogenicity in mice. The presence of specific antibodies was determined by peptide ELISA and/or immunoblotting using the *E. coli* clone expressing the given epitope embedded in LamB or FhuA platform proteins, as it is exemplified in Fig. 5A and B, respectively, and summarized in Table 4 and Table 7. 43 novel GBS antigens represented by 61 different epitope regions were shown to be immunogenic in mice. Positive sera were then analysed by immunoblotting using total bacterial lysates and culture supernatants prepared from *S. agalactiae* serotype III strain (data not shown). This analysis served as a first step to determine whether the antigenic proteins were expressed, and if, under which growth conditions, in order to evaluate surface expression of the polypeptide by FACS analysis. It was anticipated based on literature data that not all proteins would be expressed under *in vitro* conditions.

Cell surface staining of *S. agalactiae*. Cell surface accessibility for several antigenic proteins was subsequently demonstrated by an assay based on flow cytometry. GBS cells were incubated with preimmune and polyclonal mouse sera raised against *S. agalactiae* lysate or *E. coli* clones harboring plasmids encoding the platform protein fused to a *S. agalactiae* peptide, followed by detection with fluorescently tagged secondary antibody. As shown in Fig. 6A, antisera raised against *S. agalactiae* lysate contains antibodies against surface components, demonstrated by a significant shift in fluorescence of the *S. agalactiae* serotype III cell population. Similar cell surface staining of *S. agalactiae* serotype III cells was observed with polyclonal sera raised against peptides of many of the GBS antigens identified (Fig. 6B). In some instances, a subpopulation of the bacteria was not stained, as indicated by the detection of two peaks in the histograms (Fig. 6B). This phenomenon may be a result of differential expression of the gene products during the growth of the bacterium, insufficient antibody levels or partial inhibition of antibody binding caused by other surface molecules or plasma proteins. Importantly, a well-known protective GBS

antigen, Sip/gbs0031 is proved to be also positive in this assay.

In vitro bactericidal activity. Opsonophagocytic killing is the cornerstone of host defense against extracellular bacteria, such as *S. agalactiae*. Cell surface binding of antibodies to bacterial antigens are opsonizing and induce killing (bactericidal) by phagocytic cells (macrophages and neutrophil granulocytes) if the antibodies induced by the particular antigens can bind activated complement components (C3bi). In Figure 7 data are presented on bactericidal activity measured by antigen-specific antibodies generated in mice with corresponding epitopes. According to these data, several of the novel GBS antigens, for example gbs0012, gbs0016, gbs0428, gbs1306 and gbs2018 induce functional antibodies. Importantly, a well-known protective GBS antigen, Sip/gbs0031 is proved to be strongly positive in the very same assay.

These experiments confirmed the bioinformatic prediction that many of the proteins are exported due to their signal peptide sequence and in addition showed that they are present on the cell surface of *S. agalactiae* serotype III. They also confirm that these proteins are available for recognition by human antibodies with functional properties and make them valuable candidates for the development of a vaccine against GBS diseases.

Table 1A: Immunogenic proteins identified by bacterial surface display.

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogeni c region (aa)	Seq. ID (DNA, Prot.)
gbs0012	weakly similar to beta-lactamase	4-20,35-44,65-70,73-87,92-98,112-137,152-161,177- 186,193-200,206-213,229-255,282-294,308-313,320- 326,349-355,373-384,388-406,420-425	B:13, C:6	115-199	1, 218
gbs0016	glucan-binding protein B	5-24,35-41,44-70,73-89,103-109,127-143,155-161,185- 190,192-207,212-219,246-262,304-336,372-382,384- 393,398-407,412-418,438-444	B:12, C:4, D:3, E:5, H:4, I:12, M:2	1-75, 76-161, 164-239	2, 219
gbs0024	phosphoribosylformyl glycinamide synthase	4-10,16-58,60-71,77-92,100-126,132-146,149-164,166- 172,190-209,214-220,223-229,241-256,297-312,314- 319,337-343,351-359,378-387,398-418,421-428,430- 437,440-448,462-471,510-519,525-536,552-559,561- 568,573-582,596-602,608-630,637-649,651-665,681- 702,714-732,739-745,757-778,790-805,807-815,821- 829,836-842,846-873,880-903,908-914,916-923,931- 940,943-948,956-970,975-986,996-1015,1031-1040,1051- 1069,1072-1095,1114-1119,1130-1148,1150-1157,1169- 1176,1229-1238	F:4	802-812	3, 220
gbs0031	surface immunogenic protein	5-12,14-26,35-47,52-67,72-78,83-98,121-141,152-159,163- 183,186-207,209-257,264-277,282-299,301-309,312- 318,324-339,358-368,372-378,387-397,425-431	A:17, B:53, C:36, D:4	46-291	4, 221
gbs0048	Hypothetical protein	29-38,44-64,70-76,78-87,94-100,102-112,119-134,140- 149,163-173,178-186,188-194,207-234,247-262,269-290	K:13	73-92	5, 222
gbs0053	aldehyde-alcohol dehydrogenase (adhE)	10-28,36-63,77-87,103-119,127-136,141-169,171-183,195- 200,207-232,236-246,251-265,268-283,287-297,314- 322,335-343,354-363,384-390,405-411,419-436,443- 455,467-473,480-513,518-529,550-557,565-585,602- 608,616-625,632-660,665-677,685-701,726-736,738- 747,752-761,785-796,801-813,838-853,866-871	E:4	757-774	6, 223
gbs0061	rpIB ribosomal protein L2	31-38,61-66,74-81,90-115,123-145,154-167,169-179,182- 193,200-206,238-244,267-272	F:2, I:12	235-251	7, 224
gbs0084	DNA-directed RNA polymerase, alpha subunit (rpoA)	19-25,38-54,56-64,66-72,74-92,94-100,116-129,143- 149,156-183,204-232,253-266,269-275,294-307	C:4, D:6	241-313	8, 225
gbs0107	conserved hypothetical protein	5-34,50-56,60-65,74-85,89-97,108-119,159-165,181- 199,209-225,230-240,245-251,257-262,274-282,300-305	K:2	64-75	9, 226

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogeni c region (aa)	Seq. ID (DNA, Prot.)
gbs0108	deoxyuridine 5'- triphosphate nucleotidohydrolase	5-13,16-21,27-42,45-52,58-66,74-87,108-114,119-131	E:5	39-51	10, 227
gbs0113	ribose ABC transporter	6-23,46-54,59-65,78-84,100-120,128-133,140-146,159- 165,171-183,190-204,224-232,240-248,250-259,274- 280,288-296,306-315	F:4	267-274	11, 228
gbs0123	similar to argininosuccinate synthase	5-12,15-24,26-36,42-65,68-80,82-104,111-116,125- 144,159-167,184-189,209-218,235-243,254-265,269- 283,287-300,306-316,318-336,338-352,374-392	K:17	162-174	12, 229
gbs0127	rpmV 50S ribosomal protein L28	30-42,45-54	F:11	25-37	13, 230
gbs0144	oligopeptide ABC transporter, substrate-binding	10-30,53-59,86-95,116-130,132-147,169-189,195-201,212- 221,247-256,258-265,278-283,291-298,310-316,329- 339,341-352,360-367,388-396,398-411,416-432,443- 452,460-466,506-512,515-521,542-548	E:7	419-431	14, 231
gbs0183	membrane protein, putative	4-27,30-53,60-67,70-90,92-151,159-185,189-195,198- 210,215-239	F:9	173-189	15, 232
gbs0184	oligopeptide ABC transporter, oligopeptide-binding	4-26,41-54,71-78,116-127,140-149,151-158,161-175,190- 196,201-208,220-226,240-252,266-281,298-305,308- 318,321-329,344-353,372-378,384-405,418-426,429- 442,457-463,494-505,514-522	E:6	174-188	16, 233
gbs0235	glycine betaine/carnitine/chole line ABC transporter	17-25,27-39,61-67,81-89,99-110,120-131,133-139,147- 161,167-172,179-185,192-198,203-213,226-238,243- 258,261-267,284-290,296-307,311-328,340-352,356-371	G:8, H:15	239-256	17, 234
gbs0255	conserved hypothetical protein	8-30,40-49,67-80,114-123,126-142,152-162,188-194	E:2	57-70	18, 235
gbs0260	glycyl-tRNA synthetase (beta subunit)	4-23,28-34,36-47,50-61,76-81,89-94,96-104,112-119,126- 146,155-181,195-200,208-214,220-229,244-260,263- 276,282-288,292-300,317-323,336-351,353-359,363- 375,382-399,415-432,444-455,458-471,476-481,484- 492,499-517,522-529,535-541,543-568,572-584,586- 600,607-617,626-637,656-675	F:3	282-297	19, 236
gbs0268	transketolase (tkt)	6-24,30-35,38-45,63-91,134-140,146-160,167-188,214- 220,226-234,244-250,260-270,286-301,316-329,340- 371,429-446,448-459,474-481,485-491,512-526,537- 544,550-565,573-583,596-613,621-630,652-658	E:7	87-97	20, 237
gbs0286	NH ₃ -dependent	8-20,26-48,56-67,76-86,94-109,115-121,123-129,143-	F:12, G:7, H:8	237-247	21, 238

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogeni c region (aa)	Seq. ID (DNA, Prot.)
	NAD ⁺ synthetase	160,178-186,191-198,201-208,221-236,238-244,260-268			
gbs0288	similar to penicillin- binding protein 1A	4-40,42-57,73-87,98-117,126-135,150-156,166-174,196- 217,231-236,248-258,276-284,293-301,307-313,339- 347,359-365,375-387,395-402,428-440,445-456,485- 490,497-505,535-541,547-555,610-625,648-656,665-671	D:5, K:3	448-528	22, 239
gbs0343	seryl-tRNA synthetase (serS)	10-18,39-45,51-61,80-96,98-106,110-115,158-172,174- 183,191-200,220-237,249-255,274-289,308-324,331- 341,372-381,384-397,405-414	I:3	322-338	23, 240
gbs0411	Hypothetical protein	30-36,38-56,85-108,134-147,149-160,163-183,188- 201,206-211,219-238,247-254	I:11	5-13	24, 241
gbs0428	similar to fibrinogen binding protein, putative peptidoglycan linked protein (LPXTG motif)	11-40,98-103,110-115,133-145,151-159,172-179,192- 201,204-212,222-228,235-245,258-268,283-296,298- 309,322-329,342-351,354-362,372-378,385-393,407- 418,495-516	A:7, B:2, C:31	1-148	25, 242
gbs0437	glucose-6-phosphate isomerase (pgi)	5-19,21-36,73-94,112-119,122-137,139-145,152-167,184- 190,198-204,208-224,249-265,267-281,299-304,309- 317,326-333,356-364,368-374,381-389,391-414,419- 425,430-435	I:26	113-140	26, 243
gbs0460	decarboxylase	45-54,59-67,78-91	I:7, K:11	15-23	27, 244
gbs0465	oxydoreductase	11-22,33-47,52-80,88-112,124-129	F:4	6-25	28, 245
gbs0470	similar to alpha protein, putative peptidoglycan linked protein (LPXTG motif)	26-41,51-63,80-89,93-115,150-163,187-193,220-237,240- 249,286-294,296-306,316-329,345-353,361-370,407- 425,428-437,474-482,484-494,504-517,533-541,549- 558,595-613,616-625,660-668,673-685,711-726,736- 744,749-761,787-802,812-820,825-837,863-878,888- 896,901-913,939-954,964-972,977-989,1003-1008,1016- 1022,1028-1034,1041-1053,1059-1074,1101-1122	B:4, C:2, D:8	420-511, 581- 704	29, 246
gbs0489	acetyltransferase, GNAT family	18-25,27-55,71-83,89-95,102-113,120-146,150-156,174- 185	E:32	159-175	30, 247
gbs0492	gbs0492 valyl-tRNA synthetase	24-30,38-56,63-68,87-93,136-142,153-164,183-199,213- 219,226-234,244-261,269-278,283-289,291-297,320- 328,330-336,340-346,348-356,358-366,382-387,401- 408,414-419,449-455,468-491,504-512,531-537,554- 560,597-608,621-627,632-643,650-662,667-692,703- 716,724-737,743-758,783-794,800-818,846-856	A:3	806-884	31, 248

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogeni c region (aa)	Seq. ID (DNA, Prot.)
gbs0538	amino acid ABC transporter (ATP- binding protein)	4-14,21-39,86-92,99-107,121-131,136-144,147-154,158- 166,176-185,193-199,207-222,224-230	G:1	117-136	32, 249
gbs0539	similar to phosphomannomuta se	65-76,85-97,103-109,115-121,125-146,163-169,196- 205,212-219,228-237,241-247,254-262,269-288,294- 303,305-313,328-367,395-401,405-412,418-429,437- 447,481-488,506-513,519-524,530-541,546-557	K:4	266-284	33, 250
gbs0555	beta-lactam resistance factor (fibA)	5-14,37-42,49-71,78-92,97-112,127-136,147-154,156- 163,186-198,216-225,233-243,248-253,295-307,323- 332,359-366,368-374,380-398	E:3	194-223	34, 251
gbs0579	dipeptidase	4-11,33-39,45-72,100-113,119-129,136-144,169-175,177- 185,200-208,210-219,262-276,278-297,320-326,336- 344,347-362,381-394,443-453	I:4	438-454	35, 252
gbs0580	zinc ABC transporter, zinc-binding adhesion, lipoprotein	4-29,31-52,55-61,95-110,138-158,162-171,179-187,202- 229,239-248,251-256,262-267,269-285,304-310,351- 360,362-368,381-388,415-428,435-440,448-458	I:11	161-178	36, 253
gbs0628	cell wall surface anchor family protein (IP×TG)	4-17,19-28,32-43,47-59,89-110,112-126,128-134,140- 148,152-161,169-184,191-204,230-235,255-264,328- 338,341-347,401-409,413-419,433-441,449-458,463- 468,476-482,486-492,500-506,529-545	I:9, H:1	305-381	37, 254
gbs0632	cell wall surface anchor family protein, putative (FPKTG motive)	10-29,38-45,53-61,134-145,152-160,163-170,202-208,219- 229,248-258,266-275,282-288,315-320,328-334,377- 385,392-402,418-424,447-453,460-471,479-487,491- 497,500-507,531-537,581-594,615-623,629-635,644- 652,659-666,668-678,710-717,719-728,736-741,747- 760,766-773,784-789,794-800,805-817,855-861,866-887	H:3	698-715	38, 255
gbs0634	putative surface protein	16-26,29-37,44-58,62-68,74-80,88-95,97-120,125-144,165- 196	H:1	58-72	39, 256
gbs0667	regulatory protein, putative, truncation	14-21,23-46,49-60,63-74,78-92,96-103,117-129,134- 161,169-211,217-231,239-248,252-281,292-299,313-343	I:2	243-257	40, 257
gbs0672	transcriptional regulator (GntR family)	11-27,46-52,67-72,76-84,91-112,116-153,160-175,187- 196,202-211,213-220	G:11	43-76	41, 258
gbs0687	Hypothetical protein	5-29,37-56,78-86,108-118,152-161	I:4	120-130	42, 259
gbs0785	Similar to penicillin binding protein 2B	8-14,19-41,52-66,75-82,87-92,106-121,127-133,136- 143,158-175,180-187,196-204,221-228,239-245,259- 265,291-306,318-323,328-340,352-358,361-368,375-	K:3	184-196	43, 260

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogeni c region (aa)	Seq. ID (DNA, Prot.)
		381,391-399,411-418,431-442,446-455,484-496,498- 510,527-533,541-549,558-565,575-585,587-594,644- 655,661-668,671-677			
gbs0811	beta-glucosidase	4-22,29-38,55-62,75-81,102-107,110-134,143-150,161- 167,172-179,191-215,223-233,241-247,251-264,266- 272,288-309,340-352,354-366,394-402,414-438	L:13	198-218	44, 261
gbs0828	hypothetical protein	24-44,49-70,80-91,105-118,128-136,140-154	I:3	77-92	45, 262
gbs0851	hypothetical protein	5-22,31-36,41-47,67-74,83-90,105-122,135-143,160-167	E:2	118-129	46, 263
gbs0865	hypothetical protein	4-25,33-73,81-93,96-106,114-120,122-128,130-172,179- 208,210-241,251-283,296-301	K:4	92-100	47, 264
gbs0890	exonuclease RexB (rexB)	14-24,29-38,43-50,52-72,86-97,101-107,110-125,127- 141,145-157,168-175,177-184,186-195,205-226,238- 250,255-261,284-290,293-304,307-314,316-323,325- 356,363-371,383-390,405-415,423-432,442-454,466- 485,502-511,519-527,535-556,558-565,569-574,612- 634,641-655,672-686,698-709,715-722,724-732,743- 753,760-769,783-792,818-825,830-839,842-849,884- 896,905-918,926-940,957-969,979-1007,1015-1021,1049- 1057	E:5	336-349	48, 265
gbs0896	similar to acetoin dehydrogenase	6-16,26-31,33-39,62-73,75-85,87-100,113-123,127- 152,157-164,168-181,191-198,208-214,219-226,233- 254,259-266,286-329	K:2	181-195	49, 266
gbs0898	acetoin dehydrogenase, thymine PPi dependent	4-13,32-39,53-76,99-108,110-116,124-135,137-146,149- 157,162-174,182-190,207-231,242-253,255-264,274- 283,291-323,334-345,351-360,375-388,418-425,456- 474,486-492,508-517,520-536,547-560,562-577	E:13, F:2, I:2, J:2	31-45, 419- 443	50, 267
gbs0904	phosphoglucomutase /phosphomannomuta se family protein	15-26,30-37,42-49,58-90,93-99,128-134,147-154,174- 179,190-197,199-205,221-230,262-274,277-287,300- 314,327-333,343-351,359-377,388-396,408-413,416- 425,431-446	I:3	246-256	51, 268
gbs0918	weakly similar to histidine triad protein, putative lipoprotein	5-26,34-42,47-54,61-67,71-104,107-115,131-138,144- 153,157-189,196-202,204-210,228-245,288-309,316- 329,332-341,379-386,393-399,404-412,414-421,457- 468,483-489,500-506,508-517,523-534,543-557,565- 580,587-605,609-617,619-627,631-636,640-646,662- 668,675-682,705-710,716-723,727-732,750-758,784- 789,795-809,869-874	B:5, C:11, D:36, E:3, K:3	14-138, 166- 286, 372-503, 674-696, 754- 859	52, 269

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogeni c region (aa)	Seq. ID (DNA, Prot.)
gbs0931	pyruvate kinase	5-17,32-38,40-47,80-89,113-119,125-137,140-154,157-163,170-177,185-199,213-225,228-236,242-248,277-290,292-305,323-333,347-353,364-370,385-394,399-406,423-433,441-451,462-474,477-487	F:78	116-124	53, 270
gbs0947	similar to L-Lactate Dehydrogenase	7-16,18-30,32-49,53-61,63-85,95-101,105-115,119-134,143-150,159-178,185-202,212-229,236-250,254-265,268-294	K:28	63-72	54, 271
gbs0948	DNA gyrase, A subunit (gyrA)	4-12,19-47,73-81,97-103,153-169,188-198,207-213,217-223,236-242,255-265,270-278,298-305,309-317,335-347,354-363,373-394,419-424,442-465,486-492,500-507,542-549,551-558,560-572,580-589,607-614,617-623,647-653,666-676,694-704,706-714,748-754,765-772,786-792,795-806	I:4	358-370	55, 272
gbs0969	similar to unknown plasmid protein	18-28,30-38,40-46,49-55,69-78,82-98,104-134,147-153,180-190,196-202,218-236,244-261,266-273,275-286,290-295,301-314,378-387,390-395,427-434	E:3	290-305	56, 273
gbs0971	similar to putative plasmid replication protein	4-13,20-31,39-51,54-61,69-84,87-105,117-124	K:17	108-125	57, 274
gbs0972	Hypothetical protein	24-34,43-54,56-66,68-79	E:3	50-69	58, 275
gbs0983	similar to plasmid protein	5-43,71-77,102-131,141-148,150-156,159-186,191-207,209-234,255-268,280-286,293-299,317-323,350-357,363-372,391-397,406-418,428-435,455-465,484-497,499-505,525-531,575-582,593-607,621-633,638-649,655-673,684-698,711-725,736-741,743-752,759-769,781-793,813-831,843-853,894-905,908-916,929-946,953-963,970-978,1001-1007,1011-1033	D:11, E:2, F:2, J:10, K:10, L:46, M:3	165-178, 818- 974	59, 276
gbs0986	surface antigen proteins, putative peptidoglycan bound	16-44,63-86,98-108,185-191,222-237,261-274,282-294,335-345,349-362,374-384,409-420,424-430,440-447,453-460,465-473,475-504,522-534,538-551,554-560,567-582,598-607,611-619,627-640,643-653,655-661,669-680,684-690,701-707,715-731,744-750,756-763,768-804,829-837,845-853,855-879,884-890,910-928	B:3, C:12, D:2, E:3, F:20, H:3, I:3, J:5, M:2	77-90, 144- 212, 279-355, 434-536, 782- 810, 875-902	60, 277
gbs0988	similar to plasmid surface exclusion protein, putative peptidoglycan bound	4-22,29-41,45-51,53-66,70-77,86-95,98-104,106-124,129-135,142-151,153-161,169-176,228-251,284-299,331-337,339-370,380-387,393-398,406-411,423-433,440-452,461-469,488-498,501-516,523-530,532-559,562-	J:2	212-227	61, 278

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogeni c region (aa)	Seq. ID (DNA, Prot.)
	protein (LPXTG motif)	567,570-602,612-628,630-645,649-659,666-672,677- 696,714-723,727-747			
gbs0991	ATP-dependent Clp protease, ATP- binding subunit ClpA	4-9,17-31,35-41,56-61,66-75,81-87,90-124,133-138,149- 163,173-192,213-219,221-262,265-275,277-282,292- 298,301-307,333-346,353-363,371-378,419-430,435- 448,456-469,551-570,583-599,603-612	F:15	275-291	62, 279
gbs0993	similar to plasmid proteins	28-34,53-58,72-81,100-128,145-154,159-168,172-189,217- 225,227-249,256-263,299-309,322-330,361-379,381- 388,392-401,404-417,425-436,440-446,451-464,469- 487,502-511,543-551,559-564,595-601,606-612,615- 626,633-642,644-650,664-670,674-684,692-701,715- 723,726-734,749-756,763-771,781-787,810-843,860- 869,882-889,907-917,931-936,941-948,951-958,964- 971,976-993,1039-1049,1051-1065,1092-1121,1126- 1132,1145-1151,1158-1173,1181-1192,1194-1208,1218- 1223,1229-1243,1249-1254,1265-1279,1287-1297,1303- 1320,1334-1341,1343-1358,1372-1382,1406-1417,1419- 1425,1428-1434,1441-1448,1460-1473,1494-1504,1509- 1514,1529-1550	B:2, F:2, J:4, K:2, M:7	654-669, 1400-1483	63, 280
gbs0995	hypothetical protein	10-16,20-25,58-65,97-109,118-132,134-146,148-155,186- 195,226-233,244-262,275-284,295-310,317-322,330- 339,345-351,366-375,392-403,408-415,423-430,435- 444,446-457,467-479,486-499,503-510,525-537,540- 585,602-612,614-623,625-634,639-645,650-669,700- 707,717-724,727-739	H:3, I:39, J:3, M:3	205-230, 733- 754	64, 281
gbs0997	hypothetical protein	5-22,37-43,72-81,105-113,128-133,148-160,188-194,204- 230,238-245,251-257	D:2, F:52	194-213	65, 282
gbs0998	hypothetical protein	16-21,35-41,56-72,74-92,103-109	I:2	62-68	66, 283
gbs1001	hypothetical protein	4-15,17-82,90-104,107-159,163-170,188-221,234-245,252- 265	G:8	220-235	67, 284
gbs1015	hypothetical protein	16-22,36-46,61-75,92-107,113-121,139-145,148-160	K:17	30-42	68, 285
gbs1035	conserved hypothetical protein	4-12,20-26,43-49,55-62,66-78,121-127,135-141,146- 161,164-170,178-189,196-205,233-238,269-279,288- 318,325-332,381-386,400-407	E:3	328-346	69, 286
gbs1041	hypothetical protein	5-12,31-49,57-63,69-79,89-97,99-114,116-127,134- 142,147-154,160-173,185-193,199-204,211-222,229- 236,243-249,256-274	L:2	58-68	70, 287

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogeni c region (aa)	Seq. ID (DNA, Prot.)
gbs1066	hypothetical protein	10-20,28-34,39-53,68-79,84-90,99-106	K:2	73-79	71, 288
gbs1087	FbsA	14-37,45-50,61-66,77-82,93-98,109-114,125-130,141-146,157-162,173-178,189-194,205-210,221-226,237-242,253-258,269-274,285-290,301-306,316-332,349-359,371-378,385-406	A:7, B:2, C:4, E:277, G:523, J:25	34-307, 312-385	72, 289
gbs1103	ABC transporter (ATP-binding protein)	4-10,17-38,50-85,93-99,109-116,128-185,189-197,199-210,223-256,263-287,289-312,327-337,371-386,389-394,406-419,424-432,438-450,458-463,475-502,507-513,519-526,535-542,550-567	L:5	361-376	73, 290
gbs1116	xanthine permease (pbuX)	10-39,42-93,100-144,155-176,178-224,230-244,246-255,273-282,292-301,308-325,332-351,356-361,368-379,386-393,400-421	I:48	138-155	74, 291
gbs1126	similar to plasmid unknown protein	5-11,17-34,40-45,50-55,72-80,101-123,145-151,164-172,182-187,189-195,208-218,220-241,243-252,255-270,325-331,365-371,391-398,402-418,422-428,430-435,443-452,463-469,476-484,486-494,503-509,529-553,560-565,570-590,608-614,619-627,654-661,744-750,772-780,784-790,806-816,836-853,876-885,912-918,926-933,961-975,980-987,996-1006,1016-1028,1043-1053,1057-1062	E:2, K:3	994-1003, 1033-1056	75, 292
gbs1143	putative peptidoglycan linked protein (LPXTG)	17-45,64-71,73-81,99-109,186-192,223-238,262-275,283-295,336-346,350-363,375-385,410-421,425-431,441-448,454-463,468-474,476-512,523-537,539-552,568-583,599-608,612-620,628-641,644-654,656-662,670-681,685-695,702-708,716-723,725-735,757-764,769-798,800-806,808-816,826-840,846-854,856-862,874-881,885-902,907-928	C:3, D:2, F:15, J:3	274-350, 443-513	76, 293
gbs1145	surface exclusion protein Sec10	4-22,29-41,45-51,53-61,70-76,85-92,99-104,111-122,134-140,142-154,163-174,224-232,255-265,273-279,283-297,330-335,337-348,356-367,373-385,391-396,421-431,442-455,475-485,493-505,526-538,544-561,587-599,605-620,622-651,662-670,675-681,687-692,697-712,714-735	C:2	252-262	77, 294
gbs1158	Similar to oxidoreductase	4-12,15-35,40-46,50-59,67-94,110-128,143-169,182-188,207-215,218-228,238-250	K:2	74-90	78, 295
gbs1165	cysteine desulphurase (iscS-1)	9-18,42-58,78-85,88-95,97-106,115-122,128-134,140-145,154-181,186-202,204-223,261-267,269-278,284-	F:5	12-29	79, 296

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogeni c region (aa)	Seq. ID (DNA, Prot.)
		293,300-336,358-368			
gbs1195	staphylokinase and streptokinase	7-34,46-53,62-72,82-88,100-105,111-117,132-137,144- 160,166-180,183-189,209-221,231-236,246-253,268- 282,286-293,323-336,364-372,378-392,422-433	B:3, C:2, D:2, G:3, H:8	388-405	80, 297
gbs1209	ATP-dependent DNA helicase PcrA	21-27,34-50,72-77,80-95,164-177,192-198,202-220,226- 236,239-247,270-279,285-292,315-320,327-334,348- 355,364-371,388-397,453-476,488-497,534-545,556- 576,582-588,601-607,609-616,642-662,674-681,687- 697,709-715,721-727,741-755	C:3, I:5	621-739	81, 298
gbs1214	conserved hypothetical protein	4-14,16-77,79-109	B:2	25-99	82, 299
gbs1242	CpsG, beta-1,4- galactosyltransferase	4-9,17-23,30-37,44-55,65-72,77-93,102-121,123-132,146- 153	L:24	17-29	83, 300
gbs1260	ABC transporter, ATP-binding protein	4-18,25-41,52-60,83-92,104-112,117-123,149-155,159- 167,170-192,201-210,220-227,245-250	I:17	124-137	84, 301
gbs1270	gbs1270 hyaluronate lyase	8-25,50-55,89-95,138-143,148-153,159-169,173-179,223- 238,262-268,288-295,297-308,325-335,403-409,411- 417,432-446,463-475,492-501,524-530,542-548,561- 574,576-593,604-609,612-622,637-654,665-672,678- 685,720-725,731-739,762-767,777-783,820-838,851- 865,901-908,913-920,958-970,1000-1006,1009-1015,1020- 1026,1043-1052,1055-1061	C:19, D:5, L:19	1-128, 252- 341, 771-793, 1043-1058	85, 302
gbs1305	hypothetical protein	16-26,33-46	I:2	64-76	86, 303
gbs1306	Laminin binding protein	4-27,69-77,79-101,117-123,126-142,155-161,171-186,200- 206,213-231,233-244,267-273,313-329,335-344,347- 370,374-379,399-408,422-443,445-453,461-468,476- 482,518-534,544-553,556-567,578-595,601-620,626- 636,646-658,666-681,715-721,762-768,778-785,789- 803,809-819	A:6, B:7, C:17, D:72, E:8, F:91, G:2, H:4, I:26, J:3, K:14	22-108, 153- 318, 391-527, 638-757	87, 304
gbs1307	Lmb, laminin- binding surface protein	6-21,32-43,62-92,104-123,135-141,145-152,199-216,218- 226,237-247,260-269,274-283,297-303	A:2, D:3	1-72, 127-211	88, 305
gbs1308	C5a peptidase, authentic frameshift	6-26,50-56,83-89,108-114,123-131,172-181,194-200,221- 238,241-247,251-259,263-271,284-292,304-319,321- 335,353-358,384-391,408-417,424-430,442-448,459- 466,487-500,514-528,541-556,572-578,595-601,605- 613,620-631,635-648,660-670,673-679,686-693,702-	B:4, C:15, D:70, E:18, F:26, G:5, H:4, J:2, K:40	1-213, 269- 592, 992-1120	89, 306

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogeni c region (aa)	Seq. ID (DNA, Prot.)
		708,716-725,730-735,749-755,770-777,805-811,831- 837,843-851,854-860,863-869,895-901,904-914,922- 929,933-938,947-952,956-963,1000-1005,1008-1014,1021- 1030,1097-1103,1120-1130,1132-1140			
gbs1309	hypothetical protein	9-16,33-39,47-59,65-79,81-95,103-108,115-123,138- 148,163-171,176-185,191-196,205-211,213-221,224- 256,261-276,294-302,357-363,384-390	E:2, F:4, H:2, J:2	95-111, 161- 189	90, 307
gbs1311	transposase, C- terminal part	21-27,35-45,70-76,92-105,129-143,145-155,161-166,170- 191,204-211,214-231,234-246,249-255,259-275	F:3	1-18	91, 308
gbs1321	hypothetical protein	21-35,45-53,56-64,69-97	F:7	1-16	92, 309
gbs1352	putative helicase and methylase	25-33,41-47,61-68,86-101,106-114,116-129,134-142,144- 156,163-176,181-190,228-251,255-261,276-292,295- 305,334-357,368-380,395-410,424-429,454-460,469- 482,510-516,518-527,531-546,558-570,579-606,628- 636,638-645,651-656,668-674,691-698,717-734,742- 754,765-770,792-797,827-835,847-859,874-881,903- 909,926-933,942-961,964-977,989-1004,1010-1028,1031- 1047,1057-1075,1081-1095,1108-1117,1138-1144,1182- 1189,1193-1206,1220-1229,1239-1246,1257-1267,1271- 1279,1284-1301,1312-1320,1329-1335,1341-1347,1358- 1371,1399-1404,1417-1426,1458-1463,1468-1476,1478- 1485,1493-1506,1535-1541,1559-1574,1583-1590,1595- 1601,1603-1611,1622-1628,1634-1644,1671-1685,1689- 1696,1715-1720,1734-1746,1766-1775,1801-1806,1838- 1844,1858-1871,1910-1917,1948-1955,1960-1974,2000- 2015,2019-2036,2041-2063	E:3, H:2, M:4	748-847, 1381-1391	93, 310
gbs1356	Putative peptidoglycan linked protein (LPXTG motif) - Agglutinin receptor	5-12,18-24,27-53,56-63,96-113,119-124,131-136,157- 163,203-209,215-223,233-246,264-273,311-316,380- 389,393-399,425-433,445-450,457-462,464-470,475- 482,507-513,527-535,542-548,550-565,591-602,607- 613,627-642,644-664,673-712,714-732,739-764,769- 782,812-818,826-838,848-854,860-871,892-906,930- 938,940-954,957-973,990-998,1002-1021,1024-1033,1037- 1042,1050-1060,1077-1083,1085-1092,1100-1129,1144- 1161,1169-1175,1178-1189,1192-1198,1201-1207,1211- 1221,1229-1239,1250-1270,1278-1292,1294-1300,1314- 1335,1344-1352,1360-1374,1394-1405,1407-1414,1416- 1424,1432-1452,1456-1462,1474-1497,1500-1510,1516-	C:5, D:62, I:22	187-273, 306- 441	94, 311

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogeni c region (aa)	Seq. ID (DNA, Prot.)
		1522,1534-1542,1550-1559,1584-1603,1608-1627			
gbs1376	similar to ATP- dependent Clp proteinase (ATP- binding subunit), ClpL	70-80,90-97,118-125,128-140,142-148,154-162,189- 202,214-222,224-232,254-260,275-313,317-332,355- 360,392-398,425-432,448-456,464-470,476-482,491- 505,521-528,533-546,560-567,592-597,605-614,618- 626,637-644,646-653,660-666,677-691	K:4	207-227	95, 312
gbs1377	similar to homocysteine S- methyltransferase	5-19,26-34,37-55,57-66,69-83,86-102,115-134,138- 143,154-172,178-195,209-246,251-257,290-302,306-311	M:2	256-266	96, 313
gbs1386	hydroxy-3- methylglutaryl- coenzyme A synthase	10-20,22-28,35-57,72-79,87-103,108-128,130-144,158- 171,190-198,225-242,274-291,301-315,317-324,374-385	G:2	353-365	97, 314
gbs1390	hypothetical protein	4-9,17-30,34-54,59-66,73-94,118-130,135-150,158- 171,189-198,219-239,269-275,283-301	E:3, K:4	89-106, 176- 193	98, 315
gbs1391	hypothetical protein	14-20,22-74,77-86,89-99,104-109,126-135,154-165,181- 195,197-212,216-224,264-275	E:3	107-118	99, 316
gbs1403	similar to 5'- nucleotidase, putative peptidoglycan bound protein (LPXTN)	4-18,21-38,63-72,101-109,156-162,165-179,183-192,195- 210,212-218,230-239,241-256,278-290,299-311,313- 322,332-341,348-366,386-401,420-426,435-450,455- 460,468-479,491-498,510-518,532-538,545-552,557- 563,567-573,586-595,599-609,620-626,628-636,652- 657,665-681	A:3, C:12, D:4, J:2	1-198	100, 317
gbs1408	Similar to ABC transporter (ATP- binding protein)	4-10,16-38,51-68,73-79,94-115,120-125,132-178,201- 208,216-223,238-266,269-295,297-304,337-342,347- 356,374-401,403-422,440-447,478-504,510-516,519- 530,537-544	D:2, K:4	191-206	101, 318
gbs1420	similar to cell wall proteins, putative peptidoglycan linked protein (LPXTG motif)	12-40,42-48,66-71,77-86,95-102,113-120,129-137,141- 148,155-174,208-214,218-225,234-240,256-267,275- 283,300-306,313-321,343-350,359-367,370-383,398- 405,432-439,443-461,492-508,516-526,528-535	C:3, D:4	370-478	102, 319
gbs1429	hypothetical protein	6-14,20-37,56-62,90-95,97-113,118-125,140-145,161- 170,183-202,237-244,275-284,286-305,309-316,333- 359,373-401,405-412	B:2, C:2	176-187	103, 320
gbs1442	hypothetical thiamine biosynthesis protein, ThiI	33-44,50-55,59-80,86-101,129-139,147-153,157-163,171- 176,189-201,203-224,239-245,257-262,281-287,290- 297,304-320,322-331,334-350,372-390,396-401	L:28	71-88, 353- 372	104, 321

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogeni c region (aa)	Seq. ID (DNA, Prot.)
gbs1452	rplT 50S ribosomal protein L20	5-11,15-24,26-33,40-47,75-88,95-103,105-112	E:2	17-30	105, 322
gbs1464	ferrichrome ABC transporter (permease)	5-11,16-39,46-54,62-82,100-107,111-124,126-150,154- 165,167-183,204-238,245-295,301-313,316-335	F:4	8-16	106, 323
gbs1470	conserved hypothetical protein	4-19,34-48,69-74,79-107,115-127,129-135,143-153,160- 169,171-182	I:4	142-153	107, 324
gbs1528	conserved hypothetical protein	4-30,65-74,82-106,110-120,124-132,135-140,146-175,179- 184,190-196,217-223,228-233,250-267,275-292,303- 315,322-332	I:7	174-186	108, 325
gbs1529	Putative peptidoglycan bound protein (LPXTG motif)	9-16,29-41,47-57,68-84,87-109,113-119,162-180,186- 193,195-201,203-208,218-230,234-243,265-271,281- 292,305-312,323-332,341-347,349-363,368-374,383- 390,396-410,434-440,446-452,455-464,466-473,515- 522,529-542,565-570,589-600,602-613,618-623,637- 644,1019-1027,1238-1244,1258-1264,1268-1276,1281- 1292,1296-1302	C:2	883-936	109, 326
gbs1531	UvrB excinuclease ABC chain B	10-17,23-32,39-44,54-72,75-81,88-111,138-154,160- 167,178-185,201-210,236-252,327-334,336-342,366- 376,388-400,410-430,472-482,493-526,552-558,586- 592,598-603,612-621,630-635,641-660	M:2	384-393	110, 327
gbs1533	glutamine ABC transporter, glutamine-binding protein	4-22,24-39,50-59,73-84,100-105,111-117,130-138,155- 161,173-178,182-189,205-215,266-284,308-313,321- 328,330-337,346-363,368-374,388-395,397-405,426- 434,453-459,482-492,501-507,509-515,518-523,527- 544,559-590,598-612,614-629,646-659,663-684,686- 694,698-721	I:4	445-461	111, 328
gbs1536	hypothetical protein	14-22,27-33	E:10	3-17	112, 329
gbs1542	oxidoreductase, aldo/keto reductase family	29-41,66-73,81-87,90-108,140-146,150-159,165-184,186- 196,216-226,230-238,247-253,261-269	I:13	126-140	113, 330
gbs1547	small protein, SmpB	5-12,16-25,27-33,36-45,60-68,83-88,103-126	L:11	86-101	114, 331
gbs1565	hypothetical protein	14-23,36-47,56-66,84-89,94-105,111-127,140-153,160- 174,176-183,189-203,219-225,231-237,250-257	F:2, J:2, K:8, L:21	194-227	115, 332
gbs1586	peptidyl-prolyl cis- trans isomerase, cyclophilin-type	4-25,54-60,64-71,73-82,89-106,117-124,157-169,183- 188,199-210,221-232,236-244,255-264	E:3	58-98	116, 333

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogeni c region (aa)	Seq. ID (DNA, Prot.)
gbs1591	5-methylthioadenosine nucleosidase/S- adenosylhomocysteine nucleosidase (pfs)	13-19,26-36,41-53,55-71,77-84,86-108,114-135,157- 172,177-183,187-194,208-213,218-226	I:18, L:2	110-125, 156- 170	117, 334
gbs1632	similar to branched- chain amino acid ABC transporter, amino acid-binding protein	5-24,63-69,77-85,94-112,120-137,140-146,152-159,166- 172,179-187,193-199,206-212,222-228,234-240,244- 252,257-264,270-289,298-309,316-328,337-348,363-375	B:2, E:4, I:3	1-56, 340-352	118, 335
gbs1638	amino acid permease	18-39,42-71,78-120,124-144,152-173,179-189,199- 209,213-222,228-258,269-304,329-361,364-372,374- 389,396-441	E:8, G:9, H:9	313-327	119, 336
gbs1662	conserved hypothetical protein	19-25,91-98,108-120,156-162,168-174,191-204,211- 216,232-266,272-278,286-308,316-321,327-333,344- 355,358-364,384-391,395-428,464-476,487-495,497- 511,544-561,563-573,575-582,588-594	E:3, H:2	10-25, 322- 338	120, 337
gbs1666	SWI/SNF family helicase	14-26,32-49,51-57,59-72,80-91,102-112,119-125,147- 161,164-173,175-183,188-213,217-222,246-254,260- 276,282-303,308-318,321-328,333-350,352-359,371- 378,392-401,407-414,416-443,448-463,471-484,490- 497,501-514,519-527,539-551,557-570,578-590,592- 598,600-610,618-629,633-647,654-667,676-689,702- 709,718-726,728-737,741-760,764-780,786-795,808- 826,836-842,845-852,865-874,881-887,931-945,949- 957,968-974,979-986,1003-1009,1023-1029	F:4	90-103	121, 338
gbs1673	conserved hypothetical protein	11-16,37-56,60-66,69-77,80-88,93-106,117-139,166-171	E:2	72-90	122, 339
gbs1695	dihydroxyacetone kinase family protein	59-84,123-133,145-150,161-167,178-189	I:8	115-128	123, 340
gbs1754	excinuclease ABC, A subunit (uvrA)	15-33,39-46,52-64,74-87,108-124,127-144,150-156,173- 179,184-194,201-208,219-236,243-269,272-295,302- 309,343-349,356-361,370-379,405-411,414-423,430- 451,457-464,466-475,477-483,496-502,507-522,541- 548,557-563,571-577,579-585,590-605,626-642,650- 662,671-691,704-710,751-769,775-781,786-791,794- 829,851-858,868-878,884-904,913-919,931-939	I:2	132-142	124, 341
gbs1760	Similar to A/G- specific adenine	33-58,64-71,74-80,83-88,96-120,122-139,146-157,167- 177,207-213,220-225,236-242,264-279,300-305,326-	K:8	97-115, 199- 211	125, 342

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogeni c region (aa)	Seq. ID (DNA, Prot.)
	glycosylase	336,340-347,350-360			
gbs1777	glycerol uptake facilitator protein, putative	4-26,43-57,70-99,102-117,121-133,142-148,151-168,170- 183,192-220,235-249,258-279	E:4	30-41	126, 343
gbs1783	polyprenyl synthetase family protein	34-42,48-58,70-94,110-130,154-160,164-172,178-183,195- 203,211-222,229-250,256-261,274-284,286-292,312-323	I:3	222-233	127, 344
gbs1784	ABC transporter, ATP-binding protein CydC	4-9,15-36,38-45,49-74,78-88,100-112,136-191,211- 220,226-233,239-246,254-274,287-307,316-322,342- 353,356-366,373-378,384-393,405-431,449-457,459- 468,487-511,515-524,529-541,544-552,562-568,571-576	C:2, D:2	208-280	128, 345
gbs1790	hypothetical protein	10-27,31-37,39-54,71-108,124-143	A:23, C:6	2-107	129, 346
gbs1805	Similar to secreted unknown protein	16-27,38-57,64-70,90-102,104-113,116-137,160-166	A:197, C:2	1-80	130, 347
gbs1816	HD domain protein	13-21,31-36,56-67,127-136,153-171,173-180,184-200,214- 222,225-231,239-263,267-273	F:8	135-159	131, 348
gbs1821	Similar to 23S ribosomal RNA methyltransferase	12-27,31-51,68-74,77-87,94-101,108-114,117-123,127- 134,138-168,173-196,201-207,212-217,227-237,247- 257,264-280	K:5	205-223	132, 349
gbs1823	triad family protein	17-22,25-54,70-76,92-100	G:6, H:3	98-110	133, 350
gbs1834	two-component sensor histidine kinase	7-29,40-50,60-67,87-96,105-111,119-164,172-199,206- 212,220-227,237-259,272-279,282-293,295-309,313- 319,321-328,345-363,376-386	E:3, F:6	159-176	134, 351
gbs1842	transcriptional antiterminator, BglG family	4-19,24-30,36-43,50-68,71-89,93-106,141-152,154- 172,179-197,199-215,229-239,246-252,255-263,281- 298,319-325,329-356,358-368,374-390,397-409,420- 429,432-444,450-456,459-475,483-494,496-502,520- 528,532-556	I:19	362-377	135, 352
gbs1850	hypothetical transaldolase	18-25,40-62,77-85,91-97,105-116,123-133,139-184,189- 197	G:2	122-140	136, 353
gbs1869	phosphoglycerate kinase	4-49,52-58,62-70,79-105,109-133,142-150,163-168,206- 214,220-228,233-240,243-254,274-281,303-311,327- 338,357-373,378-396,403-413,420-436,441-453,461- 467,475-481,484-498,506-512,514-521,523-529,562- 579,589-595,598-603,615-648,714-722,728-742,749- 758,777-792,795-807	L:9	643-658	137, 354
gbs1875	alkyl hydroperoxide	8-27,37-48,51-56,72-79,87-106,120-138,140-147,167-	F:3	456-470	138, 355

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogeni c region (aa)	Seq. ID (DNA, Prot.)
	reductase (large subunit) and NADH dehydrogenase	176,187-197,205-216,222-229,234-239,243-249,277- 288,292-315,334-343,347-353,363-391,398-404,430- 447,461-467,478-492,498-507			
gbs1879	endopeptidase O (pepO)	5-12,18-24,59-69,80-93,95-109,119-125,130-137,139- 147,158-163,168-176,182-202,206-215,222-239,241- 249,267-277,291-298,311-318,321-327,338-344,348- 355,373-386,393-406,411-417,434-443,446-465,473- 484,514-521,532-553,584-594	I:26	221-237	139, 356
gbs1893	2-keto-3- deoxygluconate kinase	4-14,27-34,50-58,63-72,79-106,109-114,121-142,146- 154,161-167,169-175,178-201,223-238,249-254,259- 264,278-292,294-312,319-330	F:8, K:9	167-191	140, 357
gbs1899	N-acetylmuramoyl- L-alanine amidase, family 4 protein	7-28,36-42,50-61,63-80,122-152,161-174,176-191	B:2, C:2, E:3	140-190	141, 358
gbs1907	citrate carrier protein, CCS family	20-57,59-65,70-78,86-102,119-133,142-161,163-173,177- 188,192-202,204-220,222-236,240-253,279-319,326- 331,337-383,390-399,406-412,420-427,431-438	I:2	381-395	142, 359
gbs1924	similar to pneumococcal histidine triad protein B precursor (C-terminal part)	13-18,28-34,37-43,50-59,75-81,83-97,105-121,139- 147,200-206,209-227,231-247,260-271,318-327,366- 381,388-394,399-406	K:3	182-201	143, 360
gbs1925	similar to pneumococcal histidine triad protein B precursor (N-terminal part)	6-29,37-43,51-56,70-77,82-102,110-119,127-143,178- 190,201-209,216-243,261-269,281-292,305-313,327- 339,341-354,356-373,391-397,423-429,438-445,450-478	A:2, B:5, C:12, D:57	21-314	144, 361
gbs1962	conserved hypothetical protein	4-12,15-21,32-41,59-76,80-89,96-104	E:3	90-103	145, 362
gbs2008	similar to C5A peptidase, putative peptidoglycan linked protein (LPXTG motif)	9-28,30-41,44-54,69-74,77-82,90-97,104-123,125-135,149- 155,164-173,177-184,217-226,230-235,238-244,258- 272,282-297,300-305,309-315,317-322,327-336,348- 362,368-374,380-387,400-411,414-424,451-458,460- 466,483-494,497-503,506-511,521-528,540-553,569- 587,598-606,628-642,661-681,688-700,718-733,740- 749,752-764,769-783,823-834,848-854,862-872,878- 884,886-898,915-920,938-951,954-961,963-972,982-	A:253, B:2, C:3, D:6, H:2	3-82, 509-576	146, 363

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogeni c region (aa)	Seq. ID (DNA, Prot.)
		989,996-1003,1010-1016,1021-1032,1038-1044,1047-1057,1060-1070,1079-1088,1094-1102,1117-1127,1129-1135,1142-1153,1158-1204,1212-1229,1234-1263,1269-1277,1308-1313,1327-1338,1344-1376,1400-1415,1436-1443,1448-1458,1497-1504,1511-1522,1544-1566			
gbs2018	putative peptidoglycan linked protein (LPXTG motif)	8-36,40-64,71-79,88-94,102-109,118-127,138-148,151-159,163-174,192-198,200-206,220-233,268-273,290-301,304-309,316-323,331-349,378-391,414-420,427-437,455-475,494-510,541-547,549-555,616-640	A:132, B:6, C:13, D63, E:15, H:2, J:9, K:13	1-60, 55-139, 212-308, 386- 458, 458-624	147, 364
gbs2029	hypothetical protein	16-31,35-42,70-77,91-101,120-130,132-140,143-153,185-190,195-202,215-222,228-238,241-251,257-264,268-277,288-302,312-324,326-333,341-348,364-382,415-429,438-454,458-466,491-499,501-521	G:8	273-281	148, 365
gbs2042	hypothetical protein	8-14,32-57,74-149,155-177,179-212,221-266,271-296,304-324,329-346,349-359,368-401,413-419,426-454,465-478,493-510	L:11	466-490	149, 366
gbs2054	DNA mismatch repair protein HexA	22-28,33-51,64-89,96-119,126-132,138-146,152-159,161-169,172-179,193-198,205-211,221-231,235-254,273-280,297-303,312-320,328-346,351-373,378-384,391-398,448-454,460-468,470-481,516-558,574-593,597-602,613-623,626-646,649-656,668-673,675-683,696-708,715-722,724-739,745-751,759-777,780-804,816-822	E:8	102-113	150, 367
gbs2058	hypothetical protein	12-28,41-91,98-107,112-120,125-131,151-193,215-221,240-250,263-280	L:3	128-138	151, 368
gbs2060	aspartyl-tRNA synthetase (aspS)	16-24,32-38,46-62,68-81,90-105,127-133,144-150,160-166,178-184,186-202,210-219,232-240,252-258,264-273,293-324,337-344,349-357,360-369,385-398,410-416,419-427,441-449,458-476,508-515,523-539,544-549,562-569,571-579	E:3, L:12	96-109, 127- 139	152, 369
gbs2075	hypothetical protein	19-25,28-34,56-61,85-97,110-116	M:2	39-53	153, 370
gbs2106	protein of unknown function/lipoprotein, putative	4-37,41-50,62-72,91-97,99-109,114-125,136-141,149-158,160-166,201-215	A:5, B:6, C:4, D:14, E:11, I:8, K:23	27-225	154, 371
gbs2118	similar to inosine monophosphate dehydrogenase	15-31,44-51,96-105,122-130,149-157,162-168,178-183,185-192,198-204,206-213,221-234,239-245,248-255,257-266,289-335,349-357,415-422,425-441,448-454,462-468	K:17	463-481	155, 372

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogeni c region (aa)	Seq. ID (DNA, Prot.)
gbs2131	ABC transporter, permease protein, putative	5-31,39-55,63-72,76-99,106-155,160-177,179-199,207- 217,223-240,245-255,261-267,294-316,321-343,354- 378,382-452,477-488,529-536,555-569,584-591,593- 612,620-627,632-640,647-654,671-680,698-704,723- 730,732-750,769-775,781-788,822-852	I:2	505-525	156, 373
ARF0112	Hypothetical protein	none	F:6	3-18	157, 374
ARF0147	Hypothetical protein	4-14	E:3, I:3	12-24	158, 375
ARF0532	Hypothetical protein	4-11,22-30	F:10	12-25	159, 376
ARF0534	Hypothetical protein	5-12	E:2, G:2	4-18	160, 377
ARF0557	Hypothetical protein	4-28	E:2, G:6, H:4	7-14	161, 378
ARF0862	Hypothetical protein	6-16	G:7, H:4	8-16	162, 379
ARF0891	Hypothetical protein	4-15,18-33	K:6	24-36	163, 380
ARF0895	Hypothetical protein	4-10,16-21	I:21	20-31	164, 381
ARF0943	Hypothetical protein	none	C:2, K:9	6-19	165, 382
ARF0973	Hypothetical protein	11-18	D:2, G:3, H:8, I:2, K:2	3-10	166, 383
ARF0999	Hypothetical protein	13-24	B:4, K:3	3-15	167, 384
ARF1010	Hypothetical protein	15-27	K:2	7-16	168, 385
ARF1230	Hypothetical protein	11-16	K:11	1-15	169, 386
ARF1503	Hypothetical protein	4-16	E:13	9-21	170, 387
ARF1556	Hypothetical protein	4-24,40-48,54-67	F:2	22-39	171, 388
ARF1585	Hypothetical protein	6-30,34-55,62-68,78-106	I:5, J:4	68-74	172, 389
ARF1588	Hypothetical protein	none	I:2	3-14	173, 390
ARF1735	Hypothetical protein	9-19	I:13	6-21	174, 391
ARF1809	Hypothetical protein	4-17	H:2, L:17	1-9	175, 392
ARF1826	Hypothetical protein	5-30	I:6	1-8	176, 393
ARF1882	Hypothetical protein	4-16,23-46,51-56	K:23	45-55	177, 394
ARF1996	Hypothetical protein	none	F:3	7-16	178, 395
CRF0123	Hypothetical protein	none	F:32	2-14	179, 396
CRF0180	Hypothetical protein	4-36,43-65	E:6, G:6, H:12	50-62	180, 397
CRF0208	Hypothetical protein	10-30	I:2	14-21	181, 398
CRF0258	Hypothetical protein	9-17	I:2	1-10	182, 399
CRF0285	Hypothetical protein	4-12	F:2	3-16	183, 400
CRF0311	Hypothetical protein	4-15	H:4	5-23	184, 401
CRF0446	Hypothetical protein	none	L:20	10-21	185, 402

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogeni c region (aa)	Seq. ID (DNA, Prot.)
CRF0455	Hypothetical protein	none	F:5	6-16	186, 403
CRF0491	Hypothetical protein	4-29,31-38	G:4	2-14	187, 404
CRF0520	Hypothetical protein	4-35	H:4	33-42	188, 405
CRF0530	Hypothetical protein	none	G:13, H:8, K:3	2-17	189, 406
CRF0570	Hypothetical protein	9-18,30-35	I:2	15-33	190, 407
CRF0649	Hypothetical protein	4-9	G:8, H:6	6-12	191, 408
CRF0853	Hypothetical protein	none	I:6	3-17	192, 409
CRF0955	Hypothetical protein	12-21,37-44,52-61,72-80	E:7, L:44	38-48	193, 410
CRF0983.1	Hypothetical protein	4-10,29-44,54-61,69-78	K:59	13-27	194, 411
CRF0983.2	Hypothetical protein	13-23,36-53	L:33	2-15	195, 412
CRF1083	Hypothetical protein	4-25,28-46,56-72,81-99,120-132,134-142,154-160	F:18	129-141	196, 413
CRF1095	Hypothetical protein	4-15,24-33,35-41,64-86	L:15	21-33	197, 414
CRF1212.1	Hypothetical protein	9-15	I:5	4-13	198, 415
CRF1212.2	Hypothetical protein	4-11,13-19,34-48	L:30	15-32	199, 416
CRF1290	Hypothetical protein	4-21	I:7	11-31	200, 417
CRF1383	Hypothetical protein	23-57	K:13	38-50	201, 418
CRF1416	Hypothetical protein	4-32	E:16, J:7	3-13	202, 419
CRF1500	Hypothetical protein	4-10,13-25,32-42,56-68,72-84	E:16	26-38	203, 420
CRF1513	Hypothetical protein	4-20,31-48,52-58,65-71,80-93,99-108,114-123	I:2	37-49	204, 421
CRF1518	Hypothetical protein	6-12,14-20	F:28	3-25	205, 422
CRF1663	Hypothetical protein	14-25,27-38	F:10	5-14	206, 423
CRF1667	Hypothetical protein	4-41,57-105,109-118,123-136,144-152	G:4	86-99	207, 424
CRF1832	Hypothetical protein	None	E:5, L:8	6-19	208, 425
CRF1866	Hypothetical protein	none	G:3, H: 18	2-19	209, 426
CRF1892	Hypothetical protein	14-47	L:11	1-14	210, 427
CRF1942	Hypothetical protein	4-21,29-44	F:14	2-18	211, 428
CRF1992	Hypothetical protein	23-29	K:10	10-28	212, 429
CRF2047	Hypothetical protein	6-16,22-36	K:9	11-22	213, 430
CRF2050	Hypothetical protein	4-19,30-44	I:2	18-27	214, 431
CRF2096	Hypothetical protein	5-15,37-45,58-65	G:2	38-47	215, 432
CRF2113	Hypothetical protein	4-15,23-34	I:5	4-15	216, 433
NRF1311	transposase, C- terminal part	30-36,44-54,79-85,101-114,138-152,154-164,170-175,179- 200,213-220,223-240,243-255,258-264,268-284	F:3	10-28	217, 434

Table 1B: Immunogenic proteins identified by amino acid sequence identity with peptides identified by bacterial surface display.

S. <i>agalactiae</i> antigenic protein (new)	Identical region	Peptide sequence	Peptide name	Protein identified by BSD	Immunogeni c region (aa)	Sequenc e ID (DNA, protein)
gbs0384	210 – 226 738 – 753	MEYKGNFSQKTINRFKS QTQRSGKINTDFMRQL	gbs0995.1 gbs0995.2	gbs0995 gbs0995	210 – 226 738 – 753	435, 449
gbs0393	326 – 344 326 – 348 338 – 354 371 – 392 801 – 809 877 – 901	VKTIGYGKLTGKVNHHYVA VKTIGYGKLTGKVNHHYVANKDG VNHHYVANKDGSVTAFV AAVNQNIVFRVLTKDGRPIFEK TVIKKGTNL VTHITEKSKPVEPQKATPKAPAKGL	gbs0986.2 gbs1143.1 gbs0986.3 gbs1143.2 gbs0986.4 gbs0986.5	gbs0986 gbs1143 gbs0986 gbs1143 gbs0986 gbs0986	326 – 344 327 – 349 338 – 354 372 – 393 801 – 809 877 – 901	436, 450
gbs0396	893 – 906	RQELLTPTQLSKLQ	gbs0983.1	gbs0983	893 – 906	437, 451
gbs0407	51 – 69	VRYDKLEALVAYHGAKSAS	gbs0972.1	gbs0972	51 – 69	438, 452
gbs0408	110 – 125	HQPNRIYLTDKLVPYI	gbs0971.1	gbs0971	110 – 125	439, 453
gbs0410	291 – 305	QSIKQHDKEKLRTVL	gbs0969.1	gbs0969	291 – 305	440, 454
gbs0714	210 – 226 738 – 753	MEYKGNFSQKTINRFKS QTQRSGKINTDFMRQL	gbs0995.1 gbs0995.2	gbs0995 gbs0995	210 – 226 738 – 753	441, 455
gbs0723	326 – 344 326 – 348 338 – 354 371 – 392 801 – 809 877 – 901	VKTIGYGKLTGKVNHHYVA VKTIGYGKLTGKVNHHYVANKDG VNHHYVANKDGSVTAFV AAVNQNIVFRVLTKDGRPIFEK TVIKKGTNL VTHITEKSKPVEPQKATPKAPAKGL	gbs0986.2 gbs1143.1 gbs0986.3 gbs1143.2 gbs0986.4 gbs0986.5	gbs0986 gbs1143 gbs0986 gbs1143 gbs0986 gbs0986	326 – 344 327 – 349 338 – 354 372 – 393 801 – 809 877 – 901	442, 456
gbs0726	893 – 906	RQELLTPTQLSKLQ	gbs0983.1	gbs0983	893 – 906	443, 457
gbs0737	51 – 69	VRYDKLEALVAYHGAKSAS	gbs0972.1	gbs0972	51 – 69	444, 458
gbs0738	110 – 125	HQPNRIYLTDKLVPYI	gbs0971.1	gbs0971	110 – 125	445, 459
gbs0740	291 – 305	QSIKQHDKEKLRTVL	gbs0969.1	gbs0969	291 – 305	446, 460
gbs0897	32 – 44	EGDVLLEIMSDKT	gbs0898.1	gbs0898	32 – 44	447, 461
gbs0966	399 – 410	PGLTVEEKFTVF	gbs0144.1	gbs0144	420 – 431	448, 462

Table 2. Epitope serology with human sera

Peptides	positivity	aa from	aa to	Seq ID
gbs0012.1	++	120	143	218
gbs0012.2	+	138	161	218
gbs0012.3	+	156	179	218
gbs0016.2	+++	110	129	219
gbs0016.3	+	168	184	219
gbs0048.1	+	74	90	222
gbs0053.1	+++	759	773	223
gbs0061.1	+++	237	260	224
gbs0084.1	+	265	284	225
gbs0107.1	++	65	74	226
gbs0108.1	++	41	50	227
gbs0123.1	+	163	174	229
gbs0127.1	++	26	37	230
gbs0183.1	+	174	189	232
gbs0235.1	++	240	256	234
gbs0260.1	+	285	297	236
gbs0286.1	+	238	247	238
gbs0288.1	+	491	519	239
gbs0437.1	++	114	140	243
gbs0539.1	+	267	284	250
gbs0579.1	+	439	453	252
gbs0580.1	++	162	178	253
gbs0628.1	++	347	364	254
gbs0632.1	+++	699	715	255
gbs0634.1	+	60	71	256
gbs0667.1	++	244	257	257
gbs0672.1	+	44	63	258
gbs0672.2	+	57	76	258
gbs0785.1	+	185	196	260
gbs0851.1	+	119	129	263
gbs0896.1	++	182	195	266
gbs0898.1	++	32	44	267
gbs0898.2	+	424	442	267
gbs0904.1	+	247	256	268
gbs0918.1	++	678	694	269
gbs0918.2	+	785	805	269
gbs0918.4	+	55	77	269
gbs0918.5	+++	72	94	269
gbs0995.1	+	210	226	281
gbs1087.3	+	37	59	289
gbs1165.1	+	13	29	296
gbs1816.1	+	136	159	348
gbs1821.1	+	205	222	349
gbs1823.1	+	99	110	350
gbs1834.1	+	160	176	351
gbs1875.1	+	457	470	355
gbs1879.1	+	221	237	356
gbs1893.1	+	167	190	357
gbs1925.1	+	96	120	361
gbs2018.3	+++	399	417	364
gbs2018.4	+++	503	519	364
gbs2018.5	+++	544	563	364
gbs2106.2	+	46	68	371
gbs2106.7	+	159	183	371
gbs2106.8	+	184	198	371
gbs2118.1	++	463	481	372

Table 3: Gene distribution in *S. agalactiae* strains.

ORF	Common name	Gene distribution (present of 50)	Amino acid substitutions (in serotype 1A strain)*	Seq. ID (DNA, Prot.)
gbs0012	weakly similar to beta-lactamase	44/44	n.d.	1, 218
gbs0016	glucan-binding protein B (S.mutans)	40/44	0/224	2, 219
gbs0024	Phosphoribosylformylglycinamidine	46/46	10/228	3, 220
gbs0031	surface immunogenic protein	46/46	1/225	4, 221
gbs0048	Unknown	30/46	0/61	5, 222
gbs0053	aldehyde-alcohol dehydrogenase (adhE)	45/45	0/224	6, 223
gbs0061	rplB ribosomal protein L2	46/46	0/218	7, 224
gbs0084	DNA-directed RNA polymerase, alpha subunit (rpoA)	45/45	0/207	8, 225
gbs0107	conserved hypothetical protein	46/46	0/235	9, 226
gbs0108	deoxyuridine 5'-triphosphate nucleotidohydrolase	44/44	0/125	10, 227
gbs0113	ribose ABC transporter	44/45	0/227	11, 228
gbs0123	similar to argininosuccinate synthase	44/44	0/184	12, 229
gbs0127	rpmV 50S ribosomal protein L28	46/46	0/40	13, 230
gbs0144	oligopeptide ABC transporter, substrate- binding	45/45	0/282	14, 231
gbs0183	membrane protein, putative	44/44	0/223	15, 232
gbs0184	oligopeptide ABC transporter, oligopeptide-binding	46/46	1/203	16, 233
gbs0235	glycine betaine/carnitine/choline ABC transporter	46/46	0/219	17, 234
gbs0255	conserved hypothetical protein	46/46	0/180	18, 235
gbs0260	glycyl-tRNA synthetase (beta subunit	46/46	0/209	19, 236
gbs0268	transketolase (tkt)	46/46	0/208	20, 237
gbs0286	NH ₃ -dependent NAD ⁺ synthetase	45/45	0/191	21, 238
gbs0288	similar to penicillin-binding protein 1A	45/45	0/212	22, 239
gbs0343	seryl-tRNA synthetase (serS)	46/46	0/228	23, 240
gbs0428	similar to fibrinogen binding protein, putative peptidoglycan linked protein (LPXTG motif)	45/46	1/126	25, 242
gbs0437	glucose-6-phosphate isomerase (pgi)	45/45	0/232	26, 243
gbs0460	decarboxylase	46/46	1/81	27, 244

ORF	Common name	Gene distribution (present of 50)	Amino acid substitutions (in serotype IA strain)*	Seq. ID (DNA, Prot.)
gbs0465	oxydoreductase	46/46	0/126	28, 245
gbs0489	acetyltransferase, GNAT family	45/45	3/144	30, 247
gbs0492	gbs0492 valyl-tRNA synthetase	44/44	3/125	31, 248
gbs0538	amino acid ABC transporter (ATP-binding protein)	46/46	0/214	32, 249
gbs0539	similar to phosphomannomutase	46/46	0/244	33, 250
gbs0555	beta-lactam resistance factor (fibA)	46/46	0/218	34, 251
gbs0579	dipeptidase	46/46	0/218	35, 252
gbs0580	zinc ABC transporter, zinc-binding adhesion lipot	45/45	2/235	36, 253
gbs0628	cell wall surface anchor family protein - (IPxTG)	42/44	0/219	37, 254
gbs0632	cell wall surface anchor family protein, putative (FPKTG motive)	44/45	0/238	38, 255
gbs0667	regulatory protein, putative, truncation	44/44	0/229	40, 257
gbs0672	transcriptional regulator (GntR family)	43/43	0/203	41, 258
gbs0687	unknown proteins	45/45	0/149	42, 259
gbs0785	Similar to penicillin binding protein 2B	45/45	0/218	43, 260
gbs0828	unknown proteins	46/46	1/120	45, 262
gbs0851	hypothetical protein	46/46	0/140	46, 263
gbs0865	gbs0865 Unknown	44/44	0/241	47, 264
gbs0890	exonuclease RxB (rxB)	46/46	0/232	48, 265
gbs0896	similar to acetoin dehydrogenase	46/46	0/239	49, 266
gbs0898	acetoin dehydrogenase, thymine PPi dependent	45/45	0/180	50, 267
gbs0904	phosphoglucomutase/phosphomannomutase family prote	46/46	0/169	51, 268
gbs0918	weakly similar to histidine triad protein, putative lipoprotein	45/45	1/209	52, 269
gbs0931	pyruvate kinase	46/46	0/185	53, 270
gbs0947	similar to L-Lactate Dehydrogenase	46/46	0/233	54, 271
gbs0948	DNA gyrase, A subunit (gyrA)	44/44	0/172	55, 272
gbs1035	conserved hypothetical protein	46/46	0/210	69, 286
gbs1066	gbs1066 Unknown	17/46	2/92	71, 288
gbs1087	highly repetitive peptidoglycan bound protein (LPXTG motif)	42/45	n.d.	72, 289

ORF	Common name	Gene distribution (present of 50)	Amino acid substitutions (in serotype IA strain)*	Seq. ID (DNA, Prot.)
gbs1103	ABC transporter (ATP-binding protein)	46/46	1/165	73, 290
gbs1116	xanthine permease (pbuX)	45/45	1/170	74, 291
gbs1158	Similar to oxidoreductase	44/44	1/170	78, 295
gbs1165	cysteine desulphurase (iscS-1)	43/43	0/148#	79, 296
gbs1195	staphylokinase and streptokinase	45/45	60/142	80, 297
gbs1209	ATP-dependent DNA helicase PcrA	43/44	1/94#	81, 298
gbs1214	conserved hypothetical protein	43/46	0/97	82, 299
gbs1260	ABC transporter, ATP-binding protein	44/46	1/198	84, 301
gbs1306	Laminin binding protein (Spellerberg,B et al 1999)	45/46	0/215	87, 304
gbs1307	lmb laminin-binding surface protein	45/45	n.d.	88, 305
gbs1308	C5a peptidase, authentic frameshift	46/46	0/205	89, 306
gbs1309	hypothetical protein	44/46	0/214	90, 307
gbs1356	Putative peptidoglycan linked protein (LPXTG motif) - Agglutinin receptor	20/46	50/211#	94, 311
gbs1376	similar to ATP-dependent Clp proteinase (ATP-binding subunit), ClpL	45/45	0/197	95, 312
gbs1377	similar to homocysteine S-methyltransferase	45/45	0/55	96, 313
gbs1386	-hydroxy-3-methylglutaryl-coenzyme A synthase	44/44	0/219	97, 314
gbs1390	gbs1390 Unknown	43/43	0/198	98, 315
gbs1391	gbs1391 Unknown	44/44	0/214	99, 316
gbs1403	similar to 5'-nucleotidase, putative peptidoglycan bound protein (LPXTN)	45/45	3/189	100, 317
gbs1408	Similar to ABC transporter (ATP-binding protein)	45/45	0/205	101, 318
gbs1429	unknown proteins	46/46	1/193	103, 320
gbs1452	rplT 50S ribosomal protein L20	46/46	0/101	105, 322
gbs1464	ferrichrome ABC transporter (permease	44/44	2/232	106, 323
gbs1470	conserved hypothetical protein	46/46	2/164	107, 324
gbs1528	conserved hypothetical protein	45/45	0/213	108, 325
gbs1531	UvrB excinuclease ABC chain B	45/45	0/108	110, 327
gbs1533	glutamine ABC transporter, glutamine-binding prote	44/44	0/166	111, 328

ORF	Common name	Gene distribution (present of 50)	Amino acid substitutions (in serotype IA strain)*	Seq. ID (DNA, Prot.)
gbs1542	oxidoreductase, aldo/keto reductase family	45/45	1/219	113, 330
gbs1565	hypothetical protein	43/43	1/218	115, 332
gbs1586	peptidyl-prolyl cis-trans isomerase, cyclophilin-type	45/45	1/227	116, 333
gbs1591	5-methylthioadenosine nucleosidase/S- adenosylhomoc	45/45	0/203	117, 334
gbs1632	similar to branched-chain amino acid ABC transporter, amino acid-binding protein	45/45	0/223	118, 335
gbs1638	amino acid permease	45/45	0/100	119, 336
gbs1662	conserved hypothetical protein	45/45	0/213	120, 337
gbs1666	SWI/SNF family helicase	45/45	0/200	121, 338
gbs1673	conserved hypothetical protein	45/45	0/147	122, 339
gbs1695	dihydroxyacetone kinase family protein	43/43	1/165	123, 340
gbs1754	excinuclease ABC, A subunit (uvrA)	43/43	0/224	124, 341
gbs1760	Similar to A/G-specific adenine glycosylase	46/46	0/181	125, 342
gbs1777	glycerol uptake facilitator protein, putative	43/43	0/199	126, 343
gbs1783	polyprenyl synthetase family protein	45/45	0/217	127, 344
gbs1784	ABC transporter, ATP-binding protein CydC	45/45	1/220	128, 345
gbs1790	unknown proteins	41/43	3/75#	129, 346
gbs1805	Similar to secreted unknown proteins	45/45	0/66	130, 347
gbs1816	HD domain protein	43/43	1/176	131, 348
gbs1821	Similar to 23S ribosomal RNA methyltransferase	43/43	2/155#	132, 349
gbs1834	two-component sensor histidine kinase	44/44	0/213	134, 351
gbs1842	transcriptional antiterminator, BglG family	43/43	0/208	135, 352
gbs1850	hypothetical transaldolase	44/44	0/194	136, 353
gbs1875	alkyl hydroperoxide reductase (large subunit) and NADH dehydrogenase	46/46	0/192	138, 355
gbs1879	endopeptidase O (pepO)	43/43	0/135	139, 356
gbs1893	2-keto-3-deoxygluconate kinase	36/46	0/228	140, 357
gbs1899	N-acetylmuramoyl-L-alanine amidase, family 4 prote	43/43	0/149	141, 358
gbs1907	citrate carrier protein, CCS family	43/43	0/219	142, 359
gbs1925	similar to pneumococcal histidine triad protein B precursor (N-terminal part)	43/43	0/103	144, 361
gbs1962	conserved hypothetical protein	28/46	0/136	145, 362
gbs2008	similar to C5A peptidase, putative	43/43	n.d.	146, 363

- 86 -

ORF	Common name	Gene distribution (present of 50)	Amino acid substitutions (in serotype IA strain)*	Seq. ID (DNA, Prot.)
	peptidoglycan linked protein (LPXTG motif)			
gbs2018	putative peptidoglycan linked protein (LPXTG motif)	43/45	0/104	147, 364
gbs2029	unknown proteins	44/44	1/238	148, 365
gbs2054	DNA mismatch repair protein HexA	46/46	0/206	150, 367
gbs2060	aspartyl-tRNA synthetase (aspS)	46/46	2/211	152, 369
gbs2106	protein of unknown function/lipoprotein, putative	44/44	0/160	154, 371
gbs2118	similar to inosine monophosphate dehydrogenase	43/43	0/113	155, 372
gbs2131	ABC transporter, permease protein, putative	45/45	0/237	156, 373

Table 4. Immunogenicity of epitopes in mice

ORF	aa from	aa to	IB	Peptide ELISA	Seq ID
gbs0016	110	129	+		219
	168	184	+		
gbs0986	877	901	+		277
	333	354	+		
	326	344	+		
	801	809	+		
gbs1805	1	54		+++++	347
gbs2018	544	563	++	+++++	364
	31	51	+	+++	
	107	119	+		
	399	417	++	++++	
	503	519	+	++++	
gbs0012	120	198	++	+	218
gbs0016	20	35	+	++	219
gbs0031	118	201		++++	221
gbs0428	48	132	+	+++++	242
gbs0538	118	136	+	++++	249
gbs0580	162	178	+	+	253
gbs0628	347	364	+	+++++	254
gbs0632	699	715	+	+++++	255
gbs0672	50	76		+	258
gbs0918	785	819	+	+++++	269
	44	128	++		
gbs0971	90	128		+++++	274
gbs1087	314	384	+		289
gbs1143	327	349		+++	293
gbs1306	242	314	++	++++	304
	405	478	++		
	23	100	+		
gbs1307	129	210	++		305
gbs1309	162	188		++	307
gbs1352	750	772	++	+++++	310
gbs1632	1	56		++	335
gbs1662	322	337	+	+++++	337
gbs1673	72	90	+	+++++	339
gbs1784	374	395		+	345
gbs1816	136	159	+	++++	348
gbs1899	141	164	+		358
gbs1925	96	157	++	+	361
gbs2008	1	82		+	363
gbs2018	489	556	+	+++++	364
gbs2106	159	183		++	371
	49	133	+	+++++	

Table 5: Immunogenic proteins identified by bacterial surface display.

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
gbs0233	similar to glycine betaine/carnitine/choline ABC transporter (osmoprotectant- binding protein)	4-26, 35-41, 53-61, 73-84, 103-108, 114-120, 140-146, 156-162, 192-208, 214-219, 227-233, 239-252, 260-268, 284-297	A:5, B:9, H:3	1-48, 113-133	463, 475
gbs0419	protein of unknown function/lipoprotein	4-27, 38-44, 50-56, 59-64, 72-79, 83-89, 92-97, 108-116, 123-148, 152-167, 183-196, 200-220, 232-244, 255-261, 265-274, 282-302, 309-317	C:3, D:4, J:2, K:4	1-79, 231-302	464, 476
gbs0456	cell wall surface anchor family protein	6-28, 66-72, 85-105, 115-121, 144-151, 160-170, 176- 185, 223-230, 252-288, 296-310, 319-333, 367-374, 458- 464, 471-480, 483-488, 520-528, 530-549, 559-564, 593- 601, 606-616, 636-643, 655-662, 676-682, 684-699, 719- 726, 735-750, 757-764, 777-785, 799-810, 812-843, 846- 853, 868-873, 880-889, 891-899, 909-929, 934-940, 963- 969, 998-1004, 1007-1014, 1016-1022, 1030-1046	A:9, B:125, F:9	1-80, 808-821	465, 477
gbs0942	protein of unknown function/lipoprotein	7-24, 35-41, 75-81, 91-114, 122-132, 137-144, 148-156, 183-192, 194-200, 212-228, 233-238, 251-258, 275-295, 326-332, 337-346	A:3, B:9, C:2, J:3	1-79, 305-321	466, 478
gbs0973	gid protein (gid)	31-38, 42-52, 66-72, 86-92, 98-104, 115-122, 127-146, 154-164, 169-187, 198-212, 225-237, 255-269	D:2, G:3, H:8, I:2, K:2	13-92, 135-142	467, 479
gbs0975	Unknown protein	4-36, 39-49, 63-69, 71-77, 81-88, 123-131, 133-139, 160- 169, 174-180, 188-194, 210-217, 273-278, 289-300, 317- 334, 336-341, 383-401, 425-438	A:3, B:5, C:5, D:2, J:2	1-68, 212-270, 402-446	468, 480
gbs1038	permease, putative	21-29, 31-42, 49-63, 72-79, 81-93, 112-132, 159-165, 188-195, 197-232, 262-267, 279-286, 294-301, 318-326, 348-366, 381-405, 409-426, 436-465, 471-480, 484-492, 497-505, 521-544, 554-561, 567-577, 581-589, 601-609, 611-622, 636-651, 653-667, 669-685, 700-708, 716-722, 729-744, 749-766, 780-786, 789-811, 814-864	B:2, C:3, E:3, J:2	1-57, 84-106	469, 481
gbs1144	Unknown protein	6-24, 35-48, 57-63, 72-78, 87-92, 113-119, 123-137, 147- 153, 173-181, 212-233	C:30	1-124	470, 482
gbs1279	conserved domain protein	13-34, 62-69, 78-83, 86-91, 98-104, 107-115, 146-159, 179-188, 195-205, 209-221, 226-233, 239-253, 276-282, 284-294, 297-308, 331-354, 375-382, 388-399, 421-433,	A:44, B:2, C:4	1-84	471, 483

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		449-458, 464-469, 472-491, 508-513, 525-531, 534-550, 575-593, 601-618, 629-635, 654-661, 666-680, 706-721, 723-740, 771-805, 810-830, 845-851			
gbs1441	conserved hypothetical protein	4-32, 45-64, 73-83, 86-92, 100-111, 125-147, 157-163, 170-175, 177-188, 226-232, 245-252, 258-274, 320-335, 348-359	A:2, B:8, C:2	1-71	472, 484
gbs1677	sodium transport family protein	13-40, 43-71, 76-83, 87-101, 109-119, 125-156, 162-175, 182-219, 226-232, 240-262, 270-287, 306-318, 326-342, 344-408, 414-444, 449-456	B:3, C:2, K:5	1-51	473, 485
gbs2093	Membrane protein, putative	4-16, 18-34, 45-54, 99-108, 134-140, 203-212, 241-257, 266-274, 279-291, 308-315, 330-336, 355-370, 374-382, 402-410, 428-455, 466-472, 474-480, 531-554, 560-566, 572-580, 597-618, 632-660, 664-674, 676-685, 691-705, 708-735, 750-768	B :5, C :8, D :2	1-87, 342-480	474, 486

Table 6. Immune reactivity of epitopes within identified antigens with human sera

Peptides	Positivity	aa from	aa to	Seq ID
gbs0233.1	+	115	132	475
gbs0233.2	+	1	26	475
gbs0419.1	++	33	55	476
gbs0942.2	+++	1	25	478
gbs0973.1	+	37	61	479
gbs0975.1	+	1	24	480
gbs1038.1	+	1	23	481
gbs1144.3	++	46	60	482
gbs1279.1	+++	1	28	483
gbs1279.2	+	23	50	483
gbs1279.3	++	45	71	483
gbs1441.1	+	1	22	484
gbs1441.2	++	17	38	484
gbs1677.1	+	1	22	485
gbs1677.2	+	17	38	485
gbs2093.1	+	1	27	486
gbs2093.2	++	22	47	486
gbs2093.4	+	422	447	486

Table 7. Immunogenicity of epitopes in mice

ORF	aa from	aa to	Peptide ELISA	Seq ID
gbs0233	115	132	++++	475
	1	47	++	
gbs0419	1	55	++++	476
gbs0456	22	85	++	477
gbs0942	307	320	+	478
	1	44	++	
gbs0973	15	76	++	479
	40	92	+++	
gbs0975	1	59	++	480
	213	269	+	
	403	445	+	
gbs1038	1	56	++++	481
	85	105	+	
gbs1144	37	121	+++++	482
gbs1279	1	71	+++++	483
gbs1441	1	38	+++	484
gbs1677	1	38	+++	485
gbs2093	1	47	+++	486

References

- Altschul, S., et al. (1990). Journal of Molecular Biology **215**: 403-10.
- Balter, S. et al. In Gram positive pathogens ed. by Fischetti V.A. et al. AMS Press 2000, 154-160.
- Bennett, D., et al. (1995). J Mol Recognit **8**: 52-8.
- Brodeur, B., et al. (2000). Infect Immun **68**: 5610-8.
- Burnie, J., et al. (1998). J Antimicrob Chemother **41**: 319-22.
- Campbell, J., et al. (2000). Obstet Gynecol **96**: 498-503.
- Cheng, Q., et al. (2002). Infect Immun **70**: 6409-15.
- Clackson, T., et al. (1991). Nature **352**: 624-8.
- Devereux, J., et al. (1984). Nucleic acids research **12**: 387-95.
- Doherty, E., et al. (2001). Annu Rev Biophys Biomol Struct **30**: 457-475.
- Eisenbraun, M., et al. (1993). DNA Cell Biol **12**: 791-7.
- Etz, H., et al. (2001). J Bacteriol **183**: 6924-35.
- Farley, M. (2001). Clin Infect Dis **33**: 556-61.
- Ganz, T. (1999). Science **286**: 420-421.
- Georgiou, G. (1997). Nature Biotechnology **15**: 29-34.
- Glaser, P., et al. (2002). Mol Microbiol **45**: 1499-513.
- Hashemzadeh-Bonehi, L., et al. (1998). Mol Microbiol **30**: 676-678.
- Heinje, von G (1987) e.g. Sequence Analysis in Molecular Biology, Academic Press.
- Hemmer, B., et al. (1999). Nat Med **5**: 1375-82.
- Hoe, N., et al. (2001). J Infect Dis **183**: 633-9.
- Hornef, M., et al. (2002). Nat Immunol **3**: 1033-40.
- Jackson, L., et al. (1995). Ann Intern Med **123**: 415-20.
- Johanson, K., et al. (1995). J Biol Chem **270**: 9459-71.
- Jones, P., et al. (1986). Nature **321**: 522-5.
- Kajava, A., et al. (2000). J Bacteriol **182**: 2163-9.
- Kohler, G., et al. (1975). Nature **256**: 495-7.
- Larsson, C., et al. (1999). Vaccine **17**: 454-8.
- Lewin, A., et al. (2001). Trends Mol Med **7**: 221-8.
- Marks, J., et al. (1992). Biotechnology (N Y) **10**: 779-83.
- McCafferty, J., et al. (1990). Nature **348**: 552-4.
- Michel, J., et al. (1991). Infect Immun **59**: 2023-8.
- Navarre, W., et al. (1999). Microbiol Mol Biol Rev **63**: 174-229.
- Nizet, V. & Rubens, C.E. in Gram positive pathogens ed. by Fischetti V.A. et al. ASM Press 2000, pp 125-136.
- Okano, H., et al. (1991). J Neurochem **56**: 560-7.
- Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression; CRC Press, Boca Ration, FL (1988).
- Paoletti, L., et al. (2002). Semin Neonatol **7**: 315-23.
- Paoletti, L., et al. In Gram positive pathogens ed. by Fischetti V.A. et al. ASM Press 2000, pp 137-153.
- Phillips-Quagliata, J., et al. (2000). J Immunol **165**: 2544-55.
- Rammensee, H., et al. (1999). Immunogenetics **50**: 213-9.
- Seeger, C., et al. (1984). Proc Natl Acad Sci U S A **81**: 5849-52.
- Shibuya, A., et al. (2000). Nature Immunology **1**: 441-6.
- Skerra, A. (1994). Gene **151**: 131-5.
- Tang, D., et al. (1992). Nature **356**: 152-4.
- Tempest, P., et al. (1991). Biotechnology (N Y) **9**: 266-71.
- Tettelin, H., et al. (2002). Proc Natl Acad Sci U S A **99**: 12391-6.
- Tourdot, S., et al. (2000). Eur J Immunol **30**: 3411-21.
- Wiley, J., et al. (1987) Current Protocols in Molecular Biology.

Claims:

1. An isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence, which is selected from the group consisting of:
 - a) a nucleic acid molecule having at least 70% sequence identity to a nucleic acid molecule selected from **Seq ID No 14, 90, 157-216**,
 - b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
 - c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
 - d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b), or c)
 - e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid molecule defined in a), b), c) or d).
2. The isolated nucleic acid molecule according to claim 1, wherein the sequence identity is at least 80%, preferably at least 95%, especially 100%.
3. An isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence selected from the group consisting of
 - a) a nucleic acid molecule having 96 % or more than 96 %, preferably at least 98 %, especially 100 % sequence identity to a nucleic acid molecule selected from **Seq ID No 1, 3, 5-13, 15, 18-25, 27-31, 33-36, 39-68, 70-85, 92-100, 103-126, 128-145, 147, 149-156, 217, 435-448 and 463-474**.
 - b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
 - c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
 - d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b) or c),
 - e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).
4. An isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence selected from the group consisting of
 - a) a nucleic acid molecule having 98 % or more than 98%, especially 100 % sequence identity to a nucleic acid molecule selected from **Seq ID No 32, 86, 91, 101, 127**,
 - b) a nucleic acid molecule which is complementary to the nucleic acid of a),
 - c) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).
5. The nucleic acid molecule according to any one of the claims 1, 2, 3 or 4, wherein the nucleic acid is DNA.
6. The nucleic acid molecule according to any one of the claims 1,2, 3, 4, or 5 wherein the nucleic acid is RNA.
7. An isolated nucleic acid molecule according to any one of claims 1 to 5, wherein the nucleic acid molecule is isolated from a genomic DNA, especially from a *S. agalactiae* genomic DNA.
8. A vector comprising a nucleic acid molecule according to any one of claims 1 to 7.
9. A vector according to claim 8, wherein the vector is adapted for recombinant expression of the hyperimmune serum reactive antigens or fragment thereof encoded by the nucleic acid molecule according to any one of claims 1 to 7.

10. A host cell comprising the vector according to claim 8 or 9.
11. A hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to any one of the claims 1, 2, 5, 6 or 7 and fragments thereof, preferably the amino acid sequence is selected from the group consisting of **Seq ID No 231, 307, 374-433**.
12. A hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to any one of the claims 3, 5, 6, or 7 and fragments thereof, preferably the amino acid sueqnece is selected from the group consisting of **Seq ID No 218, 220, 222-230, 232, 235-242, 244-248, 250-253, 256-285, 287-302, 309-317, 320-343, 345-362, 364, 366-373, 434, 449-462 and 475-486**.
13. A hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to any one of the claims 4, 5, 6, or 7 and fragments thereof, preferably the amino acid sequence is selected from the group consisting of **Seq ID No 249, 303, 308, 318, 344**.
14. Fragments of hyperimmune serum-reactive antigens selected from the group consisting of peptides comprising amino acid sequences of column "predicted immunogenic aa" and "location of identified immunogenic region" of Table 1A, **especially peptides comprising amino acid 4-20, 35-44, 65-70, 73-87, 92-98, 112-137, 152-161, 177-186, 193-200, 206-213, 229-255, 282-294, 308-313, 320-326, 349-355, 373-384, 388-406, 420-425 and 115-199 of Seq ID No 218; 5-24, 35-41, 44-70, 73-89, 103-109, 127-143, 155-161, 185-190, 192-207, 212-219, 246-262, 304-336, 372-382, 384-393, 398-407, 412-418, 438-444, 1-75, 76-161 and 164-239 of Seq ID No 219; 4-10, 16-58, 60-71, 77-92, 100-126, 132-146, 149-164, 166-172, 190-209, 214-220, 223-229, 241-256, 297-312, 314-319, 337-343, 351-359, 378-387, 398-418, 421-428, 430-437, 440-448, 462-471, 510-519, 525-536, 552-559, 561-568, 573-582, 596-602, 608-630, 637-649, 651-665, 681-702, 714-732, 739-745, 757-778, 790-805, 807-815, 821-829, 836-842, 846-873, 880-903, 908-914, 916-923, 931-940, 943-948, 956-970, 975-986, 996-1015, 1031-1040, 1051-1069, 1072-1095, 1114-1119, 1130-1148, 1150-1157, 1169-1176, 1229-1238 and 802-812 of Seq ID No 220; 5-12, 14-26, 35-47, 52-67, 72-78, 83-98, 121-141, 152-159, 163-183, 186-207, 209-257, 264-277, 282-299, 301-309, 312-318, 324-339, 358-368, 372-378, 387-397, 425-431 and 46-291 of Seq ID No 221; 29-38, 44-64, 70-76, 78-87, 94-100, 102-112, 119-134, 140-149, 163-173, 178-186, 188-194, 207-234, 247-262, 269-290 and 73-92 of Seq ID No 222; 10-28, 36-63, 77-87, 103-119, 127-136, 141-169, 171-183, 195-200, 207-232, 236-246, 251-265, 268-283, 287-297, 314-322, 335-343, 354-363, 384-390, 405-411, 419-436, 443-455, 467-473, 480-513, 518-529, 550-557, 565-585, 602-608, 616-625, 632-660, 665-677, 685-701, 726-736, 738-747, 752-761, 785-796, 801-813, 838-853, 866-871 and 757-774 of Seq ID No 223; 31-38, 61-66, 74-81, 90-115, 123-145, 154-167, 169-179, 182-193, 200-206, 238-244, 267-272 and 235-251 of Seq ID No 224; 19-25, 38-54, 56-64, 66-72, 74-92, 94-100, 116-129, 143-149, 156-183, 204-232, 253-266, 269-275, 294-307 and 241-313 of Seq ID No 225; 5-34, 50-56, 60-65, 74-85, 89-97, 108-119, 159-165, 181-199, 209-225, 230-240, 245-251, 257-262, 274-282, 300-305 and 64-75 of Seq ID No 226; 5-13, 16-21, 27-42, 45-52, 58-66, 74-87, 108-114, 119-131 and 39-51 of Seq ID No 227; 6-23, 46-54, 59-65, 78-84, 100-120, 128-133, 140-146, 159-165, 171-183, 190-204, 224-232, 240-248, 250-259, 274-280, 288-296, 306-315 and 267-274 of Seq ID No 228; 5-12, 15-24, 26-36, 42-65, 68-80, 82-104, 111-116, 125-144, 159-167, 184-189, 209-218, 235-243, 254-265, 269-283, 287-300, 306-316, 318-336, 338-352, 374-392 and 162-174 of Seq ID No 229; 30-42, 45-54 and 25-37 of Seq ID No 230; 10-30, 53-59, 86-95, 116-130, 132-147, 169-189, 195-201, 212-221, 247-256, 258-265, 278-283, 291-298, 310-316, 329-339, 341-352, 360-367, 388-396, 398-411, 416-432, 443-452, 460-466, 506-512, 515-521, 542-548 and 419-431 of Seq ID No 231; 4-27, 30-53, 60-67, 70-90, 92-151, 159-185, 189-195, 198-210, 215-239 and 173-189 of Seq ID No 232; 4-26, 41-54, 71-78, 116-127, 140-149, 151-158, 161-175, 190-196, 201-208, 220-226, 240-252, 266-281, 298-305,**

308-318, 321-329, 344-353, 372-378, 384-405, 418-426, 429-442, 457-463, 494-505, 514-522 and 174-188 of **Seq ID No 233**; 17-25, 27-39, 61-67, 81-89, 99-110, 120-131, 133-139, 147-161, 167-172, 179-185, 192-198, 203-213, 226-238, 243-258, 261-267, 284-290, 296-307, 311-328, 340-352, 356-371 and 239-256 of **Seq ID No 234**; 8-30, 40-49, 67-80, 114-123, 126-142, 152-162, 188-194 and 57-70 of **Seq ID No 235**; 4-23, 28-34, 36-47, 50-61, 76-81, 89-94, 96-104, 112-119, 126-146, 155-181, 195-200, 208-214, 220-229, 244-260, 263-276, 282-288, 292-300, 317-323, 336-351, 353-359, 363-375, 382-399, 415-432, 444-455, 458-471, 476-481, 484-492, 499-517, 522-529, 535-541, 543-568, 572-584, 586-600, 607-617, 626-637, 656-675 and 282-297 of **Seq ID No 236**; 6-24, 30-35, 38-45, 63-91, 134-140, 146-160, 167-188, 214-220, 226-234, 244-250, 260-270, 286-301, 316-329, 340-371, 429-446, 448-459, 474-481, 485-491, 512-526, 537-544, 550-565, 573-583, 596-613, 621-630, 652-658 and 87-97 of **Seq ID No 237**; 8-20, 26-48, 56-67, 76-86, 94-109, 115-121, 123-129, 143-160, 178-186, 191-198, 201-208, 221-236, 238-244, 260-268 and 237-247 of **Seq ID No 238**; 4-40, 42-57, 73-87, 98-117, 126-135, 150-156, 166-174, 196-217, 231-236, 248-258, 276-284, 293-301, 307-313, 339-347, 359-365, 375-387, 395-402, 428-440, 445-456, 485-490, 497-505, 535-541, 547-555, 610-625, 648-656, 665-671 and 448-528 of **Seq ID No 239**; 10-18, 39-45, 51-61, 80-96, 98-106, 110-115, 158-172, 174-183, 191-200, 220-237, 249-255, 274-289, 308-324, 331-341, 372-381, 384-397, 405-414 and 322-338 of **Seq ID No 240**; 30-36, 38-56, 85-108, 134-147, 149-160, 163-183, 188-201, 206-211, 219-238, 247-254 and 5-13 of **Seq ID No 241**; 11-40, 98-103, 110-115, 133-145, 151-159, 172-179, 192-201, 204-212, 222-228, 235-245, 258-268, 283-296, 298-309, 322-329, 342-351, 354-362, 372-378, 385-393, 407-418, 495-516 and 1-148 of **Seq ID No 242**; 5-19, 21-36, 73-94, 112-119, 122-137, 139-145, 152-167, 184-190, 198-204, 208-224, 249-265, 267-281, 299-304, 309-317, 326-333, 356-364, 368-374, 381-389, 391-414, 419-425, 430-435 and 113-140 of **Seq ID No 243**; 45-54, 59-67, 78-91 and 15-23 of **Seq ID No 244**; 11-22, 33-47, 52-80, 88-112, 124-129 and 6-25 of **Seq ID No 245**; 26-41, 51-63, 80-89, 93-115, 150-163, 187-193, 220-237, 240-249, 286-294, 296-306, 316-329, 345-353, 361-370, 407-425, 428-437, 474-482, 484-494, 504-517, 533-541, 549-558, 595-613, 616-625, 660-668, 673-685, 711-726, 736-744, 749-761, 787-802, 812-820, 825-837, 863-878, 888-896, 901-913, 939-954, 964-972, 977-989, 1003-1008, 1016-1022, 1028-1034, 1041-1053, 1059-1074, 1101-1122, 420-511 and 581-704 of **Seq ID No 246**; 18-25, 27-55, 71-83, 89-95, 102-113, 120-146, 150-156, 174-185 and 159-175 of **Seq ID No 247**; 24-30, 38-56, 63-68, 87-93, 136-142, 153-164, 183-199, 213-219, 226-234, 244-261, 269-278, 283-289, 291-297, 320-328, 330-336, 340-346, 348-356, 358-366, 382-387, 401-408, 414-419, 449-455, 468-491, 504-512, 531-537, 554-560, 597-608, 621-627, 632-643, 650-662, 667-692, 703-716, 724-737, 743-758, 783-794, 800-818, 846-856 and 806-884 of **Seq ID No 248**; 4-14, 21-39, 86-92, 99-107, 121-131, 136-144, 147-154, 158-166, 176-185, 193-199, 207-222, 224-230 and 117-136 of **Seq ID No 249**; 65-76, 85-97, 103-109, 115-121, 125-146, 163-169, 196-205, 212-219, 228-237, 241-247, 254-262, 269-288, 294-303, 305-313, 328-367, 395-401, 405-412, 418-429, 437-447, 481-488, 506-513, 519-524, 530-541, 546-557 and 266-284 of **Seq ID No 250**; 5-14, 37-42, 49-71, 78-92, 97-112, 127-136, 147-154, 156-163, 186-198, 216-225, 233-243, 248-253, 295-307, 323-332, 359-366, 368-374, 380-398 and 194-223 of **Seq ID No 251**; 4-11, 33-39, 45-72, 100-113, 119-129, 136-144, 169-175, 177-185, 200-208, 210-219, 262-276, 278-297, 320-326, 336-344, 347-362, 381-394, 443-453 and 438-454 of **Seq ID No 252**; 4-29, 31-52, 55-61, 95-110, 138-158, 162-171, 179-187, 202-229, 239-248, 251-256, 262-267, 269-285, 304-310, 351-360, 362-368, 381-388, 415-428, 435-440, 448-458 and 161-178 of **Seq ID No 253**; 4-17, 19-28, 32-43, 47-59, 89-110, 112-126, 128-134, 140-148, 152-161, 169-184, 191-204, 230-235, 255-264, 328-338, 341-347, 401-409, 413-419, 433-441, 449-458, 463-468, 476-482, 486-492, 500-506, 529-545 and 305-381 of **Seq ID No 254**; 10-29, 38-45, 53-61, 134-145, 152-160, 163-170, 202-208, 219-229, 248-258, 266-275, 282-288, 315-320, 328-334, 377-385, 392-402, 418-424, 447-453, 460-471, 479-487, 491-497, 500-507, 531-537, 581-594, 615-623, 629-635, 644-652, 659-666, 668-678, 710-717, 719-728, 736-741, 747-760, 766-773, 784-789, 794-800, 805-817, 855-861, 866-887 and 698-715 of **Seq ID No 255**; 16-26, 29-37, 44-58, 62-68, 74-80, 88-95, 97-120, 125-144, 165-196 and 58-72 of **Seq ID No 256**; 14-21, 23-46, 49-60, 63-74, 78-92, 96-103, 117-129, 134-161, 169-211, 217-231, 239-248, 252-281, 292-299, 313-343 and 243-257 of **Seq ID No 257**; 11-27, 46-52, 67-72, 76-84, 91-112, 116-153, 160-175, 187-196, 202-211, 213-220 and 43-76 of **Seq ID No 258**; 5-29, 37-56, 78-86, 108-118, 152-161 and 120-130 of **Seq ID No 259**; 8-14, 19-41, 52-66, 75-82, 87-92, 106-121, 127-133, 136-143, 158-175, 180-187, 196-204, 221-228, 239-245, 259-265, 291-306, 318-323, 328-340, 352-358, 361-368, 375-381, 391-399, 411-418, 431-442, 446-455, 484-496, 498-510, 527-533, 541-549, 558-565,

575-585, 587-594, 644-655, 661-668, 671-677 and 184-196 of **Seq ID No 260**; 4-22, 29-38, 55-62, 75-81, 102-107, 110-134, 143-150, 161-167, 172-179, 191-215, 223-233, 241-247, 251-264, 266-272, 288-309, 340-352, 354-366, 394-402, 414-438 and 198-218 of **Seq ID No 261**; 24-44, 49-70, 80-91, 105-118, 128-136, 140-154 and 77-92 of **Seq ID No 262**; 5-22, 31-36, 41-47, 67-74, 83-90, 105-122, 135-143, 160-167 and 118-129 of **Seq ID No 263**; 4-25, 33-73, 81-93, 96-106, 114-120, 122-128, 130-172, 179-208, 210-241, 251-283, 296-301 and 92-100 of **Seq ID No 264**; 14-24, 29-38, 43-50, 52-72, 86-97, 101-107, 110-125, 127-141, 145-157, 168-175, 177-184, 186-195, 205-226, 238-250, 255-261, 284-290, 293-304, 307-314, 316-323, 325-356, 363-371, 383-390, 405-415, 423-432, 442-454, 466-485, 502-511, 519-527, 535-556, 558-565, 569-574, 612-634, 641-655, 672-686, 698-709, 715-722, 724-732, 743-753, 760-769, 783-792, 818-825, 830-839, 842-849, 884-896, 905-918, 926-940, 957-969, 979-1007, 1015-1021, 1049-1057 and 336-349 of **Seq ID No 265**; 6-16, 26-31, 33-39, 62-73, 75-85, 87-100, 113-123, 127-152, 157-164, 168-181, 191-198, 208-214, 219-226, 233-254, 259-266, 286-329 and 181-195 of **Seq ID No 266**; 4-13, 32-39, 53-76, 99-108, 110-116, 124-135, 137-146, 149-157, 162-174, 182-190, 207-231, 242-253, 255-264, 274-283, 291-323, 334-345, 351-360, 375-388, 418-425, 456-474, 486-492, 508-517, 520-536, 547-560, 562-577, 31-45 and 419-443 of **Seq ID No 267**; 15-26, 30-37, 42-49, 58-90, 93-99, 128-134, 147-154, 174-179, 190-197, 199-205, 221-230, 262-274, 277-287, 300-314, 327-333, 343-351, 359-377, 388-396, 408-413, 416-425, 431-446 and 246-256 of **Seq ID No 268**; 5-26, 34-42, 47-54, 61-67, 71-104, 107-115, 131-138, 144-153, 157-189, 196-202, 204-210, 228-245, 288-309, 316-329, 332-341, 379-386, 393-399, 404-412, 414-421, 457-468, 483-489, 500-506, 508-517, 523-534, 543-557, 565-580, 587-605, 609-617, 619-627, 631-636, 640-646, 662-668, 675-682, 705-710, 716-723, 727-732, 750-758, 784-789, 795-809, 869-874, 14-138, 166-286, 372-503, 674-696 and 754-859 of **Seq ID No 269**; 5-17, 32-38, 40-47, 80-89, 113-119, 125-137, 140-154, 157-163, 170-177, 185-199, 213-225, 228-236, 242-248, 277-290, 292-305, 323-333, 347-353, 364-370, 385-394, 399-406, 423-433, 441-451, 462-474, 477-487 and 116-124 of **Seq ID No 270**; 7-16, 18-30, 32-49, 53-61, 63-85, 95-101, 105-115, 119-134, 143-150, 159-178, 185-202, 212-229, 236-250, 254-265, 268-294 and 63-72 of **Seq ID No 271**; 4-12, 19-47, 73-81, 97-103, 153-169, 188-198, 207-213, 217-223, 236-242, 255-265, 270-278, 298-305, 309-317, 335-347, 354-363, 373-394, 419-424, 442-465, 486-492, 500-507, 542-549, 551-558, 560-572, 580-589, 607-614, 617-623, 647-653, 666-676, 694-704, 706-714, 748-754, 765-772, 786-792, 795-806 and 358-370 of **Seq ID No 272**; 18-28, 30-38, 40-46, 49-55, 69-78, 82-98, 104-134, 147-153, 180-190, 196-202, 218-236, 244-261, 266-273, 275-286, 290-295, 301-314, 378-387, 390-395, 427-434 and 290-305 of **Seq ID No 273**; 4-13, 20-31, 39-51, 54-61, 69-84, 87-105, 117-124 and 108-125 of **Seq ID No 274**; 24-34, 43-54, 56-66, 68-79 and 50-69 of **Seq ID No 275**; 5-43, 71-77, 102-131, 141-148, 150-156, 159-186, 191-207, 209-234, 255-268, 280-286, 293-299, 317-323, 350-357, 363-372, 391-397, 406-418, 428-435, 455-465, 484-497, 499-505, 525-531, 575-582, 593-607, 621-633, 638-649, 655-673, 684-698, 711-725, 736-741, 743-752, 759-769, 781-793, 813-831, 843-853, 894-905, 908-916, 929-946, 953-963, 970-978, 1001-1007, 1011-1033, 165-178 and 818-974 of **Seq ID No 276**; 16-44, 63-86, 98-108, 185-191, 222-237, 261-274, 282-294, 335-345, 349-362, 374-384, 409-420, 424-430, 440-447, 453-460, 465-473, 475-504, 522-534, 538-551, 554-560, 567-582, 598-607, 611-619, 627-640, 643-653, 655-661, 669-680, 684-690, 701-707, 715-731, 744-750, 756-763, 768-804, 829-837, 845-853, 855-879, 884-890, 910-928, 77-90, 144-212, 279-355, 434-536, 782-810 and 875-902 of **Seq ID No 277**; 4-22, 29-41, 45-51, 53-66, 70-77, 86-95, 98-104, 106-124, 129-135, 142-151, 153-161, 169-176, 228-251, 284-299, 331-337, 339-370, 380-387, 393-398, 406-411, 423-433, 440-452, 461-469, 488-498, 501-516, 523-530, 532-559, 562-567, 570-602, 612-628, 630-645, 649-659, 666-672, 677-696, 714-723, 727-747 and 212-227 of **Seq ID No 278**; 4-9, 17-31, 35-41, 56-61, 66-75, 81-87, 90-124, 133-138, 149-163, 173-192, 213-219, 221-262, 265-275, 277-282, 292-298, 301-307, 333-346, 353-363, 371-378, 419-430, 435-448, 456-469, 551-570, 583-599, 603-612 and 275-291 of **Seq ID No 279**; 28-34, 53-58, 72-81, 100-128, 145-154, 159-168, 172-189, 217-225, 227-249, 256-263, 299-309, 322-330, 361-379, 381-388, 392-401, 404-417, 425-436, 440-446, 451-464, 469-487, 502-511, 543-551, 559-564, 595-601, 606-612, 615-626, 633-642, 644-650, 664-670, 674-684, 692-701, 715-723, 726-734, 749-756, 763-771, 781-787, 810-843, 860-869, 882-889, 907-917, 931-936, 941-948, 951-958, 964-971, 976-993, 1039-1049, 1051-1065, 1092-1121, 1126-1132, 1145-1151, 1158-1173, 1181-1192, 1194-1208, 1218-1223, 1229-1243, 1249-1254, 1265-1279, 1287-1297, 1303-1320, 1334-1341, 1343-1358, 1372-1382, 1406-1417, 1419-1425, 1428-1434, 1441-1448, 1460-1473, 1494-1504, 1509-1514, 1529-1550, 654-669 and 1400-1483 of **Seq ID No 280**; 10-16, 20-25, 58-65, 97-109, 118-132,

134-146, 148-155, 186-195, 226-233, 244-262, 275-284, 295-310, 317-322, 330-339, 345-351, 366-375, 392-403, 408-415, 423-430, 435-444, 446-457, 467-479, 486-499, 503-510, 525-537, 540-585, 602-612, 614-623, 625-634, 639-645, 650-669, 700-707, 717-724, 727-739, 205-230 and 733-754 of **Seq ID No 281**; 5-22, 37-43, 72-81, 105-113, 128-133, 148-160, 188-194, 204-230, 238-245, 251-257 and 194-213 of **Seq ID No 282**; 16-21, 35-41, 56-72, 74-92, 103-109 and 62-68 of **Seq ID No 283**; 4-15, 17-82, 90-104, 107-159, 163-170, 188-221, 234-245, 252-265 and 220-235 of **Seq ID No 284**; 16-22, 36-46, 61-75, 92-107, 113-121, 139-145, 148-160 and 30-42 of **Seq ID No 285**; 4-12, 20-26, 43-49, 55-62, 66-78, 121-127, 135-141, 146-161, 164-170, 178-189, 196-205, 233-238, 269-279, 288-318, 325-332, 381-386, 400-407 and 328-346 of **Seq ID No 286**; 5-12, 31-49, 57-63, 69-79, 89-97, 99-114, 116-127, 134-142, 147-154, 160-173, 185-193, 199-204, 211-222, 229-236, 243-249, 256-274 and 58-68 of **Seq ID No 287**; 10-20, 28-34, 39-53, 68-79, 84-90, 99-106 and 73-79 of **Seq ID No 288**; 14-37, 45-50, 61-66, 77-82, 93-98, 109-114, 125-130, 141-146, 157-162, 173-178, 189-194, 205-210, 221-226, 237-242, 253-258, 269-274, 285-290, 301-306, 316-332, 349-359, 371-378, 385-406, 34-307 and 312-385 of **Seq ID No 289**; 4-10, 17-38, 50-85, 93-99, 109-116, 128-185, 189-197, 199-210, 223-256, 263-287, 289-312, 327-337, 371-386, 389-394, 406-419, 424-432, 438-450, 458-463, 475-502, 507-513, 519-526, 535-542, 550-567 and 361-376 of **Seq ID No 290**; 10-39, 42-93, 100-144, 155-176, 178-224, 230-244, 246-255, 273-282, 292-301, 308-325, 332-351, 356-361, 368-379, 386-393, 400-421 and 138-155 of **Seq ID No 291**; 5-11, 17-34, 40-45, 50-55, 72-80, 101-123, 145-151, 164-172, 182-187, 189-195, 208-218, 220-241, 243-252, 255-270, 325-331, 365-371, 391-398, 402-418, 422-428, 430-435, 443-452, 463-469, 476-484, 486-494, 503-509, 529-553, 560-565, 570-590, 608-614, 619-627, 654-661, 744-750, 772-780, 784-790, 806-816, 836-853, 876-885, 912-918, 926-933, 961-975, 980-987, 996-1006, 1016-1028, 1043-1053, 1057-1062, 994-1003 and 1033-1056 of **Seq ID No 292**; 17-45, 64-71, 73-81, 99-109, 186-192, 223-238, 262-275, 283-295, 336-346, 350-363, 375-385, 410-421, 425-431, 441-448, 454-463, 468-474, 476-512, 523-537, 539-552, 568-583, 599-608, 612-620, 628-641, 644-654, 656-662, 670-681, 685-695, 702-708, 716-723, 725-735, 757-764, 769-798, 800-806, 808-816, 826-840, 846-854, 856-862, 874-881, 885-902, 907-928, 274-350 and 443-513 of **Seq ID No 293**; 4-22, 29-41, 45-51, 53-61, 70-76, 85-92, 99-104, 111-122, 134-140, 142-154, 163-174, 224-232, 255-265, 273-279, 283-297, 330-335, 337-348, 356-367, 373-385, 391-396, 421-431, 442-455, 475-485, 493-505, 526-538, 544-561, 587-599, 605-620, 622-651, 662-670, 675-681, 687-692, 697-712, 714-735 and 252-262 of **Seq ID No 294**; 4-12, 15-35, 40-46, 50-59, 67-94, 110-128, 143-169, 182-188, 207-215, 218-228, 238-250 and 74-90 of **Seq ID No 295**; 9-18, 42-58, 78-85, 88-95, 97-106, 115-122, 128-134, 140-145, 154-181, 186-202, 204-223, 261-267, 269-278, 284-293, 300-336, 358-368 and 12-29 of **Seq ID No 296**; 7-34, 46-53, 62-72, 82-88, 100-105, 111-117, 132-137, 144-160, 166-180, 183-189, 209-221, 231-236, 246-253, 268-282, 286-293, 323-336, 364-372, 378-392, 422-433 and 388-405 of **Seq ID No 297**; 21-27, 34-50, 72-77, 80-95, 164-177, 192-198, 202-220, 226-236, 239-247, 270-279, 285-292, 315-320, 327-334, 348-355, 364-371, 388-397, 453-476, 488-497, 534-545, 556-576, 582-588, 601-607, 609-616, 642-662, 674-681, 687-697, 709-715, 721-727, 741-755 and 621-739 of **Seq ID No 298**; 4-14, 16-77, 79-109 and 25-99 of **Seq ID No 299**; 4-9, 17-23, 30-37, 44-55, 65-72, 77-93, 102-121, 123-132, 146-153 and 17-29 of **Seq ID No 300**; 4-18, 25-41, 52-60, 83-92, 104-112, 117-123, 149-155, 159-167, 170-192, 201-210, 220-227, 245-250 and 124-137 of **Seq ID No 301**; 8-25, 50-55, 89-95, 138-143, 148-153, 159-169, 173-179, 223-238, 262-268, 288-295, 297-308, 325-335, 403-409, 411-417, 432-446, 463-475, 492-501, 524-530, 542-548, 561-574, 576-593, 604-609, 612-622, 637-654, 665-672, 678-685, 720-725, 731-739, 762-767, 777-783, 820-838, 851-865, 901-908, 913-920, 958-970, 1000-1006, 1009-1015, 1020-1026, 1043-1052, 1055-1061, 1-128, 252-341, 771-793 and 1043-1058 of **Seq ID No 302**; 16-26, 33-46 and 64-76 of **Seq ID No 303**; 4-27, 69-77, 79-101, 117-123, 126-142, 155-161, 171-186, 200-206, 213-231, 233-244, 267-273, 313-329, 335-344, 347-370, 374-379, 399-408, 422-443, 445-453, 461-468, 476-482, 518-534, 544-553, 556-567, 578-595, 601-620, 626-636, 646-658, 666-681, 715-721, 762-768, 778-785, 789-803, 809-819, 22-108, 153-318, 391-527 and 638-757 of **Seq ID No 304**; 6-21, 32-43, 62-92, 104-123, 135-141, 145-152, 199-216, 218-226, 237-247, 260-269, 274-283, 297-303, 1-72 and 127-211 of **Seq ID No 305**; 6-26, 50-56, 83-89, 108-114, 123-131, 172-181, 194-200, 221-238, 241-247, 251-259, 263-271, 284-292, 304-319, 321-335, 353-358, 384-391, 408-417, 424-430, 442-448, 459-466, 487-500, 514-528, 541-556, 572-578, 595-601, 605-613, 620-631, 635-648, 660-670, 673-679, 686-693, 702-708, 716-725, 730-735, 749-755, 770-777, 805-811, 831-837, 843-851, 854-860, 863-869, 895-901, 904-914, 922-929, 933-938, 947-952, 956-963, 1000-1005,

1008-1014, 1021-1030, 1097-1103, 1120-1130, 1132-1140, 1-213, 269-592 and 992-1120 of **Seq ID No 306**; 9-16, 33-39, 47-59, 65-79, 81-95, 103-108, 115-123, 138-148, 163-171, 176-185, 191-196, 205-211, 213-221, 224-256, 261-276, 294-302, 357-363, 384-390, 95-111 and 161-189 of **Seq ID No 307**; 21-27, 35-45, 70-76, 92-105, 129-143, 145-155, 161-166, 170-191, 204-211, 214-231, 234-246, 249-255, 259-275 and 1-18 of **Seq ID No 308**; 21-35, 45-53, 56-64, 69-97 and 1-16 of **Seq ID No 309**; 25-33, 41-47, 61-68, 86-101, 106-114, 116-129, 134-142, 144-156, 163-176, 181-190, 228-251, 255-261, 276-292, 295-305, 334-357, 368-380, 395-410, 424-429, 454-460, 469-482, 510-516, 518-527, 531-546, 558-570, 579-606, 628-636, 638-645, 651-656, 668-674, 691-698, 717-734, 742-754, 765-770, 792-797, 827-835, 847-859, 874-881, 903-909, 926-933, 942-961, 964-977, 989-1004, 1010-1028, 1031-1047, 1057-1075, 1081-1095, 1108-1117, 1138-1144, 1182-1189, 1193-1206, 1220-1229, 1239-1246, 1257-1267, 1271-1279, 1284-1301, 1312-1320, 1329-1335, 1341-1347, 1358-1371, 1399-1404, 1417-1426, 1458-1463, 1468-1476, 1478-1485, 1493-1506, 1535-1541, 1559-1574, 1583-1590, 1595-1601, 1603-1611, 1622-1628, 1634-1644, 1671-1685, 1689-1696, 1715-1720, 1734-1746, 1766-1775, 1801-1806, 1838-1844, 1858-1871, 1910-1917, 1948-1955, 1960-1974, 2000-2015, 2019-2036, 2041-2063, 748-847 and 1381-1391 of **Seq ID No 310**; 5-12, 18-24, 27-53, 56-63, 96-113, 119-124, 131-136, 157-163, 203-209, 215-223, 233-246, 264-273, 311-316, 380-389, 393-399, 425-433, 445-450, 457-462, 464-470, 475-482, 507-513, 527-535, 542-548, 550-565, 591-602, 607-613, 627-642, 644-664, 673-712, 714-732, 739-764, 769-782, 812-818, 826-838, 848-854, 860-871, 892-906, 930-938, 940-954, 957-973, 990-998, 1002-1021, 1024-1033, 1037-1042, 1050-1060, 1077-1083, 1085-1092, 1100-1129, 1144-1161, 1169-1175, 1178-1189, 1192-1198, 1201-1207, 1211-1221, 1229-1239, 1250-1270, 1278-1292, 1294-1300, 1314-1335, 1344-1352, 1360-1374, 1394-1405, 1407-1414, 1416-1424, 1432-1452, 1456-1462, 1474-1497, 1500-1510, 1516-1522, 1534-1542, 1550-1559, 1584-1603, 1608-1627, 187-273 and 306-441 of **Seq ID No 311**; 70-80, 90-97, 118-125, 128-140, 142-148, 154-162, 189-202, 214-222, 224-232, 254-260, 275-313, 317-332, 355-360, 392-398, 425-432, 448-456, 464-470, 476-482, 491-505, 521-528, 533-546, 560-567, 592-597, 605-614, 618-626, 637-644, 646-653, 660-666, 677-691 and 207-227 of **Seq ID No 312**; 5-19, 26-34, 37-55, 57-66, 69-83, 86-102, 115-134, 138-143, 154-172, 178-195, 209-246, 251-257, 290-302, 306-311 and 256-266 of **Seq ID No 313**; 10-20, 22-28, 35-57, 72-79, 87-103, 108-128, 130-144, 158-171, 190-198, 225-242, 274-291, 301-315, 317-324, 374-385 and 353-365 of **Seq ID No 314**; 4-9, 17-30, 34-54, 59-66, 73-94, 118-130, 135-150, 158-171, 189-198, 219-239, 269-275, 283-301, 89-106 and 176-193 of **Seq ID No 315**; 14-20, 22-74, 77-86, 89-99, 104-109, 126-135, 154-165, 181-195, 197-212, 216-224, 264-275 and 107-118 of **Seq ID No 316**; 4-18, 21-38, 63-72, 101-109, 156-162, 165-179, 183-192, 195-210, 212-218, 230-239, 241-256, 278-290, 299-311, 313-322, 332-341, 348-366, 386-401, 420-426, 435-450, 455-460, 468-479, 491-498, 510-518, 532-538, 545-552, 557-563, 567-573, 586-595, 599-609, 620-626, 628-636, 652-657, 665-681 and 1-198 of **Seq ID No 317**; 4-10, 16-38, 51-68, 73-79, 94-115, 120-125, 132-178, 201-208, 216-223, 238-266, 269-295, 297-304, 337-342, 347-356, 374-401, 403-422, 440-447, 478-504, 510-516, 519-530, 537-544 and 191-206 of **Seq ID No 318**; 12-40, 42-48, 66-71, 77-86, 95-102, 113-120, 129-137, 141-148, 155-174, 208-214, 218-225, 234-240, 256-267, 275-283, 300-306, 313-321, 343-350, 359-367, 370-383, 398-405, 432-439, 443-461, 492-508, 516-526, 528-535 and 370-478 of **Seq ID No 319**; 6-14, 20-37, 56-62, 90-95, 97-113, 118-125, 140-145, 161-170, 183-202, 237-244, 275-284, 286-305, 309-316, 333-359, 373-401, 405-412 and 176-187 of **Seq ID No 320**; 33-44, 50-55, 59-80, 86-101, 129-139, 147-153, 157-163, 171-176, 189-201, 203-224, 239-245, 257-262, 281-287, 290-297, 304-320, 322-331, 334-350, 372-390, 396-401, 71-88 and 353-372 of **Seq ID No 321**; 5-11, 15-24, 26-33, 40-47, 75-88, 95-103, 105-112 and 17-30 of **Seq ID No 322**; 5-11, 16-39, 46-54, 62-82, 100-107, 111-124, 126-150, 154-165, 167-183, 204-238, 245-295, 301-313, 316-335 and 8-16 of **Seq ID No 323**; 4-19, 34-48, 69-74, 79-107, 115-127, 129-135, 143-153, 160-169, 171-182 and 142-153 of **Seq ID No 324**; 4-30, 65-74, 82-106, 110-120, 124-132, 135-140, 146-175, 179-184, 190-196, 217-223, 228-233, 250-267, 275-292, 303-315, 322-332 and 174-186 of **Seq ID No 325**; 9-16, 29-41, 47-57, 68-84, 87-109, 113-119, 162-180, 186-193, 195-201, 203-208, 218-230, 234-243, 265-271, 281-292, 305-312, 323-332, 341-347, 349-363, 368-374, 383-390, 396-410, 434-440, 446-452, 455-464, 466-473, 515-522, 529-542, 565-570, 589-600, 602-613, 618-623, 637-644, 1019-1027, 1238-1244, 1258-1264, 1268-1276, 1281-1292, 1296-1302 and 883-936 of **Seq ID No 326**; 10-17, 23-32, 39-44, 54-72, 75-81, 88-111, 138-154, 160-167, 178-185, 201-210, 236-252, 327-334, 336-342, 366-376, 388-400, 410-430, 472-482, 493-526, 552-558, 586-592, 598-603, 612-621, 630-635, 641-660 and 384-393 of **Seq ID No 327**; 4-22, 24-39, 50-59, 73-84, 100-105, 111-117, 130-138,

155-161, 173-178, 182-189, 205-215, 266-284, 308-313, 321-328, 330-337, 346-363, 368-374, 388-395, 397-405, 426-434, 453-459, 482-492, 501-507, 509-515, 518-523, 527-544, 559-590, 598-612, 614-629, 646-659, 663-684, 686-694, 698-721 and 445-461 of **Seq ID No 328**; 14-22, 27-33 and 3-17 of **Seq ID No 329**; 29-41, 66-73, 81-87, 90-108, 140-146, 150-159, 165-184, 186-196, 216-226, 230-238, 247-253, 261-269 and 126-140 of **Seq ID No 330**; 5-12, 16-25, 27-33, 36-45, 60-68, 83-88, 103-126 and 86-101 of **Seq ID No 331**; 14-23, 36-47, 56-66, 84-89, 94-105, 111-127, 140-153, 160-174, 176-183, 189-203, 219-225, 231-237, 250-257 and 194-227 of **Seq ID No 332**; 4-25, 54-60, 64-71, 73-82, 89-106, 117-124, 157-169, 183-188, 199-210, 221-232, 236-244, 255-264 and 58-98 of **Seq ID No 333**; 13-19, 26-36, 41-53, 55-71, 77-84, 86-108, 114-135, 157-172, 177-183, 187-194, 208-213, 218-226, 110-125 and 156-170 of **Seq ID No 334**; 5-24, 63-69, 77-85, 94-112, 120-137, 140-146, 152-159, 166-172, 179-187, 193-199, 206-212, 222-228, 234-240, 244-252, 257-264, 270-289, 298-309, 316-328, 337-348, 363-375, 1-56 and 340-352 of **Seq ID No 335**; 18-39, 42-71, 78-120, 124-144, 152-173, 179-189, 199-209, 213-222, 228-258, 269-304, 329-361, 364-372, 374-389, 396-441 and 313-327 of **Seq ID No 336**; 19-25, 91-98, 108-120, 156-162, 168-174, 191-204, 211-216, 232-266, 272-278, 286-308, 316-321, 327-333, 344-355, 358-364, 384-391, 395-428, 464-476, 487-495, 497-511, 544-561, 563-573, 575-582, 588-594, 10-25 and 322-338 of **Seq ID No 337**; 14-26, 32-49, 51-57, 59-72, 80-91, 102-112, 119-125, 147-161, 164-173, 175-183, 188-213, 217-222, 246-254, 260-276, 282-303, 308-318, 321-328, 333-350, 352-359, 371-378, 392-401, 407-414, 416-443, 448-463, 471-484, 490-497, 501-514, 519-527, 539-551, 557-570, 578-590, 592-598, 600-610, 618-629, 633-647, 654-667, 676-689, 702-709, 718-726, 728-737, 741-760, 764-780, 786-795, 808-826, 836-842, 845-852, 865-874, 881-887, 931-945, 949-957, 968-974, 979-986, 1003-1009, 1023-1029 and 90-103 of **Seq ID No 338**; 11-16, 37-56, 60-66, 69-77, 80-88, 93-106, 117-139, 166-171 and 72-90 of **Seq ID No 339**; 59-84, 123-133, 145-150, 161-167, 178-189 and 115-128 of **Seq ID No 340**; 15-33, 39-46, 52-64, 74-87, 108-124, 127-144, 150-156, 173-179, 184-194, 201-208, 219-236, 243-269, 272-295, 302-309, 343-349, 356-361, 370-379, 405-411, 414-423, 430-451, 457-464, 466-475, 477-483, 496-502, 507-522, 541-548, 557-563, 571-577, 579-585, 590-605, 626-642, 650-662, 671-691, 704-710, 751-769, 775-781, 786-791, 794-829, 851-858, 868-878, 884-904, 913-919, 931-939 and 132-142 of **Seq ID No 341**; 33-58, 64-71, 74-80, 83-88, 96-120, 122-139, 146-157, 167-177, 207-213, 220-225, 236-242, 264-279, 300-305, 326-336, 340-347, 350-360, 97-115 and 199-211 of **Seq ID No 342**; 4-26, 43-57, 70-99, 102-117, 121-133, 142-148, 151-168, 170-183, 192-220, 235-249, 258-279 and 30-41 of **Seq ID No 343**; 34-42, 48-58, 70-94, 110-130, 154-160, 164-172, 178-183, 195-203, 211-222, 229-250, 256-261, 274-284, 286-292, 312-323 and 222-233 of **Seq ID No 344**; 4-9, 15-36, 38-45, 49-74, 78-88, 100-112, 136-191, 211-220, 226-233, 239-246, 254-274, 287-307, 316-322, 342-353, 356-366, 373-378, 384-393, 405-431, 449-457, 459-468, 487-511, 515-524, 529-541, 544-552, 562-568, 571-576 and 208-280 of **Seq ID No 345**; 10-27, 31-37, 39-54, 71-108, 124-143 and 2-107 of **Seq ID No 346**; 16-27, 38-57, 64-70, 90-102, 104-113, 116-137, 160-166 and 1-80 of **Seq ID No 347**; 13-21, 31-36, 56-67, 127-136, 153-171, 173-180, 184-200, 214-222, 225-231, 239-263, 267-273 and 135-159 of **Seq ID No 348**; 12-27, 31-51, 68-74, 77-87, 94-101, 108-114, 117-123, 127-134, 138-168, 173-196, 201-207, 212-217, 227-237, 247-257, 264-280 and 205-223 of **Seq ID No 349**; 17-22, 25-54, 70-76, 92-100 and 98-110 of **Seq ID No 350**; 7-29, 40-50, 60-67, 87-96, 105-111, 119-164, 172-199, 206-212, 220-227, 237-259, 272-279, 282-293, 295-309, 313-319, 321-328, 345-363, 376-386 and 159-176 of **Seq ID No 351**; 4-19, 24-30, 36-43, 50-68, 71-89, 93-106, 141-152, 154-172, 179-197, 199-215, 229-239, 246-252, 255-263, 281-298, 319-325, 329-356, 358-368, 374-390, 397-409, 420-429, 432-444, 450-456, 459-475, 483-494, 496-502, 520-528, 532-556 and 362-377 of **Seq ID No 352**; 18-25, 40-62, 77-85, 91-97, 105-116, 123-133, 139-184, 189-197 and 122-140 of **Seq ID No 353**; 4-49, 52-58, 62-70, 79-105, 109-133, 142-150, 163-168, 206-214, 220-228, 233-240, 243-254, 274-281, 303-311, 327-338, 357-373, 378-396, 403-413, 420-436, 441-453, 461-467, 475-481, 484-498, 506-512, 514-521, 523-529, 562-579, 589-595, 598-603, 615-648, 714-722, 728-742, 749-758, 777-792, 795-807 and 643-658 of **Seq ID No 354**; 8-27, 37-48, 51-56, 72-79, 87-106, 120-138, 140-147, 167-176, 187-197, 205-216, 222-229, 234-239, 243-249, 277-288, 292-315, 334-343, 347-353, 363-391, 398-404, 430-447, 461-467, 478-492, 498-507 and 456-470 of **Seq ID No 355**; 5-12, 18-24, 59-69, 80-93, 95-109, 119-125, 130-137, 139-147, 158-163, 168-176, 182-202, 206-215, 222-239, 241-249, 267-277, 291-298, 311-318, 321-327, 338-344, 348-355, 373-386, 393-406, 411-417, 434-443, 446-465, 473-484, 514-521, 532-553, 584-594 and 221-237 of **Seq ID No 356**; 4-14, 27-34, 50-58, 63-72, 79-106, 109-114, 121-142, 146-154, 161-167, 169-175, 178-201, 223-238, 249-

254, 259-264, 278-292, 294-312, 319-330 and 167-191 of Seq ID No 357; 7-28, 36-42, 50-61, 63-80, 122-152, 161-174, 176-191 and 140-190 of Seq ID No 358; 20-57, 59-65, 70-78, 86-102, 119-133, 142-161, 163-173, 177-188, 192-202, 204-220, 222-236, 240-253, 279-319, 326-331, 337-383, 390-399, 406-412, 420-427, 431-438 and 381-395 of Seq ID No 359; 13-18, 28-34, 37-43, 50-59, 75-81, 83-97, 105-121, 139-147, 200-206, 209-227, 231-247, 260-271, 318-327, 366-381, 388-394, 399-406 and 182-201 of Seq ID No 360; 6-29, 37-43, 51-56, 70-77, 82-102, 110-119, 127-143, 178-190, 201-209, 216-243, 261-269, 281-292, 305-313, 327-339, 341-354, 356-373, 391-397, 423-429, 438-445, 450-478 and 21-314 of Seq ID No 361; 4-12, 15-21, 32-41, 59-76, 80-89, 96-104 and 90-103 of Seq ID No 362; 9-28, 30-41, 44-54, 69-74, 77-82, 90-97, 104-123, 125-135, 149-155, 164-173, 177-184, 217-226, 230-235, 238-244, 258-272, 282-297, 300-305, 309-315, 317-322, 327-336, 348-362, 368-374, 380-387, 400-411, 414-424, 451-458, 460-466, 483-494, 497-503, 506-511, 521-528, 540-553, 569-587, 598-606, 628-642, 661-681, 688-700, 718-733, 740-749, 752-764, 769-783, 823-834, 848-854, 862-872, 878-884, 886-898, 915-920, 938-951, 954-961, 963-972, 982-989, 996-1003, 1010-1016, 1021-1032, 1038-1044, 1047-1057, 1060-1070, 1079-1088, 1094-1102, 1117-1127, 1129-1135, 1142-1153, 1158-1204, 1212-1229, 1234-1263, 1269-1277, 1308-1313, 1327-1338, 1344-1376, 1400-1415, 1436-1443, 1448-1458, 1497-1504, 1511-1522, 1544-1566, 3-82 and 509-576 of Seq ID No 363; 8-36, 40-64, 71-79, 88-94, 102-109, 118-127, 138-148, 151-159, 163-174, 192-198, 200-206, 220-233, 268-273, 290-301, 304-309, 316-323, 331-349, 378-391, 414-420, 427-437, 455-475, 494-510, 541-547, 549-555, 616-640, 1-60, 55-139, 212-308, 386-458 and 458-624 of Seq ID No 364; 16-31, 35-42, 70-77, 91-101, 120-130, 132-140, 143-153, 185-190, 195-202, 215-222, 228-238, 241-251, 257-264, 268-277, 288-302, 312-324, 326-333, 341-348, 364-382, 415-429, 438-454, 458-466, 491-499, 501-521 and 273-281 of Seq ID No 365; 8-14, 32-57, 74-149, 155-177, 179-212, 221-266, 271-296, 304-324, 329-346, 349-359, 368-401, 413-419, 426-454, 465-478, 493-510 and 466-490 of Seq ID No 366; 22-28, 33-51, 64-89, 96-119, 126-132, 138-146, 152-159, 161-169, 172-179, 193-198, 205-211, 221-231, 235-254, 273-280, 297-303, 312-320, 328-346, 351-373, 378-384, 391-398, 448-454, 460-468, 470-481, 516-558, 574-593, 597-602, 613-623, 626-646, 649-656, 668-673, 675-683, 696-708, 715-722, 724-739, 745-751, 759-777, 780-804, 816-822 and 102-113 of Seq ID No 367; 12-28, 41-91, 98-107, 112-120, 125-131, 151-193, 215-221, 240-250, 263-280 and 128-138 of Seq ID No 368; 16-24, 32-38, 46-62, 68-81, 90-105, 127-133, 144-150, 160-166, 178-184, 186-202, 210-219, 232-240, 252-258, 264-273, 293-324, 337-344, 349-357, 360-369, 385-398, 410-416, 419-427, 441-449, 458-476, 508-515, 523-539, 544-549, 562-569, 571-579, 96-109 and 127-139 of Seq ID No 369; 19-25, 28-34, 56-61, 85-97, 110-116 and 39-53 of Seq ID No 370; 4-37, 41-50, 62-72, 91-97, 99-109, 114-125, 136-141, 149-158, 160-166, 201-215 and 27-225 of Seq ID No 371; 15-31, 44-51, 96-105, 122-130, 149-157, 162-168, 178-183, 185-192, 198-204, 206-213, 221-234, 239-245, 248-255, 257-266, 289-335, 349-357, 415-422, 425-441, 448-454, 462-468 and 463-481 of Seq ID No 372; 5-31, 39-55, 63-72, 76-99, 106-155, 160-177, 179-199, 207-217, 223-240, 245-255, 261-267, 294-316, 321-343, 354-378, 382-452, 477-488, 529-536, 555-569, 584-591, 593-612, 620-627, 632-640, 647-654, 671-680, 698-704, 723-730, 732-750, 769-775, 781-788, 822-852 and 505-525 of Seq ID No 373; 3-18 of Seq ID No 374; 4-14 and 12-24 of Seq ID No 375; 4-11, 22-30 and 12-25 of Seq ID No 376; 5-12 and 4-18 of Seq ID No 377; 4-28 and 7-14 of Seq ID No 378; 6-16 and 8-16 of Seq ID No 379; 4-15, 18-33 and 24-36 of Seq ID No 380; 4-10, 16-21 and 20-31 of Seq ID No 381; 6-19 of Seq ID No 382; 11-18 and 3-10 of Seq ID No 383; 13-24 and 3-15 of Seq ID No 384; 15-27 and 7-16 of Seq ID No 385; 11-16 and 1-15 of Seq ID No 386; 4-16 and 9-21 of Seq ID No 387; 4-24, 40-48, 54-67 and 22-39 of Seq ID No 388; 6-30, 34-55, 62-68, 78-106 and 68-74 of Seq ID No 389; 3-14 of Seq ID No 390; 9-19 and 6-21 of Seq ID No 391; 4-17 and 1-9 of Seq ID No 392; 5-30 and 1-8 of Seq ID No 393; 4-16, 23-46, 51-56 and 45-55 of Seq ID No 394; 7-16 of Seq ID No 395; 2-14 of Seq ID No 396; 4-36, 43-65 and 50-62 of Seq ID No 397; 10-30 and 14-21 of Seq ID No 398; 9-17 and 1-10 of Seq ID No 399; 4-12 and 3-16 of Seq ID No 400; 4-15 and 5-23 of Seq ID No 401; 10-21 of Seq ID No 402; 6-16 of Seq ID No 403; 4-29, 31-38 and 2-14 of Seq ID No 404; 4-35 and 33-42 of Seq ID No 405; 2-17 of Seq ID No 406; 9-18, 30-35 and 15-33 of Seq ID No 407; 4-9 and 6-12 of Seq ID No 408; 3-17 of Seq ID No 409; 12-21, 37-44, 52-61, 72-80 and 38-48 of Seq ID No 410; 4-10, 29-44, 54-61, 69-78 and 13-27 of Seq ID No 411; 13-23, 36-53 and 2-15 of Seq ID No 412; 4-25, 28-46, 56-72, 81-99, 120-132, 134-142, 154-160 and 129-141 of Seq ID No 413; 4-15, 24-33, 35-41, 64-86 and 21-33 of Seq ID No 414; 9-15 and 4-13 of Seq ID No 415; 4-11, 13-19, 34-48 and 15-32 of Seq ID No 416; 4-21 and 11-31 of Seq ID No 417; 23-57 and 38-

50 of Seq ID No 418; 4-32 and 3-13 of Seq ID No 419; 4-10, 13-25, 32-42, 56-68, 72-84 and 26-38 of Seq ID No 420; 4-20, 31-48, 52-58, 65-71, 80-93, 99-108, 114-123 and 37-49 of Seq ID No 421; 6-12, 14-20 and 3-25 of Seq ID No 422; 14-25, 27-38 and 5-14 of Seq ID No 423; 4-41, 57-105, 109-118, 123-136, 144-152 and 86-99 of Seq ID No 424; 6-19 of Seq ID No 425; 2-19 of Seq ID No 426; 14-47 and 1-14 of Seq ID No 427; 4-21, 29-44 and 2-18 of Seq ID No 428; 23-29 and 10-28 of Seq ID No 429; 6-16, 22-36 and 11-22 of Seq ID No 430; 4-19, 30-44 and 18-27 of Seq ID No 431; 5-15, 37-45, 58-65 and 38-47 of Seq ID No 432; 4-15, 23-34 and 4-15 of Seq ID No 433; 30-36, 44-54, 79-85, 101-114, 138-152, 154-164, 170-175, 179-200, 213-220, 223-240, 243-255, 258-264, 268-284 and 10-28 of Seq ID No 434; the peptides comprising amino acid sequences of column "Identical region" of the Table 1B, especially peptides comprising amino acid 210-226 and 738-753 of Seq ID No 449; 326-344, 326-348, 338-354, 371-392, 801-809 and 877-901 of Seq ID No 450; 893-906 of Seq ID No 451; 51-69 of Seq ID No 452; 110-125 of Seq ID No 453; 291-305 of Seq ID No 454; 210-226 and 738-753 of Seq ID No 455; 326-344, 326-348, 338-354, 371-392, 801-809 and 877-901 of Seq ID No 456; 893-906 of Seq ID No 457; 51-69 of Seq ID No 458; 110-125 of Seq ID No 459; 291-305 of Seq ID No 460; 32-44 of Seq ID No 461; 399-410 of Seq ID No 462; the serum reactive epitopes as specified in the column of "aa from" to "aa to" of Table 2, especially peptides comprising amino acid 120-143, 138-161 and 156-179 of Seq ID No 218; 110-129 and 168-184 of Seq ID No 219; 74-90 of Seq ID No 222; 759-773 of Seq ID No 223; 237-260 of Seq ID No 224; 265-284 of Seq ID No 225; 65-74 of Seq ID No 226; 41-50 of Seq ID No 227; 163-174 of Seq ID No 229; 26-37 of Seq ID No 230; 174-189 of Seq ID No 232; 240-256 of Seq ID No 234; 285-297 of Seq ID No 236; 238-247 of Seq ID No 238; 491-519 of Seq ID No 239; 114-140 of Seq ID No 243; 267-284 of Seq ID No 250; 439-453 of Seq ID No 252; 162-178 of Seq ID No 253; 347-364 of Seq ID No 254; 699-715 of Seq ID No 255; 60-71 of Seq ID No 256; 244-257 of Seq ID No 257; 44-63 and 57-76 of Seq ID No 258; 185-196 of Seq ID No 260; 119-129 of Seq ID No 263; 182-195 of Seq ID No 266; 32-44 and 424-442 of Seq ID No 267; 247-256 of Seq ID No 268; 678-694, 785-805, 55-77 and 72-94 of Seq ID No 269; 210-226 of Seq ID No 281; 37-59 of Seq ID No 289; 13-29 of Seq ID No 296; 136-159 of Seq ID No 348; 205-222 of Seq ID No 349; 99-110 of Seq ID No 350; 160-176 of Seq ID No 351; 457-470 of Seq ID No 355; 221-237 of Seq ID No 356; 167-190 of Seq ID No 357; 96-120 of Seq ID No 361; 399-417, 503-519 and 544-563 of Seq ID No 364; 46-68, 159-183 and 184-198 of Seq ID No 371; 463-481 of Seq ID No 372; the immunogenic epitopes as specified in the column of "aa from" to "aa to" of Table 4; especially peptides comprising amino acid 110-129 and 168-184 of Seq ID No 219; 877-901, 333-354, 326-344 and 801-809 of Seq ID No 277; 1-54 of Seq ID No 347; 544-563, 31-51, 107-119, 399-417 and 503-519 of Seq ID No 364; 120-198 of Seq ID No 218; 20-35 of Seq ID No 219; 118-201 of Seq ID No 221; 48-132 of Seq ID No 242; 118-136 of Seq ID No 249; 162-178 of Seq ID No 253; 347-364 of Seq ID No 254; 699-715 of Seq ID No 255; 50-76 of Seq ID No 258; 785-819 and 44-128 of Seq ID No 269; 90-128 of Seq ID No 274; 314-384 of Seq ID No 289; 327-349 of Seq ID No 293; 242-314, 405-478 and 23-100 of Seq ID No 304; 129-210 of Seq ID No 305; 162-188 of Seq ID No 307; 750-772 of Seq ID No 310; 1-56 of Seq ID No 335; 322-337 of Seq ID No 337; 72-90 of Seq ID No 339; 374-395 of Seq ID No 345; 136-159 of Seq ID No 348; 141-164 of Seq ID No 358; 96-157 of Seq ID No 361; 1-82 of Seq ID No 363; 489-556 of Seq ID No 364; 159-183 and 49-133 of Seq ID No 371; The peptides comprising amino acid sequences of column "predicted immunogenic aa" and "location of identified immunogenic region (aa)" of Table 5, especially peptides comprising amino acid 4-26, 35-41, 53-61, 73-84, 103-108, 114-120, 140-146, 156-162, 192-208, 214-219, 227-233, 239-252, 260-268, 284-297, 1-48 and 113-133 of Seq ID No 475; 4-27, 38-44, 50-56, 59-64, 72-79, 83-89, 92-97, 108-116, 123-148, 152-167, 183-196, 200-220, 232-244, 255-261, 265-274, 282-302, 309-317, 1-79 and 231-302 of Seq ID No 476; 6-28, 66-72, 85-105, 115-121, 144-151, 160-170, 176-185, 223-230, 252-288, 296-310, 319-333, 367-374, 458-464, 471-480, 483-488, 520-528, 530-549, 559-564, 593-601, 606-616, 636-643, 655-662, 676-682, 684-699, 719-726, 735-750, 757-764, 777-785, 799-810, 812-843, 846-853, 868-873, 880-889, 891-899, 909-929, 934-940, 963-969, 998-1004, 1007-1014, 1016-1022, 1030-1046, 1-80 and 808-821 of Seq ID No 477; 7-24, 35-41, 75-81, 91-114, 122-132, 137-144, 148-156, 183-192, 194-200, 212-228, 233-238, 251-258, 275-295, 326-332, 337-346, 1-79 and 305-321 of Seq ID No 478; 31-38, 42-52, 66-72, 86-92, 98-104, 115-122, 127-146, 154-164, 169-187, 198-212, 225-237, 255-269, 13-92 and 135-142

of Seq ID No 479; 4-36, 39-49, 63-69, 71-77, 81-88, 123-131, 133-139, 160-169, 174-180, 188-194, 210-217, 273-278, 289-300, 317-334, 336-341, 383-401, 425-438, 1-68, 212-270 and 402-446 of Seq ID No 480; 21-29, 31-42, 49-63, 72-79, 81-93, 112-132, 159-165, 188-195, 197-232, 262-267, 279-286, 294-301, 318-326, 348-366, 381-405, 409-426, 436-465, 471-480, 484-492, 497-505, 521-544, 554-561, 567-577, 581-589, 601-609, 611-622, 636-651, 653-667, 669-685, 700-708, 716-722, 729-744, 749-766, 780-786, 789-811, 814-864, 1-57 and 84-106 of Seq ID No 481; 6-24, 35-48, 57-63, 72-78, 87-92, 113-119, 123-137, 147-153, 173-181, 212-233 and 1-124 of Seq ID No 482; 13-34, 62-69, 78-83, 86-91, 98-104, 107-115, 146-159, 179-188, 195-205, 209-221, 226-233, 239-253, 276-282, 284-294, 297-308, 331-354, 375-382, 388-399, 421-433, 449-458, 464-469, 472-491, 508-513, 525-531, 534-550, 575-593, 601-618, 629-635, 654-661, 666-680, 706-721, 723-740, 771-805, 810-830, 845-851 and 1-84 of Seq ID No 483; 4-32, 45-64, 73-83, 86-92, 100-111, 125-147, 157-163, 170-175, 177-188, 226-232, 245-252, 258-274, 320-335, 348-359 and 1-71 of Seq ID No 484; 13-40, 43-71, 76-83, 87-101, 109-119, 125-156, 162-175, 182-219, 226-232, 240-262, 270-287, 306-318, 326-342, 344-408, 414-444, 449-456 and 1-51 of Seq ID No 485; 4-16, 18-34, 45-54, 99-108, 134-140, 203-212, 241-257, 266-274, 279-291, 308-315, 330-336, 355-370, 374-382, 402-410, 428-455, 466-472, 474-480, 531-554, 560-566, 572-580, 597-618, 632-660, 664-674, 676-685, 691-705, 708-735, 750-768, 1-87 and 342-480 of Seq ID No 486; The serum reactive epitopes as specified in the column of "aa from" to "aa to" of Table 6, especially peptides comprising amino acid 115-132 and 1-26 of Seq ID No 475; 33-55 of Seq ID No 476; 1-25 of Seq ID No 478; 37-61 of Seq ID No 479; 1-24 of Seq ID No 480; 1-23 of Seq ID No 481; 46-60 of Seq ID No 482; 1-28, 23-50 and 45-71 of Seq ID No 483; 1-22 and 17-38 of Seq ID No 484; 1-22 and 17-38 of Seq ID No 485; 1-27, 22-47 and 422-447 of Seq ID No 486; The immunogenic epitopes as specified in the column of "aa from" to "aa to" of Table 7, especially peptides comprising amino acid 115-132 and 1-47 of Seq ID No 475; 1-55 of Seq ID No 476; 22-85 of Seq ID No 477; 307-320 and 1-44 of Seq ID No 478; 15-76 and 40-92 of Seq ID No 479; 1-59, 213-269 and 403-445 of Seq ID No 480; 1-56 and 85-105 of Seq ID No 481; 37-121 of Seq ID No 482; 1-71 of Seq ID No 483; 1-38 of Seq ID No 484; 1-38 of Seq ID No 485; 1-47 of Seq ID No 486.

15. A process for producing a *S. agalactiae* hyperimmune serum reactive antigen or a fragment thereof according to any one of the claims 11 to 14 comprising expressing the nucleic acid molecule according to any one of claims 1 to 7.
16. A process for producing a cell, which expresses a *S. agalactiae* hyperimmune serum reactive antigen or a fragment thereof according to any one of the claims 11 to 14 comprising transforming or transfecting a suitable host cell with the vector according to claim 8 or claim 9.
17. A pharmaceutical composition, especially a vaccine, comprising a hyperimmune serum-reactive antigen or a fragment thereof, as defined in any one of claims 11 to 14 or a nucleic acid molecule according to any one of claims 1 to 7.
18. A pharmaceutical composition, especially a vaccine, according to claim 17, characterized in that it further comprises an immunostimulatory substance, preferably selected from the group comprising polycationic polymers, especially polycationic peptides, immunostimulatory deoxynucleotides (ODNs), peptides containing at least two LysLeuLys motifs, neuroactive compounds, especially human growth hormone, alum, Freund's complete or incomplete adjuvants or combinations thereof.
19. Use of a nucleic acid molecule according to any one of claims 1 to 7 or a hyperimmune serum-reactive antigen or fragment thereof according to any one of claims 11 to 14 for the manufacture of a pharmaceutical preparation, especially for the manufacture of a vaccine against *S. agalactiae* infection.
20. An antibody, or at least an effective part thereof, which binds at least to a selective part of the

hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14.

21. An antibody according to claim 20, wherein the antibody is a monoclonal antibody.
22. An antibody according to claim 20 or 21, wherein said effective part comprises Fab fragments.
23. An antibody according to any one of claims 20 to 22, wherein the antibody is a chimeric antibody.
24. An antibody according to any one of claims 20 to 23, wherein the antibody is a humanized antibody.
25. A hybridoma cell line, which produces an antibody according to any one of claims 20 to 24.
26. A method for producing an antibody according to claim 20, characterized by the following steps:
 - initiating an immune response in a non-human animal by administering an hyperimmune serum-reactive antigen or a fragment thereof, as defined in any one of the claims 11 to 14, to said animal,
 - removing an antibody containing body fluid from said animal, and
 - producing the antibody by subjecting said antibody containing body fluid to further purification steps.
27. Method for producing an antibody according to claim 21, characterized by the following steps:
 - initiating an immune response in a non-human animal by administering an hyperimmune serum-reactive antigen or a fragment thereof, as defined in any one of the claims 12 to 15, to said animal,
 - removing the spleen or spleen cells from said animal,
 - producing hybridoma cells of said spleen or spleen cells,
 - selecting and cloning hybridoma cells specific for said hyperimmune serum-reactive antigens or a fragment thereof,
 - producing the antibody by cultivation of said cloned hybridoma cells and optionally further purification steps.
28. Use of the antibodies according to any one of claims 20 to 24 for the preparation of a medicament for treating or preventing *S. agalactiae* infections.
29. An antagonist, which binds to the hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14.
30. A method for identifying an antagonist capable of binding to the hyperimmune serum-reactive antigen or fragment thereof according to any one of claims 11 to 14 comprising:
 - a) contacting an isolated or immobilized hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14 with a candidate antagonist under conditions to permit binding of said candidate antagonist to said hyperimmune serum-reactive antigen or fragment, in the presence of a component capable of providing a detectable signal in response to the binding of the candidate antagonist to said hyperimmune serum reactive antigen or fragment thereof; and
 - b) detecting the presence or absence of a signal generated in response to the binding of the antagonist to the hyperimmune serum reactive antigen or the fragment thereof.
31. A method for identifying an antagonist capable of reducing or inhibiting the interaction activity of a hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to

- 14 to its interaction partner comprising:
- a) providing a hyperimmune serum reactive antigen or a hyperimmune fragment thereof according to any one of claims 11-14,
 - b) providing an interaction partner to said hyperimmune serum reactive antigen or a fragment thereof, especially an antibody according to any one of the claims 20 to 24,
 - c) allowing interaction of said hyperimmune serum reactive antigen or fragment thereof to said interaction partner to form a interaction complex,
 - d) providing a candidate antagonist,
 - e) allowing a competition reaction to occur between the candidate antagonist and the interaction complex,
 - f) determining whether the candidate antagonist inhibits or reduces the interaction activities of the hyperimmune serum reactive antigen or the fragment thereof with the interaction partner.
32. Use of any of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 11 to 14 for the isolation and/or purification and/or identification of an interaction partner of said hyperimmune serum reactive antigen or fragment thereof.
33. A process for *in vitro* diagnosing a disease related to expression of the hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14 comprising determining the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen and fragment according to any one of claims 1 to 7 or the presence of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 11-14.
34. A process for *in vitro* diagnosis of a bacterial infection, especially a *S. agalactiae* infection, comprising analysing for the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen and fragment according to any one of claims 1 to 7 or the presence of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 11 to 14.
35. Use of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 11 to 14 for the generation of a peptide binding to said hyperimmune serum reactive antigen or fragment thereof, wherein the peptide is selected from the group comprising anticalines.
36. Use of the hyperimmune serum-reactive antigen or fragment thereof according to any one of claims 11 to 14 for the manufacture of a functional nucleic acid, wherein the functional nucleic acid is selected from the group comprising aptamers and spiegelmers.
37. Use of a nucleic acid molecule according to any one of claims 11 to 14 for the manufacture of a functional ribonucleic acid, wherein the functional ribonucleic acid is selected from the group comprising ribozymes, antisense nucleic acids and siRNA.

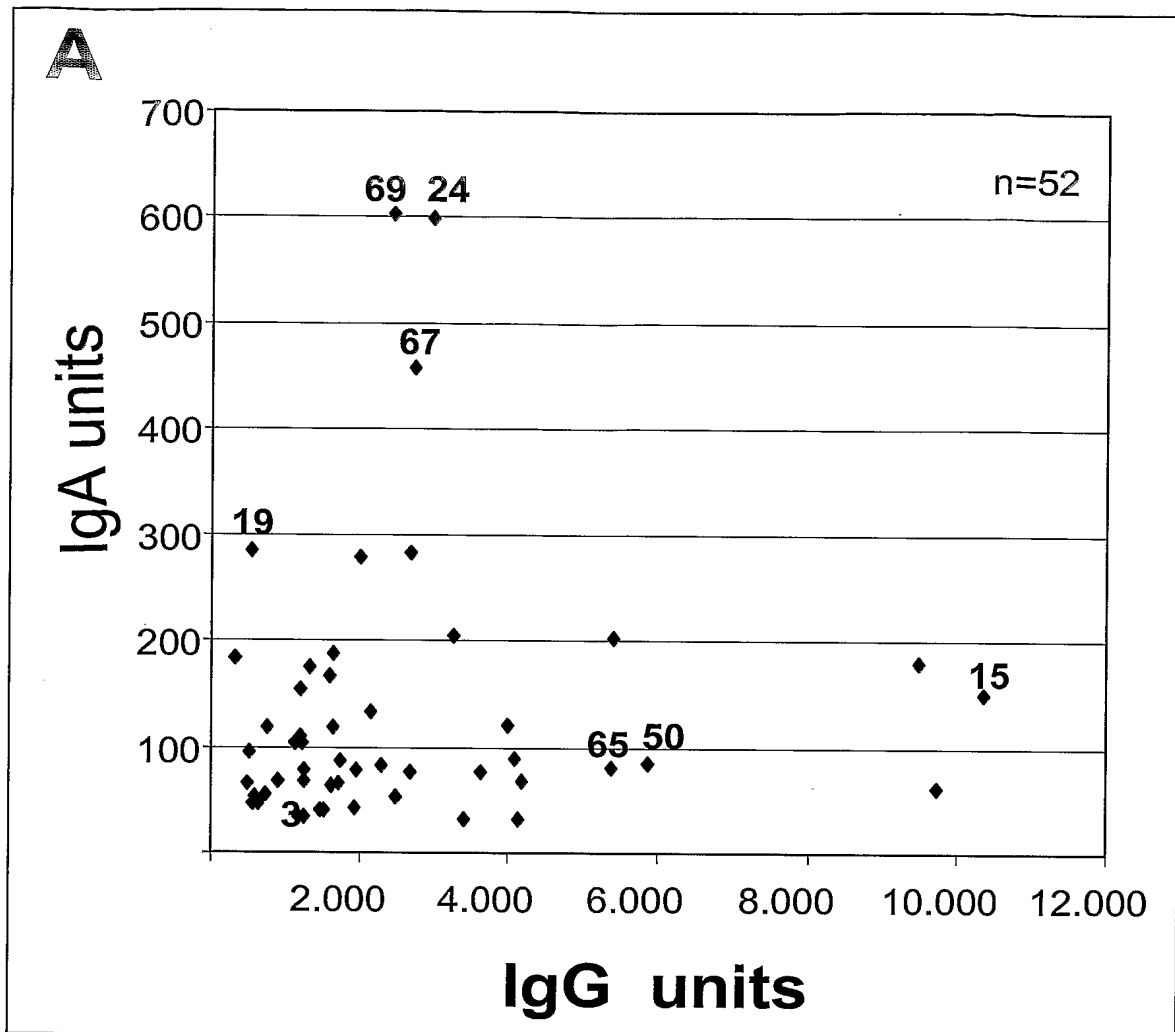


Fig. 1

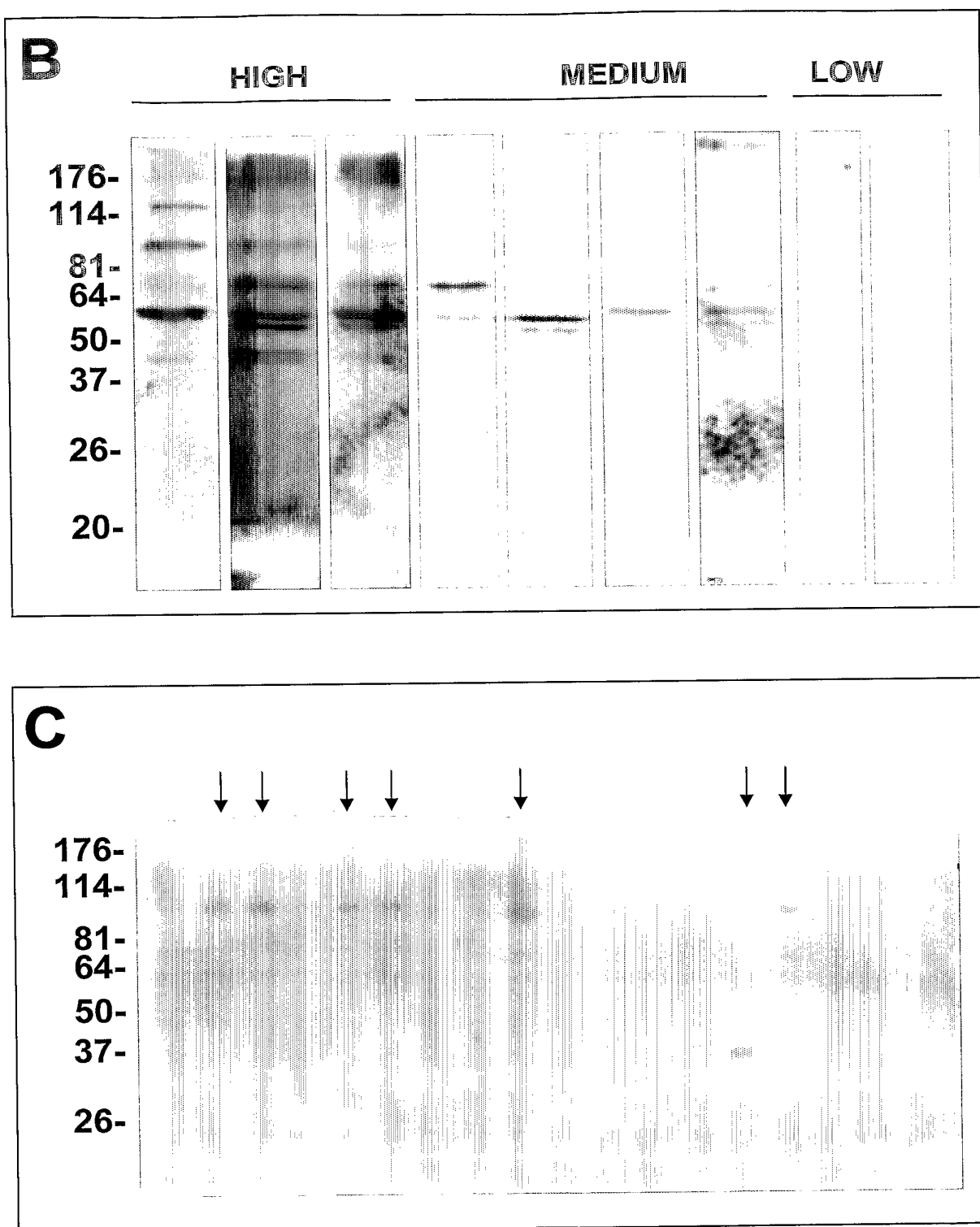


Fig. 1

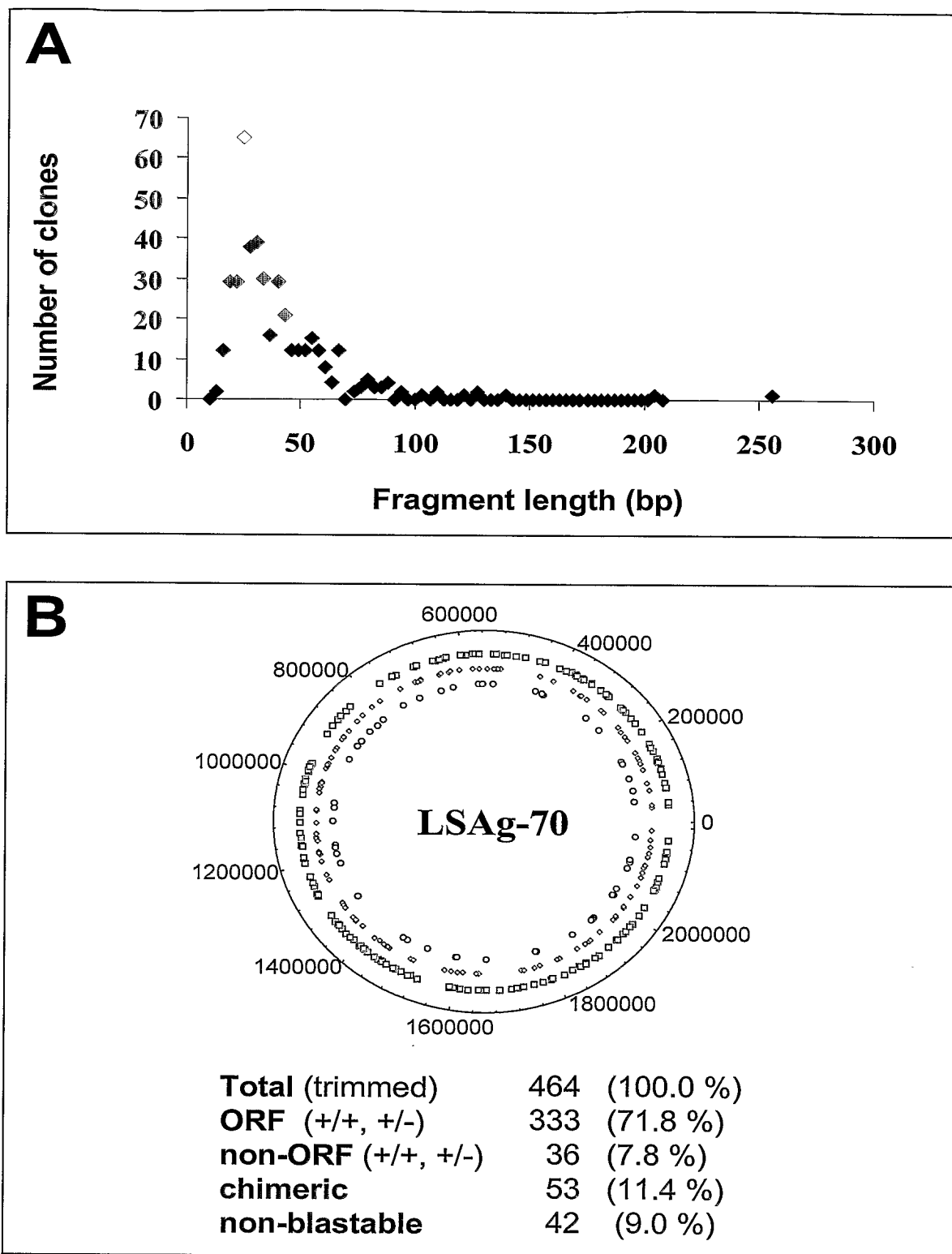


Fig. 2

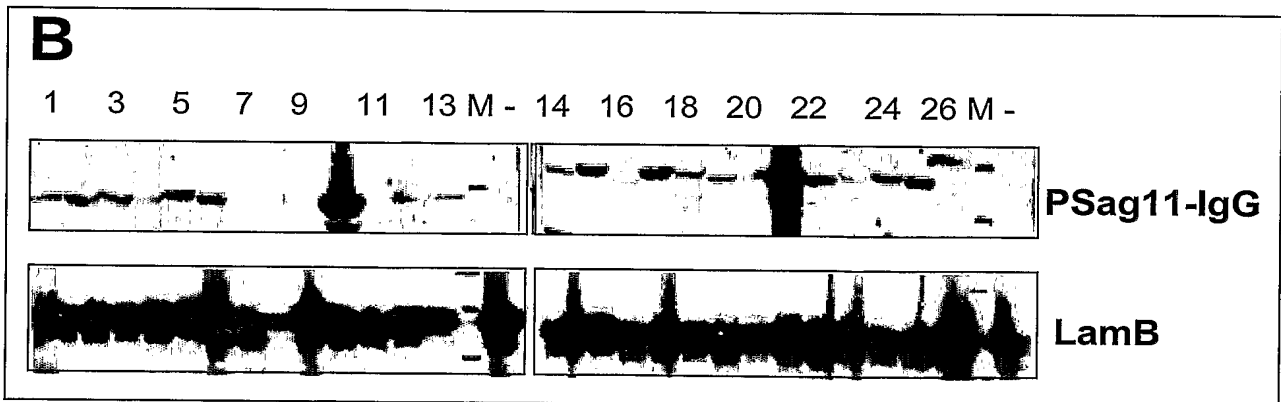
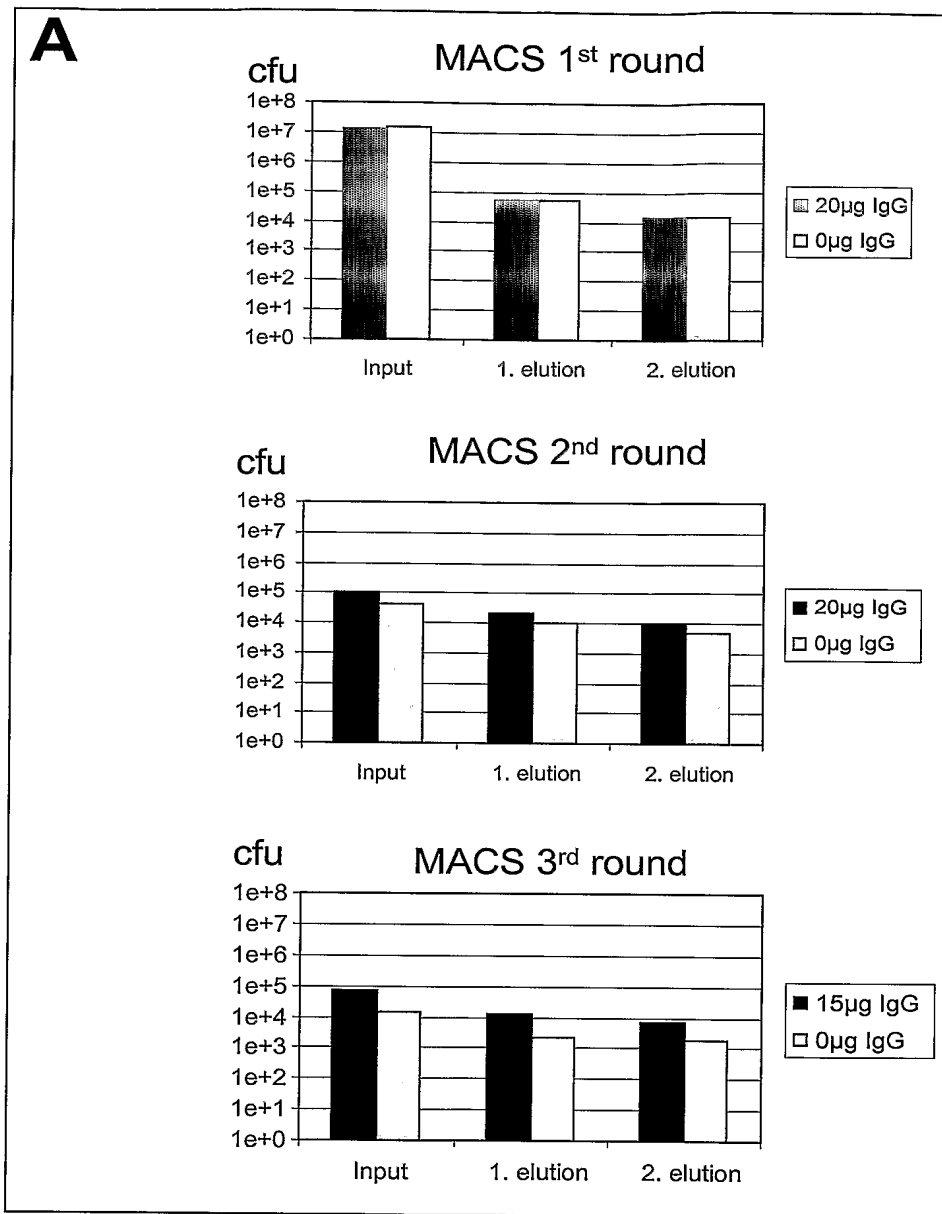


Fig. 3

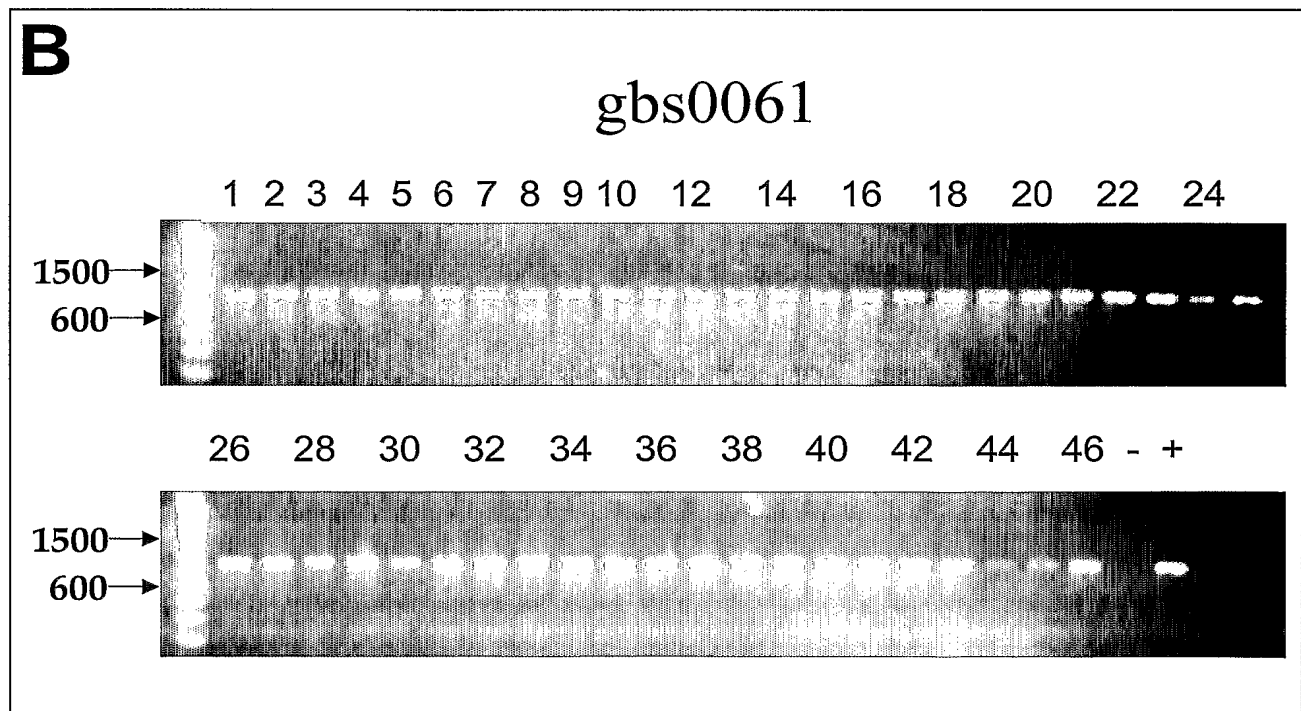
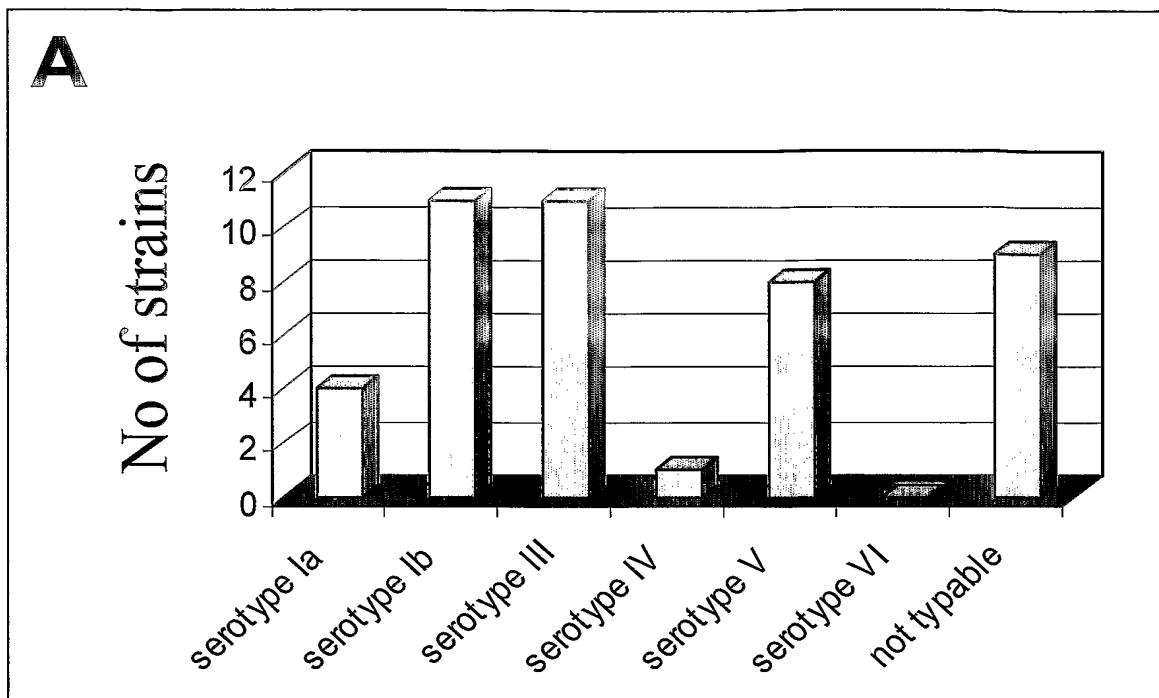


Fig. 4

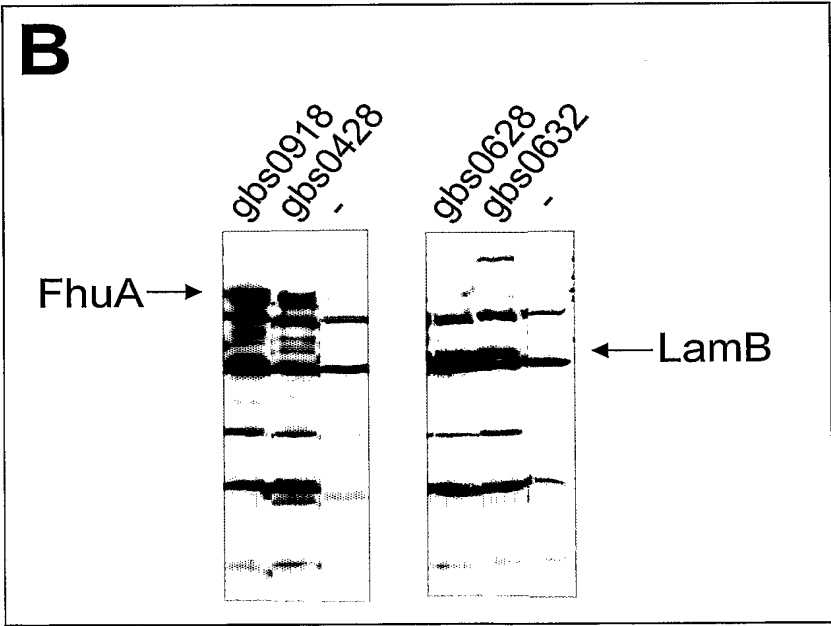
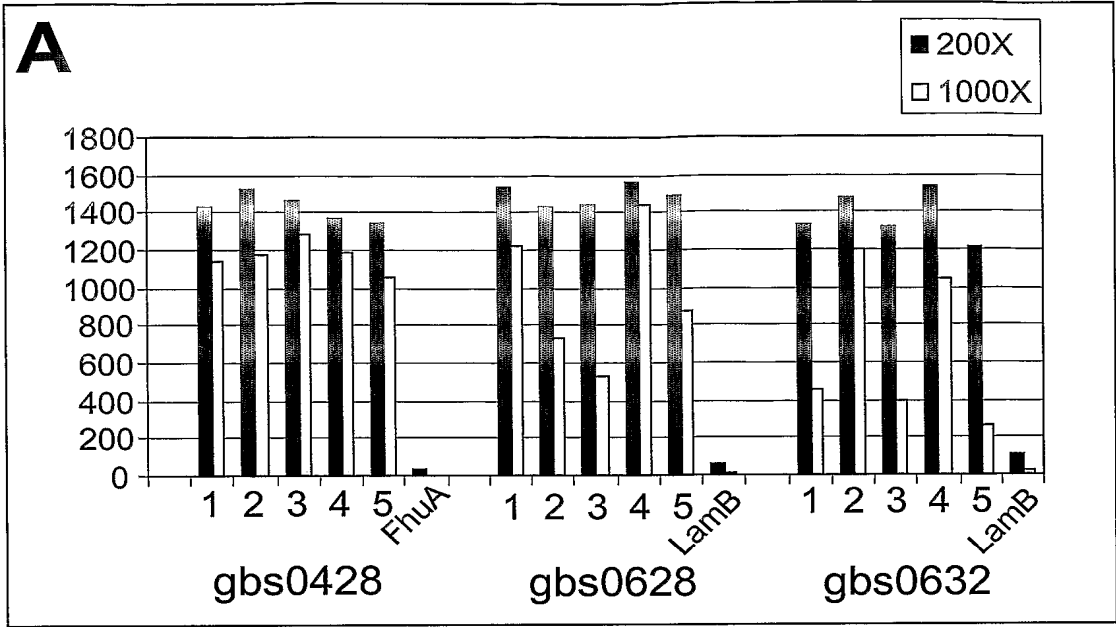


Fig. 5

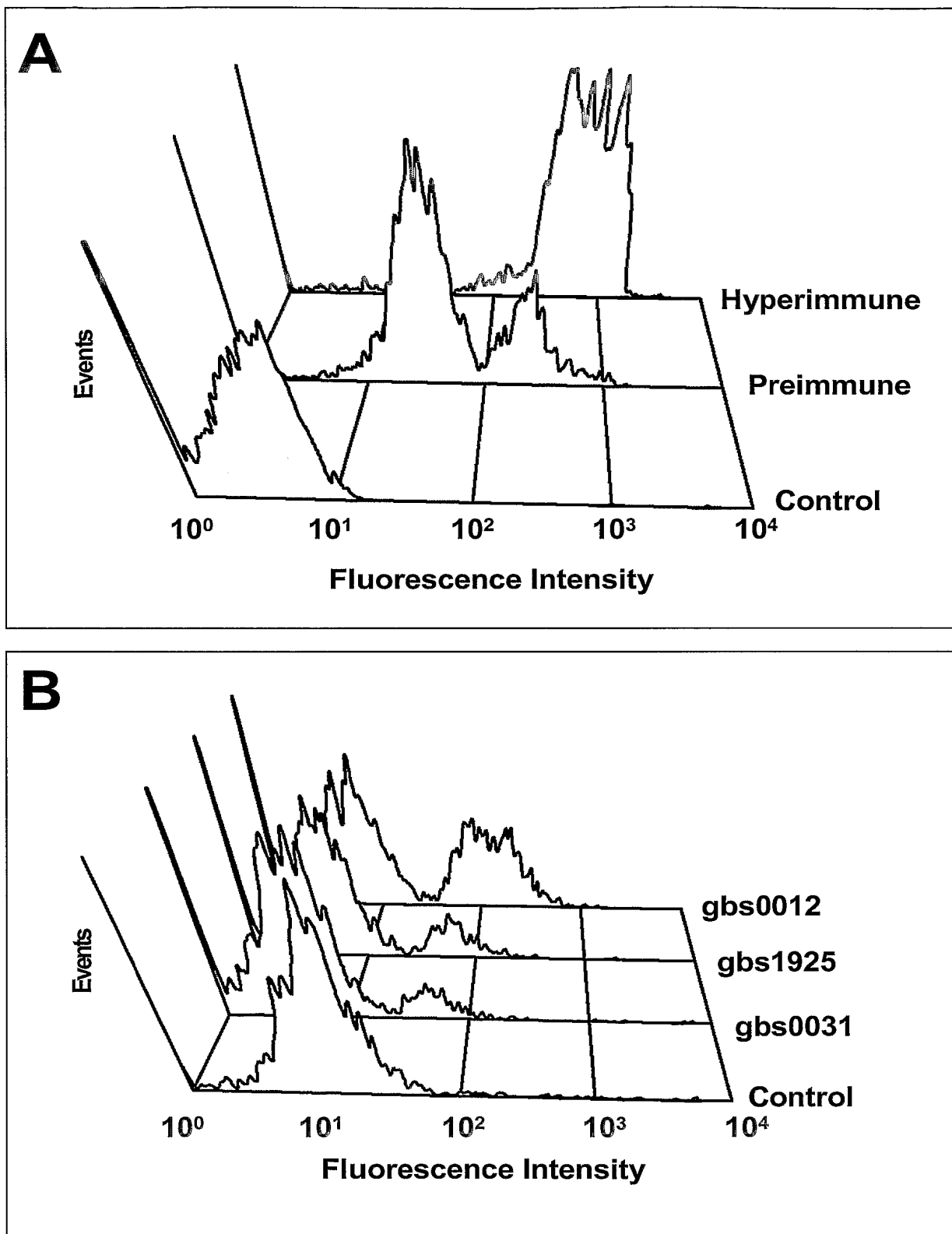


Fig. 6

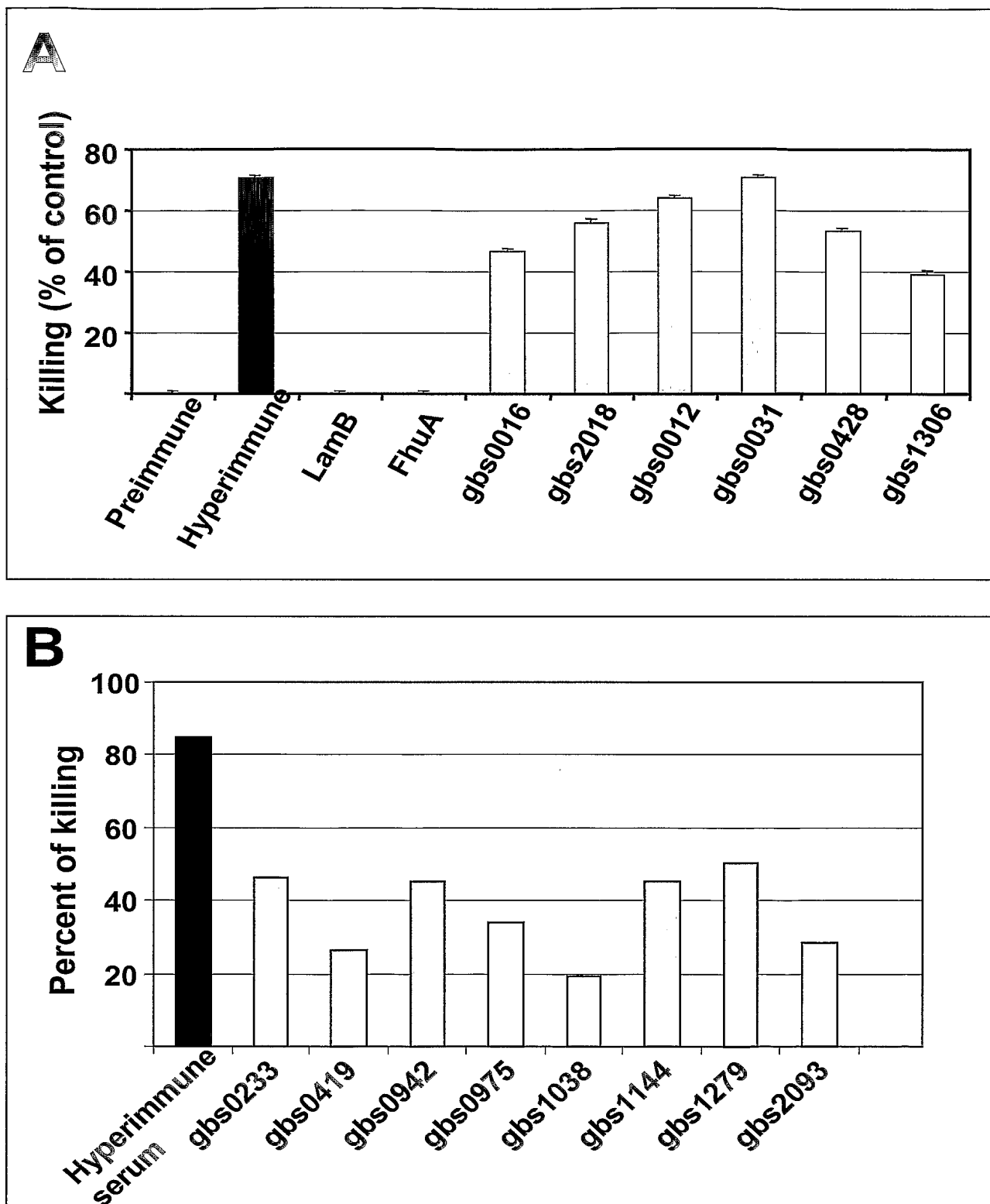


Fig. 7

SEQUENCE LISTING

SeqID 1

atgaagaaaag	ttttaaacctt	cttattatgt	agcttatatt	ttgtatcaat	cccagctata	60
agtaccgagg	agccattaac	gctttctcaa	aatagacgat	acgccttaac	tcagacagtt	120
gtggataaag	aaatgtat	tgatgctatt	ccagagagac	caactacaaa	aattgaaata	180
agcagttttc	aagatgaagc	tttaaccata	acaggagaga	ctttagttcc	aaatacttta	240
ttgtcgattg	tttctcttac	aattaattca	aatggaattc	cagtatttac	tttgtccaat	300
ggacagttca	ttaaaggctag	tcgtgaagct	atttttaatg	atttagtttc	taagcagcaa	360
tctgtctcat	tggattattg	gttaaaacct	tcttttgtga	cttatgaagc	accttacaca	420
aatggtgtta	gtgaagttta	aaataattta	aaaccttatt	ccagagtgc	tttagtagaa	480
caagcagaaa	cagaacatgg	tatttattat	aaaacggaca	gtggtttttg	gatatcagta	540
gaagatctat	cggttgctga	taatcgtatg	gctaagggtc	aagaagtatt	attggaaaaa	600
tataataaag	ataaatatgg	tatatacatc	aaacaattaa	atacacagac	agtagctggt	660
attaatatgg	ataggtcaat	gtactctgca	agtattgcaa	aattagcaac	actttatgct	720
agccaagagc	agtaaaaatt	aggaaaaactg	tcattggaca	gcaaatttga	atacaaatgat	780
aatgttaatc	aatttcctaa	tagctatgat	ccaagtggta	gtgggaaatt	agagaaaaaa	840
gctgatcata	aattatatac	cgtaaggag	ttacttgaag	caactgcaa	ggaatcagat	900
aatgttgcaa	caaatatgct	aggttattat	gtcaataatc	aatatgattc	aatgtttcaa	960
acacaagtag	acacaatttc	tggatgac	tgggatatga	aaaaacgcca	gatttctcca	1020
caagctgcgg	gtaaaatgat	ggaagcaatt	tattatcaaa	atggagatat	tgtaattac	1080
ctatcaaaga	ctgattttga	taatacaaga	atccctaaaa	atataccagt	taagtagaca	1140
cataaaattg	gagatgctta	tgactacaaa	catgatgcgg	ctattgttta	tcagaaacaa	1200
ccttttatta	tgattatctt	tacggataaa	tcactctacg	atgatatcac	taagattgct	1260
gacgacgttt	accaggtttt	aaaataa				1287

SeqID 2

atgaaaaaaaa	gaatattatc	agcagtcctt	gtgagtgagg	taactcttgg	aactgctgcc	60
gtaacagtaa	acgtgatga	ctttgactcg	aaaattgctg	ctactgattc	agtaatcaat	120
actttatcag	ggcaacaagc	agcagcacia	aaccaggtga	ctgctattaa	aggacaagtt	180
ggtgcttttag	agtctcaaca	atcagaatta	gaagcgcaaa	atgctcaact	tgaggctgta	240
tctcagcagt	taggtcaaga	gattcaaact	ctttctaata	aaattggtgc	acgtaacgaa	300
tctttgaaaa	agcaagttcg	tagtgcctca	aagggttaact	tgactaacta	tattaatact	360
attttaaaatt	cgaatcagt	atctgatgct	gttaatcgtg	ttgttgctat	tcgtgaggtt	420
gtttcagcta	atgaaaagat	gttagcacia	acaagggctg	acaaagcggc	cttagaagct	480
aaacaaattg	aaaatcaaaa	tgctataaat	actgtagcag	ctaacaagca	agctatcgaa	540
aataataaag	cagccttagc	aacacaaaaga	gcacaattag	aagcagctca	attagagtta	600
tctgctcaat	tgactacagt	ccaaaatgaa	aaagcatctt	taattcaggc	aaaagcacia	660
gctgaggaag	ctgcgcgtaa	ggcagctgaa	gcacaagcag	cagctgaagc	gaaagcacia	720
gctgaagcga	aagcacaagc	tgagtctgta	gcaaaagcac	aggcagcagc	acaagttgag	780
tctgccacag	ctcctactga	aacagttcaa	acacaaccga	gaactgaaat	aaagccttct	840
aatcttacgg	ctacttcttc	ggcaactact	cttgctacaa	ctacagctac	agctactaat	900
gagccaaaag	ttactcaacc	ttctgtagta	actaaagcag	ttgaagcacc	taaagcagtt	960
gtttcttcaa	cacctagagc	ggtatcaaaa	cctgttgtca	gaagttatga	ttcaagtaac	1020
acatacccaa	tgggacaatg	tacttgggga	gctaagtcaa	tggcttcttg	ggttggtaac	1080
tattggggaa	atgctaatac	gtggggtgct	agtgcacgtg	cagctggtta	ttctgttagga	1140
actacccttc	gtgttggtgc	agtagctggt	tggccatatg	atggtgggtg	ttacgggcac	1200
gttgacgtag	taacgtcagt	ggctaacaat	tcacttatcc	aagttatgga	atcaaatcat	1260
gctggaaata	tgagtattgg	caattacogt	gggttcattta	accctagtgc	ttctggctct	1320
gtttactata	tttaccocaaa	ttaa				1344

SeqID 3

atgaataaac	gtatTTTTgt	tgagaaaaag	gctgactttg	acattaaatc	ggctagtctt	60
gtgaaagagt	tgacgcataa	tctacaactg	acttctttga	aggatttgcg	tattgtgcag	120
gtctatgag	tcttcaattt	ggctgaggat	ttgctggcgc	gtgctgagaa	gcataatttc	180
tctgagcagg	tgacagactg	tcttttgacg	gaaactgaaa	tcactgcgga	gcttgataag	240
gttgccctct	ttgccattga	ggcgcttcc	gggtcaattt	accaacgtgc	tgctagtctg	300
caagaatctt	tgctattgct	tggaggtgac	agtcagggtta	agggtcaatac	agcccagctt	360
tacttggtca	ataaggatat	tgacgaagca	gagcttgaag	ccgttaagaa	ctatcttttg	420
aatcctgttg	attcacgttt	caaggacatt	accttgccgc	ttgaagagca	ggctttctct	480
tggtctgata	agacaatccc	tagtcttgat	ttctttgaaa	cttataaggc	tgacgatttt	540
gcggccata	aggcagagca	gggcttggtc	atggaggctg	atgatcttct	cttcattcaa	600
gattattttca	aatcaatcgg	gggtgtgcca	actgagactg	agttgaaagt	tttgataact	660
tactgggtcag	accactgccg	tcacacaacc	tttgaaactg	agttgaaaaa	catcgacttt	720
tcagcttcta	aattccaaaa	acaattgcag	gcgacttatg	acaaatatat	cgccatgcgt	780

gatgaacttg	gtcgttctga	aaagccgcag	acacttatgg	atatggcgac	tatcttttgg	840
cggttatgaac	gtgccaatgg	acgactggat	gatatggaag	tctcagatga	aatcaatgcc	900
tgctcagttg	aaattgaagt	agatgttgat	gggtgaaaag	agccttggct	cctcatgttt	960
aagaatgaga	ctcacaatca	cccaacagaa	attgagccat	ttggtggcgc	agcaacttgt	1020
atcgggtggg	ccattcgtga	cccgttgtca	ggacgttcat	acgtttatca	ggctatgcgt	1080
atttcaggcg	caggcgatat	tacgactccg	attgcggaaa	cacgtgctgg	taaattgccg	1140
caacaggtta	tttctaaaaa	tgccggcgac	ggctattctt	catatggtaa	ccagattggg	1200
cttgcgacaa	cttatgtgcg	tgagtacttt	caccctggct	ttgtagccaa	acgcattggg	1260
cttgagagctg	tggttgggtgc	tgacacctaag	gaaaatgtgg	ttcgtgaaaa	accagaagca	1320
ggcgatgtgg	tcatcttgct	cggtggtaaa	acaggtcgtg	acgggtgctgg	cggtgcgaca	1380
ggttcatcta	aggttcaaac	ggttgaatct	gtggaaacag	ctggcgcgaga	ggtaaaaaaa	1440
gggaatgcca	tccaagaacg	taagattcaa	cgccttttcc	gtaatggtaa	tgtcactcgc	1500
ctaatacaaga	aatcaaatga	cttcgggtgca	gggtgtgtct	gtgttgccat	cggtgaattg	1560
gctcaggttc	tttgaaatga	tttggaacga	gtaccgttta	aataccaaag	tcttaattgg	1620
actgaaattg	caatctcaga	atcacaagag	cgtatgtcag	tcgttgttcg	tcctagtgcg	1680
gtggatacct	tcatcgcagc	ctgcaacaag	gaaaatatcg	atgccgttgt	ggttgctact	1740
attactgcaa	aaccaaacct	tgtcatgact	tgggatgggt	aaacaattgt	tgacttggaa	1800
cgccgtttcc	ttgataccaa	cggtgtccgt	gtcgttgttg	atgctaaagt	cgttgacaaa	1860
gacttgacag	ttccagaggt	acgcacaaca	tcagcagaga	cacttgaagc	ggatacgcct	1920
aaggtcttgt	ctgacctcaa	ccacgctagt	caaaaaggct	tccaaactat	ctttgactca	1980
tctgttgggtc	gctcaaccgt	taaccaccca	atcgggtggc	gttaccaaat	cacaccaaca	2040
gaaagctctg	ttcaaaaatt	gccagttcaa	cacgggtgtca	caacaactgc	atctgttatg	2100
gctcaagggt	acaatcctta	tattgcagaa	tggtcacctt	accacgggtg	tgcttatgct	2160
gtcattgaag	cgacagctcg	cttggttagca	acgggtgctg	actggtctcg	tgacagtttc	2220
tcttaccaag	agtatttcga	gcgtatggat	aaacaggcag	agcgttttgg	tcagccagta	2280
tcagctcttc	ttgggtctat	tgaggctcag	attcaacttg	gattgccatc	aatcgccggg	2340
aaggactcta	tgtctgggtac	tttcgaagaa	ttgacagtac	cgccaaacct	ggtagctttc	2400
gggtgtgacaa	cagcggacag	ccgcaagggt	ctctctcctg	agttttaaag	ggctgggtgag	2460
aatatctact	acattccagg	tcaagctatt	tcagaagata	ttgattttga	ccttatcaag	2520
gctaacttta	gccagttcga	gactattcaa	gctcaacata	agattactgc	tgcttcagct	2580
gttaaatatcg	gtgggtgtcct	agaaagtctt	gctctcatga	cttttggtaa	ccgtatcggg	2640
gcctctgttg	aaattgcaga	gcttgacagt	agcttgacag	ctcaactcgg	aggtcttgtc	2700
tttacctcag	ctgaggaaat	tgctgactcg	gtgaaaatcg	gtcaaaactca	ggcagccttt	2760
acacttactg	tcaatggaaa	tgaccttgct	ggggcaagcc	ttctatcagt	cttcgaaggc	2820
aaattggaag	aggtttaccg	aacagagttt	gaacaggcag	acgtctctga	agaagttcct	2880
gctgtggtat	cagatactgt	tatcaaggct	aaggaaacaa	ttgaaaaacc	agtgggtttac	2940
attccagctc	tccctgggtac	caactcagaa	tatgattcag	ctaaggcctt	tgaacagggt	3000
ggagctagtg	tcaacttggg	agcattttgt	accttgaatg	aggctgctat	tgctgactca	3060
gttgacacaa	tggtcgctaa	tattgctaag	gcaaatatca	tcttctttgc	tgaggagattc	3120
tcagcagcgg	atgaaccaga	tggtgtcgtc	aagtttatcg	tcaatatctt	gcttaacaag	3180
aagggttcg	cagctattga	cagcttcctc	gaaaaagggt	gccttatcat	cggtatctgt	3240
aatgggtttcc	aagcccttgt	taaatacagg	cttcttccat	acggaaaact	cgagggaagct	3300
gggtgagacaa	gtccaaccct	cttctataac	gatgccaaac	agcacgttgc	caagatgggt	3360
gagactcgta	tcgcaaatat	caactcacct	tggttggtag	gagttgagg	cgccgatatt	3420
catgccatcc	cagtttcaca	cggtgaagg	aaatttgttg	tcagcgcctc	tgaatttgca	3480
gagctaagag	acaatgggtc	aatctggagc	caatatgtgg	actttgacgg	acaaccatct	3540
atggattcta	ataacaatcc	aaatggctct	gtcaatggcca	tcgaagggat	taccagcaag	3600
aatgggtcaaa	tcatcggtaa	gatggggcac	tcagaacgct	gggaagacgg	cctcttccaa	3660
aatatccctg	gtaacaaaga	ccaagccttg	tttgctagt	cagtaaaaata	ttttacagga	3720
aaataa						3726

SeqID 4

atgaaaaatga	ataaaaaagg	actattgaca	tcgacaatgg	cagcttcgct	attatcagtc	60
gcaagtgttc	aagcacaaga	aacagatacg	acgtgggacag	cacgtactgt	ttcagaggta	120
aaggctgatt	tggtaaagca	agacaataaa	tcatcatata	ctgtgaaata	tggtgataca	180
ctaagcggtta	tttcagaagc	aatgtcaatt	gatatgaatg	tcttagcaaa	aataaataac	240
attgcagata	tcaatcctat	ttatcctgag	acaacactga	cagtaactta	cgatcagaag	300
agtcatactg	ccacttcaat	gaaaatagaa	acaccagcaa	caaatgctgc	tggtcaaaaca	360
acagctactt	tggtattgaa	aaccaatcaa	gtttctgttg	cagacaaaaa	agtttctctc	420
aatacaattt	cgggaaggat	gacaccagaa	gcagcaacaa	cgattgtttc	gccaatgaag	480
acataattct	ctgcgccagc	tttgaaatca	aaagaagtat	tagcacaaga	gcaagctgtt	540
agtcaagcag	cagctaataga	acaggtatca	ccagctcctg	tgaagtccat	tacttcagaa	600
gttccagcag	ctaaagagga	agttaaacca	actcagacgt	cagtcagtca	gtcaacaaca	660
gtatcaccag	cttctgttgc	cgctgaaaca	ccagctccag	tagctaaagt	agcaccggta	720
agaactgtag	cagcccctag	agtggcaagt	gttaagtag	tcactcctaa	agtagaaact	780

ggtgcatcac	cagagcatgt	atcagctcca	gcagttcctg	tgactacgac	ttcaccagct	840
acagacagta	agttacaagc	gactgaagtt	aagagcggtc	cggtagcaca	aaaagctcca	900
acagcaacac	cggtagcaca	accagcttca	acaacaaatg	cagtagctgc	acatcctgaa	960
aatgcagggc	tccaacctca	tggtgcagct	tataaagaaa	aagtagcgtc	aacttatgga	1020
gttaatgaat	tcagtacata	ccgtgcggga	gatccaggtg	atcatggtaa	aggtttagca	1080
gttgacttta	ttgtaggtac	taatcaagca	cttggttaata	aagttgcaca	gtactctaca	1140
caaaatatgg	cagcaaatata	catttcatat	gttatctggc	aacaaaagtt	ttactcaaat	1200
acaaacagta	tttatggacc	tgctaatact	tggaatgcaa	tgccagatcg	tggtggcggt	1260
actgccaaac	actatgacca	cgttcacgta	tcattttaaca	aataa		1305

SeqID 5

atgttaaaac	attttggtag	taaagtaaga	aatttgagag	taactagaaa	tattactcgc	60
gaagattttt	gtggtgatga	aactgagtta	tctgtaagac	aattagctag	gattgaaagt	120
ggacagtcaa	ttccaaactt	gactaaagct	cactacatag	ctaaacaatt	gaatgtaaaa	180
ttggatat	taacaggagg	agagagctta	gaattaccta	aacggtataa	agagttgaag	240
tacaaattgt	tgcgtacccc	gacttacgga	gatgctaata	gacttgcaat	tagagaagca	300
tattttgatg	aaatctatga	agtattttat	gaggagctcc	cagaagatga	aagactaatt	360
attgattgta	tgcaatcaaa	attagatggt	catttttctg	ttaatgataa	ttttggaatc	420
actattttac	atgactactt	tgatcaaatt	aagaaaaaaa	aggaatatac	cacaaatgat	480
tttgttatga	tagatttata	tttactttgc	ttttctatta	actatggaat	gaagagcttg	540
tattcttttag	agaactatca	ttttattatg	tcaaaattgt	tagagcaaga	taattttactt	600
cctgaggata	attttcaatt	gaacaacggt	ttattaaatc	atgtcgaatt	agcttttcaa	660
tttaagcaga	aaaaatatgt	acagcaaatt	attcatagaa	gtaatgctat	tatgacagaa	720
atccatgatt	ttcaaaaaag	accaatacta	agcttaatat	agtggaaata	tttattaatt	780
attgaaaaag	atagaacaaa	agcagaaaca	tgttttaaac	aatcaattct	atttgacagag	840
ttaatagggtg	atctatat	aaaaggaaaa	ttaatagagg	agtggataa	agatttaaca	900
tga						903

SeqID 6

atgactgaaa	aaactaaagc	ggtagaaact	acagatgttg	ctcttgcaat	tgatacattg	60
gttcaaaacg	gtttaaaagc	acttgatgag	atgcgtcaac	ttaatcaaga	acaagttgat	120
tatatgtgat	ctaaagcttc	tggtgcagcc	ttggatgcc	atggagaact	tgctcttcac	180
gcagtagaag	aaactggctg	tggtgtcttt	gaagataaag	cgacaaaaaa	tttatttgca	240
tgtgaacacg	tcgttaacaa	catgcgtcat	acaaagacag	tgaggagtat	tgaagaagac	300
gatgtcacag	gcttgacatt	aattgctgaa	ccagtgagg	ttgtctgtgg	tattacgcca	360
acaaccaacc	cgacttcaac	tgctattttc	aagtcattaa	tctctcttaa	aacacgtaat	420
ccaattat	ttgccttcca	cccatcagca	caagaatcat	cagcacatgc	agcacgtatt	480
gttcgtgatg	ctgctattgc	tgctggagct	cctgaaaatt	gtgtccaatg	gattgaacaa	540
ccatcgattg	atgcaactaa	tgctttgatg	aacctgatg	gtattgccac	tatccttgog	600
acagggtggt	atgcgatggt	taaagctgcc	tactcatgtg	ggaaaacctg	ccttggtgta	660
ggtgctggga	atgttccagc	ttatgttgaa	aaatcagcta	atatccgaca	agccgctcac	720
gatattgtta	tgtctaaatc	atgtgataac	ggtatggtat	gtgcatcaga	acaggctggt	780
attatttgata	aagaaattta	taaagaattt	gttgagaat	ttaaatctta	tcatacttat	840
ttcgttaata	agaaagaaaa	agctcttctt	gaagaattct	gttttggtgc	aaaagcaaat	900
agcaaaaact	gtgctgggtc	aaaattaaat	ccaaatattg	ttggaaaatc	agcagtttgg	960
attgctgaac	agctggatt	tactgttcca	gaaggaacaa	atattcttgc	cgcagaatgt	1020
actgaagtta	gtgaaaaaga	acctttgaca	cgtgaaaaac	tatcacctgt	tattgocgta	1080
ttgaaagctg	aatctacaga	agatggtggt	gaaaaagctc	gtcaaattgg	tgagtttaat	1140
ggtctaggac	actcagctgc	tattcatata	aaagatgcag	acttagctcg	tgaatttgga	1200
actagaattc	gtgctatccg	tgttatttgg	aattctcctt	ctacttttgg	tggtattggg	1260
gatgtttaca	atgctttctt	gccatcattg	actcttggtt	gtggttcgta	tggacgtaac	1320
tcagttgggtg	ataacggttag	tgctataaat	ctcttgaaat	tcaaaaaagt	aggaagacgt	1380
agaaataata	tgcaatgggt	taaagtcctt	tcaaaaaacat	acttcgaacg	tgattctatt	1440
caatatttgc	aaaaatgtcg	cgatgttgaa	cgtgtcatga	ttgttacaga	tcacgccatg	1500
gttgagcttg	gtttcttgga	tcgtatcatt	gaacaacttg	atcttcgtcg	caataaagtt	1560
gtttatcaga	tttttgctga	agtagaacca	gatccagaca	ttacaacagt	aatgaaagga	1620
acagatttga	tgcgtaacct	caaaccagac	actattattg	cattaggtgg	tggttctcct	1680
atggatgctg	cgaaagttat	gtggctcttc	tatgaacaac	cagaagttga	tttccatgac	1740
ctcgttcaaa	aattcatgga	tatccgtaaa	cgtgcgttca	aattcccaga	acttggttaag	1800
aaaacaaaaat	ttgttgctat	tccaacaact	cttggaacag	gttctgaagt	gacaccattt	1860
gccgttatct	ctgacaaagc	aaataatcgt	aaatatccaa	tcgctgatta	ttcattaaca	1920
ccaactgtag	ctatcggtga	tccggccctt	gttatgactg	ttcctgggtt	tattgcccgt	1980
gatacgggta	tggatgtatt	gacacatgca	acagaggctt	atgtttcaca	gatggcaaat	2040
gattatacag	acggacttgc	ccttcaagca	attaaaaattg	tgtttgacta	cttagaacgc	2100
tcagtaaaaag	atgctgattt	tgaagcacgt	gaaaagatgc	acaatgcgtc	aactatggca	2160

ggtatggcctt	tgcgcaatgc	attcttaggt	atttctcact	caatggcgca	taaaattggc	2220
gcacaattcc	ataccgtaca	cggacgtaca	aatgcaattc	ttttgccgta	tgttatccgc	2280
tataatggaa	ctcgtccagc	taaaacagca	acatggccta	agtacaatta	ctatcgtgct	2340
gatgaaaaat	atcaagatat	cgctaaatta	ctcggcttac	cagcagcaac	accagaagaa	2400
gctgtcgaat	catatgcaaa	agctgtgtat	gaccttggaa	cacgtttagg	tattaagatg	2460
aatttccgcg	accaaggcat	tgatgaaaaa	gaatggaaag	aaaaatctcg	tgaactagct	2520
ttcttagcat	atgaagatca	atgttcacca	gcaaatccac	gccttcgat	ggtagatcac	2580
atgcaagaaa	tcacggaaga	tgtttattat	ggttatgagg	aacgtccagg	acgtcgtatg	2640
taa						2643

SeqID 7

gtgggtatta	aagtttataa	accaacgaca	aatggccgtc	gtaatatgac	ttctttggat	60
tttgacagaa	tcactacaaa	cactcctgag	aaatcattgc	ttgtttcact	aaagaataaa	120
gcaggacgta	acaacaacgg	acgtattact	gttcgtcacc	aagggtggtg	acacaaacgt	180
cattaccgtt	tgattgactt	caaacgtaat	aaagatgggtg	ttgaagcagt	tgttaaaaca	240
attgaatacg	atccaaatcg	tactgcaaat	attgctcttg	tacactatac	tgatgggtgt	300
aaagcttaca	ttcttgccgc	taaaggcctt	gaagtaggtc	aacgcattat	ttctgggtcca	360
gaagcagata	tcaaagttgg	taacgcactt	ccacttgota	acattccagt	cggtagcagtt	420
atccataata	ttgaattgca	accaggtaaa	gggtgctgaat	tgattcgtgc	cgcggtgct	480
tctgtctcaag	tacttggtca	agaaggtaaa	tatgttcttg	ttcgccttca	atcaggtgaa	540
gtacgtatga	tccttggtac	ttgccgtgca	acaattggta	ctgttggtaa	tgaacaacaa	600
tcacttggtta	acattggtaa	agcaggacgt	aatcgttggg	aagggtgttcg	ccctacagtt	660
cgtgggtctg	taatgaaccc	taatgatcac	ccacacgggtg	gtggtgaagg	taaagcacca	720
gttggtcgtg	aagcaccatc	tactccatgg	ggtaaacctg	cacttggact	taaaactcgt	780
aataagaaaag	ctaaatcaga	caaacttatt	gttcgtcgtc	gtaacccaaa	ataa	834

SeqID 8

atgattgagt	ttgaaaaacc	aataataaca	aaaattgatg	aaaataaaga	ttacggcgaga	60
tttgtcatcg	aaccactaga	acgtggctac	ggtacaactc	taggaaactc	tcttcgtcgt	120
gtgcttctgt	cttcacttcc	aggtgcagca	gtcacatcaa	tcaaaattga	tggagtatta	180
cacgaatttg	atactatccc	aggtgtacgt	gaagatgtga	tgcaaatcat	ccttaatgta	240
aaaggacttg	ctgtgaaatc	ttacgtcgaa	gacgaaaaga	ttatcgaact	agacgttgaa	300
ggtcctgcag	aaattactgc	cggagataat	ttaacagata	gtgatatcga	aattgtaaac	360
cctgaccatt	atcttttcc	aattgctgaa	ggtcacagtt	tgaaagcaac	aatgacagtt	420
gctaaaaacc	gaggttatgt	tccagcgaga	ggaaataaaa	aagatgatgc	accagtggga	480
acattggctg	tagattcaat	ctatacacca	gtgaaaaaag	ttaattatca	agttgaacct	540
gctcgtgtag	gtagtaacga	tggctttgat	aaattaacta	ttgaaatcat	gacaaatggc	600
acaatcattc	ctgaggatgc	tcttggctct	tcagctcgcg	tcttaattga	acacttaaac	660
ttgtttactg	atttaacaga	ggttgctaaa	gcaactgaag	taatgaagga	aacagagaaa	720
gtgaacgatg	agaaagtgc	tgaccgcaca	attgaggaac	ttgatttgtc	agtgcgctca	780
tataactgtt	taaaacgtgc	tggaaattaat	acagtatttg	atttaacaga	aaaaactgag	840
cctgaaatga	tgaaagtccg	aaacttagga	cgtgaagagtc	ttgaagaagt	taaaatcaaa	900
cttgccgatc	taggtcttgg	attaaaaaac	gataaataa			939

SeqID 9

atgaaaaaga	ttcgattatc	aaagtttatt	aaaatgattg	ttgttatttt	gtttttaatt	60
agtgtagcag	ctagttttta	ttttttccac	gttgcccaag	ttcgagatga	taaatccttt	120
atttcaaagt	gtcaacgtaa	gcctggaaac	tcttttatatg	cttatgataa	atcctttgat	180
aagctattaa	agcaaaaaat	agaaatgaca	aacccaaaata	taaagcaagt	tgcttgggtat	240
gttcctgctg	ctaagaaaac	tcataagaca	gctgttgctg	ttcatgggtt	tgcgaaatagc	300
aaagagaata	tgaaggcata	tggttggctg	tttcataagt	taggatacaa	tgttcttatg	360
cctgacaata	ttgcacatgg	tgaaagtcat	gggcagttga	taggctatgg	ctggaacgac	420
cgcgagaaca	ttatcaaatg	gacagaaatg	atagttgata	agaatccatc	aagccaaatt	480
actttatttg	gtgtttcaat	gggtggagca	acagtcatga	tggttagtgg	tgaaaaatta	540
cctagtcagg	ttgttaatat	cattgaagat	tgcggttatt	ctagtgtttg	ggatgaatta	600
aaatttcagg	ctaaagagat	gtatggttta	ccagccttcc	cactcttata	tgaagtttca	660
acaatttcta	aaatcagagc	aggtttttcg	tatggacaag	caagtagtgt	cgaacaattg	720
aaaaagaata	atttaccagc	cctctttatt	catgggtgata	aggataattt	tgttccaaca	780
agtatggttt	atgacaacta	taaagctaca	gcaggtaaga	aagagcttta	tattgtaaaa	840
ggggcaaaac	atgcgaaatc	ttttgaaaaca	gagccagaaa	aatatgagaa	acgtatctct	900
agttttttga	aaaaatatga	aaaataa				927

SeqID 10

atgtcaaaaag	tacgtggcctt	tgaattagtt	agccaatttta	gcaataaaga	gttattacca	60
aaacgagaaa	cagctcacgc	agctggctat	gatttaaaaag	tagctaaaaa	aacgggttatt	120

gaacctggtg	aaattacatt	ggccccgacc	ggtattaaag	cacacatgca	accagggggag	180
gtcctgtacc	tttatgatcg	ttcatcgaat	ccacgtaaaa	aagggattgt	cctaataaat	240
tcagttggtg	ttattgatgg	tgactactat	aataaccaag	tcaatgaagg	acataattttt	300
gcacagatgc	aaaatattac	tgatcaggct	gttatttttag	aagaagggga	acggattggt	360
caggctgttt	ttgccccatt	cttattggca	gatgacgatc	aggctacagg	aatgcgtaca	420
ggtggttttg	gtagtactgg	aaaataa				447

SeqID 11

atgaaatttg	gaaaaaaact	tggcttttcta	gccttattga	tgtctattgt	cctcattcta	60
ggtgcatgtg	gtaaaaactgg	acttggaaat	tctactggga	attctacaaa	aaatgtaacc	120
aaaaaatctg	ctaaaaaactt	gaaactaggt	gtatctatctt	caacaactaa	caatccctac	180
tttggtgoga	tgaaagacgg	tattgacaaa	tatgctagca	ataaaaaaat	aagcattaag	240
gtagtggatg	ctcaagatga	cgccgcacgt	caagcagatg	atgtccaaaa	ctttattagt	300
caaaacgtag	atgctatctt	gattaatccc	gttgactcaa	aagctattgt	aacagctatt	360
aagtctgcaa	acaacgctaa	tattcctggt	attctaattg	accgtggtag	tgagggaggc	420
aaagtattaa	ctactgtcgc	ttcagataac	gttgctgctg	gtaagatggc	tgcggtattat	480
gctgttaaaa	aactaggcaa	aaaagcaaaa	gcctttgaat	tatctggagt	accaggtgcc	540
tctgtcactg	tagaccgtgg	taaaggattt	cattcagttg	caaaaactaa	acttgacatt	600
ctttcaagcc	aacttgccaa	ttttgaccgc	gccaaagctt	tgaatactac	acaaaatatg	660
attcaaggac	ataaagatgt	ccaaattatt	ttcgcacaaa	atgatgaaat	ggcacttggg	720
gctgcacagg	ctgtcaaatc	tgctggcttg	caaaatgttc	ttatcgtagg	aattgatggg	780
cagccagatg	cccatgatgc	cattaaaaaa	ggagatattt	cagccactat	tgcaacaaca	840
ccagctaaga	tgggagaaat	agcaattcaa	gcagcaattg	atcattataa	aggcaaaaaa	900
gtagagaaag	aaacaatttc	tccaattttac	cttgttacca	aagacaatgt	tgaaaaatac	960
aattggttaa						969

SeqID 12

atgggaaaaag	aaaaattaat	tttagcttat	tctgggtggtt	tagatacctc	tggtgctata	60
gcttggttaa	aaaaagatta	tgacgttatt	gctgtctgta	tggatgttgg	cgaaggtaaa	120
gatcttgatt	ttattcacga	taaggcttta	acaatagggtg	ccatagaatc	ttatatttta	180
gatgttaaag	atgagttcgc	tgagcatttt	gtgttaccag	ctttacaggc	acatgcgatg	240
tatgaacaaa	aatacccgct	tgtttcagcg	cttagtcgtc	caattattgc	tcaaaaaatta	300
gttgaaatgg	cacatcaaac	aggtgcgacc	acaattgcc	atggatgtac	aggtaaagga	360
aatgaccaag	tgcgttttga	agttgcaatt	gcagcactag	atcctgaatt	aaaagtaatt	420
gcccctgttc	gtgagtggaa	gtggcatcgt	gaagaggaaa	ttacttttgc	aaaagctaac	480
ggcgtaacct	ttccagcaga	tttagataac	ccttattcta	tagaccaaaa	tttatgggga	540
cgtgccaatg	aatgtggtgt	gcttgagaat	ccttggaatc	aagcgccaga	agaagctttt	600
ggtattacaa	aatcaccaga	agaagctcct	gattgtgcag	aatatattga	tattacgttc	660
caaaatggga	agcctatagc	tataaacaat	caagaaatga	cactagcaga	tttgatttta	720
tcgctaaatg	aaattgcagg	aaaacatggg	attggacgca	ttgatcatgt	tgaaaatcgt	780
ttagtccgta	tcaaatcacg	tgaaatttat	gaatgtcctg	cggcaatggg	actgttagct	840
gctcataaag	aaattgaaga	tttaacatta	gtccgtgaag	tgtctcattt	taaacctatc	900
cttgaaaatg	aactatcaaa	tcttattttat	aatgctttat	ggtttagtcc	agctacaaaa	960
gctatcattg	cctatgtcaa	agaaacacaa	aaagtgggta	atgggtactac	aaaagttaag	1020
ttatataaag	gttctgccaa	agtcgttgct	cgccactcgt	ctaattcatt	atatgatgag	1080
aacttagcaa	cttatacagc	tgctgataac	tttgatcaag	atgcagcagt	tggtttttatc	1140
aaactctggg	gacttccaac	ccaagttaat	gcacaagtaa	acaaaggata	a	1191

SeqID 13

atggctaaag	tatgttattt	cacaggacgt	aaaacagttt	ctggtaacaa	cogttcacac	60
gcgatgaacc	aaacaaaacg	tactgttaaa	ccaaaccttc	aaaaagttac	tgttcttattc	120
gacggtaaac	caaaaaaagt	ttgggtttca	gctcgtgcgc	ttaaatctgg	taaagtagaa	180
cgcgttttaa						189

SeqID 14

atggcaaaac	agaaaaataa	ctggcgccgt	gttgaggttg	gtgtccttac	acttgcttca	60
gttgcgactc	ttgctgcatg	tggaaagtaa	tcagcttccc	aggattctaa	tggagcgatt	120
aattgggcta	ttccaacaga	aatcaatata	ctagatttat	ctaaagttac	agacacttac	180
tcaaatctag	ctattggtaa	ctctagtagt	aatttccctc	gcttagataa	ggatggaaag	240
acgagaccag	atttggctac	taaagttgat	gtttcaaaaag	atgggtttaac	ttatacagct	300
acattacgta	aaggcttgaa	gtggtcagat	ggcagtaaac	ttactgcaaa	ggattttggt	360
tattcatggc	aacgttttagt	tgatcctaag	acagcttcac	aatatgctta	ccttgctggt	420
gaagggcatg	tgcttaatgc	cgataaaaatc	aacgaaggac	aagagaaaga	cttgaataag	480
ctaggtgtta	aggcagaagg	cgatgacaaa	gttggttatta	ctttatctag	tccgtctcca	540
caattcatct	actaccttgc	attcactaat	ttcatgccac	aaaaacaaga	agttgttgaa	600

aaatatggaa	aagattacgc	aactacttca	aaaaatacag	tttactcagg	accatatact	660
gttgaagggt	ggaatgggtc	aaatgggtact	ttcacccctga	agaaaaacaa	aaattatttg	720
gacgctaaaa	atgtaaaaac	aaaagaagtt	cgcattccaga	ctgttaaaaa	accagatacc	780
gccgttcaaa	tgtataaacg	tgggtgaatta	gatgcagcta	atatctcaaa	tacttctgct	840
atztatcaag	ctaataaaaa	taataaagat	gtcacagatg	ttctagaagc	gaccactgcc	900
tatatgcaat	ataatactac	tgggtctctg	aaagggcctg	ataatgttaa	gattcgtcgc	960
gccttaaaact	tagcaactaa	cogtaaaagga	gttggttcaag	cagccgttga	tacaggctca	1020
aaaccggcaa	ttgcttttgc	accgactggg	ttagccaaaa	caccagatgg	aactgatttg	1080
gcaaaatatg	ttgccccagg	ttatgaatat	aataaaaactg	aagcagcaaa	actcttttaa	1140
gaagggttgg	ctgaatcagg	cttgactaag	ctaaaattaa	caattacagc	agatgctgat	1200
gttcctgctg	ccaaaaactc	tgttgactat	atcaagtcta	cttgggaagc	tgctcttcca	1260
ggacttactg	ttgaagaaaa	atgtgttaacc	tttaaacacac	gcttagaaga	cagtagaaaa	1320
caaaaactttg	atatcgtagt	ttctggttgg	gggtggggatt	atccagaagg	gtcaactttc	1380
tacggcctct	ttaagtcaga	ttcacaaaaat	aacgattgaa	aatttgctaa	caaggactat	1440
gacgtgctt	ataacaaggc	aatttccgaa	gatgccttaa	aaccagaaga	atcagcaaa	1500
gactataaag	aagcagagaa	aattctattt	gagcaaggcg	cttataaccc	actctacttc	1560
cgtagtggta	aaggtttaca	aaatccaaaa	ttaaaagggtg	ttattcgtaa	tactacaggt	1620
ttgtcaatag	actttacaca	tgcttataaa	aaataa			1656

SeqID 15

atggaactct	taaaaacacc	catcttttgg	atgtgctttt	ctttaatact	ctatacgata	60
ggacaacatt	tattttaagaa	gagtaaagg	ttcttccctt	tgcagcctct	tttcttttga	120
atgggttagtg	gtattgtcat	tctttggctt	atgtcaaaaag	gttttaggaac	cgatgttaag	180
acattttata	cacaagctta	taaaccaggt	ggcgatttaa	tatttttggt	tttaaatcca	240
gcaacaattg	cttttgcagt	tctctctctat	aagaaaaatg	acgttggttaa	aaaatatttg	300
gtagaaattc	tcagcagttt	agtaatcggt	atgattggtt	cccttatgct	tatcgtcgct	360
atttctaaaa	tggttgggct	tagtcaagtc	ggaattgctt	caatgttgcc	acaagcagca	420
acaacagcaa	ttgctcttcc	aataacagca	gcaattggag	ggaacacagc	tgtgacagca	480
atggcggtgta	tcttaaatgc	agttattatt	tatgcattag	gtaaaaaatt	agtgtcattt	540
ttccatttga	atgatagtaa	gattggtgca	ggattagggtc	tagggacctc	tggtcataca	600
gtcggagcag	cctttgcatt	ggaattggga	gaactgcaag	gtgcgatggc	agctatagcg	660
gtgggtggtta	tcggtttggg	agttgatttg	gttattccta	tcttttagtca	tttgattggg	720
ttgctataa						729

SeqID 16

gtgactaaat	atgtgaagta	catctctttt	gttgctttgt	ttctggcgag	tatctttttta	60
gtagcttggtc	aaaatcaaaa	ttcacaaaaca	aaggagcgaa	cacgaaaaca	acgacccaaa	120
gatgaattgg	ttgtttctat	gggggcaaaag	cttccctcatg	aattcgatcc	aaaggaccgt	180
tatggaatcc	ataatgaagg	taatattact	catagtaccc	tattgaaacg	ttctcctgaa	240
ctagatataa	aaggagagct	tgctaaaaaaa	tataaaaatct	ctaaggatgg	cttaacgtgg	300
tcgttcgact	taaatgatga	ttttaaattc	tccaatgggtg	agcctgttac	tgctgacgat	360
gttaagttaa	cttatgatat	gttgaaagca	gatggaaaag	cttgggattt	gacctttatt	420
aagaatgttg	aagtagttgg	gaaaaaccag	gtaaatattc	atgtgactga	ggcgcatctg	480
acattttacag	cacagttgac	agaaatccca	atcgcccta	aaaaacatta	caatgataag	540
tataagagca	atcctatcgg	ttcaggacct	tacatggtaa	agaatataa	ggctggagaa	600
caagcaatct	tcgttcgaaa	tccatattgg	cacggtaaaa	agccttattt	taaaaagtgg	660
acttgggtat	tacttgatga	aaatacacgca	ctagctgctt	tagaatctgg	tgatgttgac	720
atgatttacg	caacgccaga	gcttgctagc	aagaaagtca	aaggaacacg	tcttctagat	780
attgcttcaa	atgatgttcg	tgggttatcg	ctaccttatg	tgaagaaagg	tggtgtgaaa	840
aattcaccag	acggttatcc	agtaggaaat	gatgtcacta	gtgatccagc	aatcagaaaa	900
gccttgacta	ttggtttaaa	tagacaaaaa	gttctggata	ctgttttaaa	tggttatggg	960
aaaccagctt	attcaattat	tgatagaaca	ccattctgga	atccaaaaac	agcaatttaa	1020
gataataaag	tagctaaagc	taagcaactt	ttgacaaaag	ctggatggaa	agaacaagca	1080
gacggtagcc	gcaaaaaagg	aaatcttaaa	gcggaatttg	acctttacta	ccctactaat	1140
gatcaattac	gagcaaaact	agccgttgaa	gtagcggagc	aagctaaagc	cttaggtatt	1200
actattaaac	tcaaggctag	taactgggat	gaaatggcaa	ctaagtcaca	tgattcagcc	1260
ttacttttatg	cgggaggacg	tcatcatgcg	cagcaatttt	atgaatcaca	ttacccaagt	1320
ttagctggta	aagggttgac	caatattact	ttttataaca	atcctactgt	gactaagtac	1380
cttgacaaag	caatgacatc	tcccgcacct	gataaagcta	acaaatattg	gaagttagct	1440
cagtgggatg	gcacaaacag	tgcttccact	cttgagagatt	taccaaattg	atgggtgggt	1500
agtcttaacc	atacttatat	tggtgataaa	cgtatcaatg	taggtaaaca	aggtgtccat	1560
agtcatgggc	atgattgggc	attattgact	aacattgctg	aatggacttg	ggatgaatct	1620
gctaagtaa						1629

SeqID 17

atggggccaag	aacctatcat	cgaatatcaa	aatatcaata	aagtgtatgg	ggaaaatggt	60
gcggttggaag	atattaacct	taaaatttac	cctggtgatt	tcgtttgttt	catcggtacg	120
agtggatcag	gtaaaacaac	attaatgctg	atgggttaacc	atatgttaaa	accaacaaat	180
ggtactctat	tatttaagg	aaaagatatt	tctactatta	acccattga	attaagacgc	240
agaattggat	atgttatoca	aaacattgg	ttaatgcctc	atatgaccat	ttacgaaaaat	300
atagttcttg	taccaaatt	attgaaatgg	tcagaagaag	ctaaaagagc	taaagcaagg	360
gaacttatta	aattagttga	attacccgaa	gaatatttgg	atcgctaccc	tagtgagttg	420
tctggcggtc	agcaacaacg	tatcggtgtc	attcgcgctc	ttgcagcaga	ccaagatatt	480
attttaatgg	atgagccttt	tggagctctg	gatcctatta	ctagagaagg	tattcaagac	540
ttagtcaagt	ctcttcagga	agaaatgggg	aaaactatca	tcttagttac	tcatgatatg	600
gatgaagccc	tcaagttagc	aacaaaaatt	attgttatgg	acaatggtaa	aatgggtccaa	660
gaagggacac	ccaatgatct	cttacatcat	cctgctacca	gtttcggtga	acaaatgatt	720
ggggaagagc	gtcttcttca	tgcgcaggct	gatattaccc	ctgttaaaca	gataatgtta	780
aataatcctg	tttcaataac	tgctgaaaaa	acataactg	aagctattac	actaatgcgc	840
caaaaaacgcg	ttgactcact	tctagtaacc	gataacggta	aattaattgg	ttttattgac	900
ttagaatctc	taagcagtaa	atataagaaa	gaccgacttg	tttctgatat	cttaaaacat	960
actgattttt	atgttatgga	agacgactta	cttagaaata	ctgctgagcg	tattttaaaa	1020
cgtgggttaa	aatacgctcc	agttgttgac	catgagaata	acctaagggg	cattgttact	1080
cgtgcatccc	tagttgatat	gttatacgat	attatttggg	gcgatactga	aacggaggat	1140
caataa						1146

SeqID 18

atgaaaatag	ataaaaaaga	atTTTTtagca	cttattgcta	gtattatttt	attaatTTTT	60
gcttctgtta	cgTTTTtctt	atttaaagat	catggcacta	ctcaaattgga	tactgtagaa	120
agcagtgtta	accatgtcag	tgattctcaa	ttaactgagg	cacaagatat	gttagataaa	180
tttgagaaga	aaccttcaga	aaaattattg	aaggatgtcg	aacttgcttt	aaataaattg	240
tccaattctt	ctaaaaaaga	agctttgcga	aaacgtttta	agaaagcaaa	agataagtat	300
cttaagagcgt	aagcagataa	gaaagctacc	aaagatgcta	cagatttagt	agaaattcta	360
gaacaagccc	cttcagaaga	aaatgtgtta	aaagctgaag	cagcagtcga	taagttaact	420
gtcaaagaat	ctaaagaagc	tttacaaaaa	cgtattgata	ctgttaagac	acaatatggt	480
ttgattggga	atcaaactcc	ctctagttca	gtagctgaaa	ctacagaaca	agggacagct	540
aatcctgcta	gtcaggatac	ttctagttac	gttaatcaga	atgtagcacc	aacttatgag	600
caaccgcaaa	cgaataatac	accagttact	ccaggggtta	acaatactgt	tccgactcca	660
ggaactggta	ctgcacctgc	tactaatggg	acgggtgttg	ctcagtaa		708

SeqID 19

atgactaaag	atTTattatt	ggagcttggc	cttgaagagt	tgccagctta	tgttgtgaca	60
ccgagtggaga	agcaattggg	ccaaaaaatg	gtcaagtttt	tagaggatca	tcgtttatca	120
tttgaaaactg	ttcaaacttt	ttcaactcca	cgtcgttttg	ctggtcgtgt	taaaggattg	180
gcagaccagc	agacagattt	aacagaagat	ttcaagggtc	cttctaagaa	aattgctttg	240
gatgcagaag	ggaaattttt	taaagcagcc	caaggttttg	ttcgcgga	agggttaagt	300
gttgatgata	tcgaatttct	tgaagttaag	ggagaagaat	atgtttatgt	cactaagcat	360
gaaactggaa	aaagtgcgat	tgatgtttta	gcaagtgtga	cagaggtatt	aacagaattg	420
actttcccag	tgaacatgca	ttgggcaaat	aatagttttg	aatatattcg	tccagttcac	480
acttttagtg	tattattaga	tgatcaagcc	ttagagctag	acttccttga	tattcattca	540
gggcgtatta	gtcgagggca	ccgtttcttg	ggttctgaca	ctgaaatttt	atctgctagt	600
tcgtatgaag	atgacttgcg	acaacaattt	gttattgtcg	atgcaaaaga	acgccagcaa	660
atgatcgttg	atcaaattca	tgctatcgaa	gaaaaggaaa	atatttcagt	tgaaattgac	720
gaagattttac	taaatgaagt	gcttaattta	gttgagtatc	cgacagcatt	cttgggttct	780
tttgacgaga	aataccttga	tgtacctgaa	gaagtttttag	tcacttcaat	gaaaaatcat	840
caacgctatt	ttgttggtcg	cgacagggat	ggaaaattgt	taccaaactt	tatttctgtg	900
cgtaattggaa	atgctgagca	tatcgaaaaa	gttataaaag	gtaatgaaaa	agtttttagtg	960
gctcgtctcg	aagatgggtga	attcttcttg	caagaagatc	agaaacttaa	tattgcagat	1020
ttagttgaga	aattaaaaca	agtaactttc	catgaaaaaa	ttggttcact	ttatgaacat	1080
atggatcgtg	taaaagttat	ttcacaatat	ttggctgaga	aggcagatct	ttctgatgaa	1140
gaaaaatttag	ctgtgcttct	agctgcaagt	atTTataaat	ttgacctctt	aaactggaatg	1200
gttgatgagt	ttgatgaatt	acaaggattt	atgggtgaga	aatatgcctt	acttgcaggg	1260
gaacagcccg	cagtagcagc	agcgatacgt	gaacattata	tgccgacatc	ggccgatgga	1320
gagcttccag	aaaccagagt	tgggtcaatt	ctagcgttag	ctgataaaat	tgacacctta	1380
ctttcattct	tctcagtttg	tttgattcca	agcggttcaa	atgatccata	tgtctctcgt	1440
cgagctactc	aggggatttg	ccgtattttg	gaagcttttg	gttgggatat	cccacttgat	1500
gaattagtaa	ctaaccctta	tgggtctatcg	tttgctagtt	tagattatgc	taatcaaaaa	1560
gaggtcatgg	cttttatttc	agctcgtatt	gaaaagatga	ttggctctaa	gggtccctaaa	1620
gatattcgag	aagccgtttt	agaatcagac	acttatattg	ttagccttat	tctagaagct	1680
agccaagcat	tgggtgcaaaa	gagcaaggat	gctcaatata	aagtttccat	tgaaagtttg	1740

tcacgtgcat	ttaattttagc	tgaaaaagtt	actcattctg	tatcgggtgga	ctatttcattg	1800
tttgaaaata	atcaggagaa	ggcgctatat	caagctatctt	tgtcacttga	actgactgag	1860
gatatgcatg	acaacttaga	taagcttttc	gcacttagtc	caattattaa	tgatttcttt	1920
gataatacaa	tggtaatgac	agatgatgaa	aaaatgaaac	aaaatcgtct	ggctttactc	1980
aatagccttg	ttgcaaaaagc	aagaacagtc	gctgctttta	acttattaaa	cacaaaataa	2040

SeqID 20

atgacatttg	acaccattga	tcaattagcg	gttaatacag	tccgcacgct	ttctattgat	60
gctatccaag	cagcaaattc	tgggcaccca	gggtcttcta	tgggagctgc	gcctatggct	120
tatgtgcttt	ggaataaatt	cttaaatgta	aacccaaaaa	caagtcgcaa	ttggacaaac	180
cgtgaccgtt	ttgtgctatc	agctgggcat	gggttcagctc	ttctttatag	cctacttcat	240
ttagctggct	atgcatttatc	aattgatgat	ttaaaacaat	tccgccaatg	gggatcaaaa	300
acacctggac	atccagaagt	taaccatact	gatgggtgtag	aagcaacaac	tggaccttta	360
gggcaaggta	ttgctaatgc	tgttgggtatg	gcaatggctg	aagctcattt	ggctgctaaa	420
tttaataaac	caggctttga	tttagttgat	cattacactt	atacacttca	tggatgatgg	480
tgtttgatgg	aggggtgtag	ccaagaagct	gccagtcttg	ctggacactt	aaaacttggt	540
aaattggctc	ttctttatga	ttcaaatgat	atctcacttg	atgggtccaa	gtctcaatca	600
tttacagaag	atgttaaagg	gcgttttgaa	tcatatgggt	ggcaacatat	cttagttaaa	660
gatggtaagt	atttagaagc	gattgctgca	gcaattgaag	ctgctaaagc	tgaactgat	720
aaaccaacca	ttattgaagt	taaaactatt	attggatttg	gcgcagagaa	acagggaaca	780
tcttcagttc	atggagcgcc	acttgggtgca	gaaggattta	cttttgccaa	gaaggcttat	840
ggatgggaat	atccagactt	tactgttcct	gctgaagttg	tagctcgatt	tgcctcagat	900
cttcaagcgc	gtgggtgcga	ggcagaagag	gcatggaatg	atctttttgc	taaatatgaa	960
gttgagtatc	cagaattagc	agctgaatac	aaagaagctt	ttgctggcca	agctgagaca	1020
gttgaattga	aagctcatga	cctaggttca	tcagtggcta	gtcgtgtttc	aagccaacaa	1080
gctattcaac	aattatcgac	tcaattaccg	aacctctggg	gaggggtcagc	agacctctca	1140
gcttctaata	acacaatggt	agcagcagaa	acagatttcc	aagcaagtaa	ttacgctggg	1200
cgtaacattt	ggtttgggtg	acgtgaattt	gcaatggctg	ctgcaatgaa	tgggaattgcg	1260
cttcacggtg	ggactcgtgt	ttatgggggt	acattctttg	tcttctcaaa	ctacttggtt	1320
ccagcagtac	gtatggctgc	acttcaaaac	ttgccaaactg	tctatgttat	gacacatgat	1380
tctattgctg	ttggagaaga	tgggccaaact	catgagccaa	tagaacaatt	agcatcagtg	1440
cgctcaatgc	ctaatttgaa	cgttatccgt	cccgcagacg	gtaatgaaac	aaacgctgca	1500
tggcaacgag	ctgtatcaga	gacagatcga	ccaacgatgc	ttgttttaac	acgtcaaaac	1560
ttaccagttc	ttgaaggaa	atcagaatta	gccccagaag	gggttaataa	aggtgcttat	1620
attttatcag	aagctaaagg	tgaacttgat	gggtatcatc	ttgcaacagg	ttcagaagtt	1680
aaattagctt	tagatactca	agacaaaact	gagtcagagg	gcattccatgt	tgcgctcgta	1740
tctatgccag	cacaaaacat	ttttgatgaa	caagaggctt	catatcaaga	gcaagtgcct	1800
ccatcagctg	ttacaaaacg	tcttgctatt	gaggcaggat	caagcttcgg	ttggggtaaa	1860
tatgttgggt	taaatgggct	aacacttact	attgataact	ggggagcatc	agcaccaggt	1920
aacagaattt	tcgaagagta	tggctttaca	gttgagaatg	ctgtatcgct	atataaagaa	1980
ctttaa						1986

SeqID 21

atgactttgc	aagatcaaat	tatcaaagaa	ctcgggtgtaa	aacctgttat	taatccaagt	60
caagaaatcc	gtcgttccgt	agaattttta	aaagactatc	tattaaaaca	tagttttcta	120
aagacctatc	tactgggtat	ttcagggggg	caagatttcaa	ctttagcagg	acgtctagta	180
caactagcag	ttgaagagtt	gcgtgctgat	acagggggaaa	actatcaatt	tatagctatt	240
cgtttaccat	atgggtattca	ggccgatgaa	gaagatgcac	aaaaagcatt	agattttatc	300
aagccagata	ttgctttgac	cattaatatt	aaagaagctg	ttgatggcca	agtttagagct	360
cttaatgcag	caggagtaga	gattacagac	tttaataaag	gaaatattaa	agctcgtcaa	420
agaatgatta	gtcaatatgc	agttgcaggt	caatatgctg	gagcgggtat	tggtagtgat	480
catgctgcag	aaaatattac	aggttttttc	accaaatttg	gtgatggagg	tgctgactta	540
ttacctctct	ttagacttaa	taaaagtcag	gggaaacagt	tattagctga	acttggtgct	600
gataaagcct	tgtacgaaaa	gattccaaac	gcagatttag	aagaaaataa	accaggaatc	660
gctgatgaaa	tagcccttgg	agtaacctac	caagaaattg	atgcttatct	tgaaggggaag	720
gtgggttcgg	acaagtctcg	aggtatcatt	gaaaattggg	ggtataaggg	tcaacataaa	780
cgtcatcttc	caatcacaa	ttttgatgat	ttctggaaat	aa		822

SeqID 22

attaaaaagg	aatctgttat	caaactattg	aagtatgctt	ttggcattat	aatgggattt	60
attatcttag	ctattgtaat	aggtgggctc	ctatttgcat	actacgttag	tcgttctccg	120
aaattaaccg	atcaagcttt	aaaatccgtt	aactctagtt	tggtttatga	tggtaataat	180
aaacttattg	ccgatttagg	ctcagaaaag	cgtgaaagtg	ttagtgcgga	tagcattcca	240
ctaaatttgg	ttaacgctat	cacttctatc	gaagataaac	gtttctttta	acatagaggt	300
gtcgatattt	atcgtatttt	aggtgcagct	tggcataatc	ttgttagtag	taatacgcaa	360

ggtggttcaa	cccttgatca	acagttgatt	aaactggcctt	acttttctac	caataaatct	420
gaccaaacgt	taaaacgtaa	atcacaggaa	gttttggttg	cgcttcaaat	ggagcgtaaa	480
tacaccaaaag	aagaaattct	tactttctat	attaataaag	tttatatggg	aaatgggaat	540
tatggatatga	gaacaacagc	taaatcatac	tttggtaaag	acctaagga	attatctatt	600
gcacaacttg	ctttgctcgc	tggtattcct	caagcaccta	cacaatatga	cccttataaa	660
aaccacagaat	ctgctcaaac	aagacgtaat	accgttcttc	agcagatgta	tcaagataaa	720
aacattttcta	aaaagggaata	cgaccaagct	gttgcaactc	cagtaactga	tggcttaaaa	780
gaattaaagc	aaaaatctac	ttatccaaaa	tatatggata	actacttaaa	acaagttatt	840
agtgaagtta	aacaaaaaac	tggtaaagat	atctttactg	ctgggctaaa	agtgtatact	900
aatatcaaca	ctgatgcaca	aaaacaacta	tatgacatct	acaacagtga	cacttacatc	960
gcttatccaa	acaatgaatt	acaaatagca	tctaccatca	tggatgcgac	taatggtaaa	1020
gtcattgcac	aattaggcgg	gcgtcatcag	aatgaaaata	tttcatttgg	gacaaatcaa	1080
tctgtcttaa	cagaccgcga	ttggggttct	acaatgaaac	ctatctcagc	ttatgcacct	1140
gctattgata	gtgggtgcta	taattcaaca	gggtcaatcat	taaacgactc	agtttactac	1200
tggcctggta	cttctactca	actatatgac	tgggatcgtc	aatatatggg	ttggatgagt	1260
atgcagaccg	ctattcaaca	atcacgtaac	gtccctgctg	tcagagcact	tgaagccgct	1320
ggatttagacg	aagcaaaaatc	tttccttgaa	aaattaggca	tatactatcc	agaaatgaac	1380
tattcaaatg	ctatttcaag	taacaacagt	agcagtgatg	caaaatatgg	tgcaagtatg	1440
gagaaaatgg	cagcggctta	ctcggttttt	gcaaaccggc	gaacttacta	taaaccgcaa	1500
tatgttaata	aaattgaatt	tagcgatgga	accaatgata	cttatgcagc	gtctggtagc	1560
cgtgcgatga	aagagactac	tgccctacatg	atgacggata	tgctgaaaac	agtactaaca	1620
tttggtactg	gtactaaagc	agctatccct	gggtgtgcac	aagctggtaa	gactggtagc	1680
tccaactata	cgggaagatga	gttagctaaa	attgaagcaa	ctactgggat	ctacacatagc	1740
gccgttggta	caatgggtcc	tgatgaaaac	tttgcggct	atacttctaa	gtacacaatg	1800
gcaatttgga	ctggttataa	aaatcgccct	acaccacttt	atggtagcca	actggatatt	1860
gctactgagg	tttatcgtgc	aatgatgtcc	tacctaaactg	gcggtacag	tgcatgattg	1920
acaatgccag	aagggctcta	tcgaagcgga	agctacttgt	atatcaatgg	gacaactaca	1980
accggcactt	actcttcttc	tgtctataag	aatatctatc	aaaattctgg	acagtcaagt	2040
caaagcagta	gttcaacatc	ctctgagaaa	caaaaagagg	ataagaatac	agcaaatgat	2100
gccaaattcat	catcccaca	agtcgaaaca	cctaataatg	gtaatgctac	taccctaat	2160
aattccaatc	aaactgtgcc	aggaactgga	catggtaatg	gtaatggtaa	caacaataca	2220
gtacctaacg	gtaattaa					2238

SeqID 23

atgttagact	taaaacgtat	tcgtacagat	tttgatgttg	tcgctaaaaa	attggccacg	60
ctgtggtgtg	accaagaaac	attaacaacc	cttaagaac	ttgatataaa	acgccgtgaa	120
ctacttatca	aagctgaaga	ggcgaaagcg	caacgtaatg	ttgcttctgc	tgccattgct	180
caagcaaaac	gaaataaaga	gaatgcagac	gagcaaatcg	cagctatgca	aacactttcc	240
gctgatataca	aagcaattga	tgcggaattg	gcagatgtgg	atgctaattt	acaatcaatg	300
gtgaccgtac	ttcctaatac	accagctgat	gatgtgccgc	ttggagcaga	cgaggatgaa	360
aatggtgaag	ttcgctcgtg	gggaactcct	cgtgaatttg	attttgagac	caaagctcac	420
tggtgatttg	gtgaaagcct	tggaattctc	gattgggaac	gtggtgcaaa	agttactggc	480
tctcgcttcc	tcttctacaa	aggtctaggt	actcgtttag	agcgtgctat	ctacagcttc	540
atgctggatg	aacacgctaa	ggagggtgac	gctgaagtga	tccctcctta	tatggttaac	600
cacgattcaa	tggtcggtac	gggacaatat	ccaaagttca	aggaagatac	tttcgaatta	660
gcagatagcc	cattcgtaact	tatcccaaca	gctgaagttc	ctttaacaaa	ctattatcgt	720
gatgaaatta	tcgatgggaa	agaattacct	atatacttta	ctgccatgag	tccatcattc	780
cgttcagaag	caggctctgc	aggacgtgac	acacgtggat	taattcgctc	tcatcaattc	840
cataaagtga	aaatggtgaa	atlttgccaag	cctgaggaat	cataccaaga	attagaaaaa	900
atgacagcaa	atgctgaaaa	tattcttcaa	aaacttaatc	tccataccg	tgctattacc	960
ttgtgtacag	gagatatggg	attctcagca	gctaaaacgt	atgacttaga	ggtatggatt	1020
cccgtcctaa	atacttatcg	agaaatttct	tcatgttcta	atactgaaga	tttccaagca	1080
cgctcgtgctc	aaattcggtta	ccgtgacgaa	gttgatggca	aagttagggt	gottcatact	1140
ttaaatgggt	caggacttgc	agttggacgt	actgtagcag	caatcctcga	aaattatcaa	1200
aatgaagatg	gttctgtgac	tatcccagaa	gttcttcgtc	catatatggg	taatatcgat	1260
attattaaac	caaattag					1278

SeqID 24

gtgacaatat	caaatacaaga	attgacgctt	actcccttaa	gaggaaaaag	tggaacagcc	60
tatattggta	cttatccaaa	tggtgaacgt	gtctttgtca	aatataatac	gacacctatt	120
ttgccagcct	tagctaagga	acagattgcy	ccacaactac	tgtggggcag	ccgtacaagt	180
aatggcgata	tgatgagtgc	tcaagaatgg	ttagatggtc	gaacattgac	taaagaagat	240
atgggtagta	aacagattat	tcatatttta	ttgcgcctgc	acaagtctcg	tcccttagta	300
aatcagctgt	tacaattagg	gtataaaatt	gaaaaccctt	atgatttggt	gatggattgg	360
gaaaaacaaa	ctcctattca	aatccgggaa	aacacttatt	tgcaatctat	tgtgactgag	420

ttaaagcgta	gtttacctga	gtttcgaaca	gaggttgcaa	caatcggtca	cggagatatc	480
aaacatagca	actgggttat	tacaacaagt	ggtttaattt	atttggttga	ttgggattct	540
gttcgtttaa	cagatcgcat	gtatgacgtt	gcataatatt	taagtcatta	tattccacaa	600
aaacactgga	aagattggct	gtcttactac	ggttataaag	ataatgagaa	agtctggagc	660
aaaattatct	ggatatgggca	attttcatat	ttatcacaga	taatcaaattg	ttttgataaa	720
cgagatatgg	agcatgtcaa	tcaagaaatt	tatgaattac	gaaagtttag	agagttaatt	780
aaaaagcata	atgcgagtta	g				801

SeqID 25

atgaaaatat	cacaatacaa	taaatgggtca	atcgccgat	tgaaagttgg	agctgcatct	60
gtaatgattg	ctagtgggaag	cattgtttgct	ttagggcaat	ctcatattgt	ttcagcagat	120
gagatgtccc	aacctaaaac	aaccattaca	gtcccaacag	ctaacacttc	tacaaatgta	180
gaaagtagta	ctgataaggc	attatcaaaa	gttactacga	tggagacaag	ttcagaaatg	240
cctaaaatgc	aaaatatggc	aaaagttgaa	aaaacgagtg	acaaacctat	gatgggtggct	300
acctctgtta	gaaaaatgat	ggcaacgccc	acacctgtag	cgatgaccaa	aacgcatagt	360
gtagatgagg	taaagaaatc	aactgatact	gcttttaaac	agacagtaga	cgttccggct	420
cattatgtta	atgcagcaaaa	agggaatggc	ccatttctag	caggtgtaaa	tcaaacgatt	480
ccatatgaag	cgtttggtgg	agatggcatg	ttaacgcgtt	taatccttaa	atcttctgaa	540
ggagcaaaat	ggtcagataa	tgggtgttgat	aaaaatagtc	cattattacc	attgaaaggc	600
ttaactaaag	gtaaatatitt	ctatcaagtt	tcttttaaatg	gtaatacgac	aggtaaagag	660
ggacaagctc	tcttagatca	aattaaagct	aatgataaac	atagctacca	agccacaatt	720
agagtttatg	gtgctaaaga	tggtaaaagt	gatttaaaaa	acatgattag	ccaaaaaatg	780
gtaaccatta	acattcctca	cattacaact	gatatggaag	taaaaaattc	tctaaagatg	840
gccttttaag	aaaaagtaga	cgtcccagca	aaatatgtta	gtgctgcaaa	agctaaaggc	900
ccatttttag	caggtgttaa	cgaaacgatt	ccatatgaag	cgtttggtgg	ggatggcatg	960
ttaacgcgtt	taatccttaa	agcttcagag	ggagcaaaat	ggtcagacaa	tgggtgttgat	1020
aaaaatagtc	cattattacc	gttaaaaagt	ttaactaagg	gtaaatactt	ctaccaagtc	1080
tctcttaagt	gcaatacagc	cggtaaaaaa	ggccaagctc	tcttagatca	aattaaggca	1140
aatggaagcc	ataacttatca	agcaactatc	actattttatg	gtacgaaaga	tggcaaaagt	1200
gatatgaata	ctatttttagg	acaaaagaca	gtgatgatcc	atattaatgt	cgctaaaaaa	1260
gatatgaata	gcacatcaat	gatgatgaaa	aaagataaga	tgacaatgcc	tatgaagaaa	1320
gaaatgactt	catctaaaat	aaataccggg	atgatgatgt	ctaacaacaa	gatgtcagct	1380
aatatgcaaa	tgtcatcaca	agccaaatca	aatgataaag	ctggtaaaaa	aatgtctatg	1440
atgtctaaaa	atttacctaa	tacaggtgaa	acaaagcaac	aaaatgtagg	tgtgctaggc	1500
atgcttagtc	tagcctttgc	gacaggtcta	actgcgctag	gccttaaaaa	atctaaacaa	1560
agatag						1566

SeqID 26

atgacacata	ttacatttga	ctattcaaaa	gtcttggtgc	aattttagtg	cgaacacgag	60
ttagactacc	tacaaccaca	agtaagtgc	gcagatgctt	tccttcgtca	agggactggc	120
cctggctcag	atcttctcgg	atggatggac	ctcccagaaa	actatgacaa	agaagaattt	180
tctcgatttc	aaaaagccgc	tgaaaagatt	aaatcagata	gcgaagtact	cgtgggtatt	240
ggtattggtg	gttcgtacct	tggcgcaaaa	gcagcaattg	actttttgaa	taatcatttt	300
gctaatttgc	aaaccgcaga	agaacgtaaa	gcgcctcaga	ttcttttatgc	tggaaattct	360
atttcatcta	cttaccttgc	cgatttagtt	gaatacgtcc	aagataaaga	attctcagta	420
aatgtcattt	caaaatcagg	tacaacaact	gaaccagcga	ttgctttccg	tgtattttaa	480
gaacttctag	ttaaaaagta	cgggtcaaga	gaagctaata	aacgtatcta	cgctacaact	540
gataaaagta	aaggtgccgt	aaaagttgaa	gcagatgcta	acaattggga	aacatttgta	600
gttcctgata	atgttgggtg	tgcgttctca	gtactgacag	ccgtaggctc	tcttccaatt	660
gctgcttcag	gagcagatat	tactgctctt	atggaaggcg	caaagtctgc	tcgtaaagat	720
ttatcttcag	ataaaaatctc	tgaaaacatt	gcttatcagt	acgctgcagt	tcgtaattgt	780
ctttatcgca	aagggttatat	cacagagatt	ttagctaact	acgaaccatc	attacaatac	840
tttggtgaat	ggtggaaaca	attagcaggt	gaatcagaag	gtaaagatca	aaaaggatc	900
tatcctacat	cagcaaaactt	ctcaactgat	ctcactcac	ttgggtcaatt	tattcaagaa	960
ggttacogta	acctctttga	gacagttggt	cgcgttgaga	aacctcgtaa	aaatgtgact	1020
attcctgaat	taaccgaaga	tttagatggg	cttggttatc	ttcaaggaaa	agatgtagat	1080
tttggttaata	aaaaagcaac	agatgggtgta	ctccttgctc	atacagatgg	tgggggtcca	1140
aatatgtttg	taacgcttcc	tacacaagac	gcttacaccc	ttgggttacac	tatttacttc	1200
tttgagttag	caattggcct	ttcaggttat	cttaactcag	taaatccatt	tgatcaacca	1260
ggggtagaag	catataaacg	taatatgttt	gctcttctag	gtaaacctgg	attcgaagag	1320
cttagcgctg	aattgaatgc	acgtctttaa				1350

SeqID 27

atgaaagaaa	aaacaaacagc	cggacgtcgt	caattagaag	aatttgcacc	tgaatttgcc	60
agatataatg	atgatatttt	atttggtgag	gtttgggcaa	aagaggatca	tttaacagat	120

aaaacacggt	ctattattac	tatatctgcc	ttaattagcg	gaggaaatct	tgaacagtta	180
gagcatcatc	ttcaatttgc	caaacaaaac	ggagttaacta	aagaagaaat	tgctgacatt	240
atcactcacc	ttgcttttta	tgttggtatg	cctaaagcct	ggtcagcctt	taataaagct	300
aaggaaat	ggatataa					318

SeqID 28

gcttggagag	cttttagagga	tgctcaaaaa	tctggtaagg	taaaatccat	cggtgtctca	60
aacttttttag	aaaaagactt	agaaaatatc	ttaaaaaatg	gtcatgttaa	acctgctgtc	120
aatcaaatct	tagctcacat	cggaaataca	cctttcgact	tgattgatta	ctgtcaaagt	180
aaaggtattc	aagttgaagc	ttattcacca	attgcacatg	gacaagcatt	gaaatctgat	240
ggatttcaaa	aaatggctga	aaaatatggg	gttagtgttg	ctcaattatg	tattcaatat	300
ttactacaat	taaacctgat	cgttttacca	aaggcttcta	gtaaagaaca	tttacagtct	360
aatctagact	ttgactttgt	aattagtgc	gaagatatgt	cgatattaaa	atcacttatg	420
tttgacgatt	atggggaatt	ttctaacttc	cctgttttta	gtgaaaaatg	a	471

SeqID 29

atgtttagaa	ggtctaaaaa	taacagttat	gatacttcac	agacgaaaca	acggtttttca	60
attaagaagt	tcaagtttgg	tgacgcttct	gtactaattg	gtcttagttt	tttgggtggg	120
gttacacaag	gtaatcttaa	tatttttgaa	gagtcaatag	ttgctgcac	tacaattcca	180
gggagtgcag	cgaccttaaa	tacaagcatc	actaaaaata	tacaaaacgg	aaacgcttac	240
atagatttat	atgatgtaa	gaatggattg	attgatcctc	aaaacctcat	tgtattaaat	300
ccatcaagct	attcagcaaa	ttattatatc	aaacaagggtg	ctaaatatta	tagtaatccg	360
agtgaattta	caacaactgg	ttcagcaact	attactttta	atatacttga	tgaaactgga	420
aatccacata	aaaaagctga	tggacaaatt	gatatagtta	gtgtgaattt	aactatatat	480
gattctacag	ctttaagaaa	taggatagat	gaagtaataa	ataatgcaaa	tgatcctaag	540
tggagtgatg	ggagtctgtg	tgaagtctta	actggattag	aaaaaataaa	aaaagatatt	600
gataataatc	caaaaacaca	aatagatatt	gataataaaa	ttaatgaagt	caatgaaata	660
gagaaattgt	tagttgtatc	gctaccagat	aaaattaaat	attcaccaga	ggctaagcat	720
aggactgttg	aacaacacgc	ggaattagat	gcaaaagata	gcattgcaaa	tacagatgaa	780
ttgcccatac	attcaacgta	taactggaaa	aatggtcata	aaccagacac	ctcaacatca	840
ggtgaaaaag	acggaattgt	tgaagttcac	tatccagatg	gtactgttga	tgatgtgaat	900
gttaaagtta	ccgttacatc	gaaaaaaact	gataatacag	ctccaacatt	aaccgtcact	960
ccagagcaac	agactgttaa	agtggatgaa	gatattacct	ttacggttac	agctgaagac	1020
gaaaatgaag	ttgaactagg	tttagatgat	cttaaagcta	agtatgaaa	tgatatcatt	1080
ggagctcgtg	ttaaaattaa	gtatcttact	aaagaacctta	ataagaaagt	catggaagtg	1140
acaattatga	aagctacttt	agcagataag	ggcgcaatta	cctttactgc	aaaagataaa	1200
gcaggtaatc	aagcagaacc	taagacagtt	accatcaatg	ttcttcgcgc	agataaaatt	1260
aagtattcac	cagaggctaa	gcataggact	gttgaacaac	acgcggaatt	agatgcaaaa	1320
gatagcattg	caaatacaga	tgaattgcc	tcaaatcaaa	cgtataactg	gaaaaatggt	1380
cataaaccag	acacctcaac	atcaggtgaa	aaagacggaa	ttgttgaaat	tcaactatcca	1440
gatggtactg	ttgatgatgt	gaatgttaaa	gtaacggtta	catcgaaaaa	aactgataat	1500
acagctccaa	cattaaccgt	cactccagag	caacagactg	ttaaagtgg	tgaaagatatt	1560
acctttacgg	ttacagctga	agacgaaaa	gaagttgaac	taggtttaga	tgatcttaaa	1620
gctaagtatg	aaaatgatgt	cattggagct	ctgtttaaaa	ttaagtatct	tactaaagaa	1680
cctaataaga	aagtcattgga	agtgacaatt	atgaaagcta	cttttagcaga	taagggcgca	1740
attaccttta	ctgcaaaaga	taaagcaggt	aatcaagcag	aacctaaagac	agttaccatc	1800
aatgttcttc	cgccagataa	aattaagtat	tcaccagagg	ctaagcatag	gactgttgaa	1860
caacacgcgg	aattagatgc	aaaagatagc	attgcaaaata	cagatgaatt	gccatcaaat	1920
tcaacgtata	actggaaaaa	tggtcataaa	ccagatacct	caacaccagg	agagaaaaac	1980
gctgtttgtg	ttgtgacct	tccagataag	tcaacagatg	aagttcctgt	aaaagttaca	2040
gtggttgacc	cacgtacaga	cgcagagaaa	aatgatccag	caggtaaaga	tcaaactgtc	2100
aaagtgggtg	aacaaccaga	tccgacaaaa	tctcttgaag	cagtaccagc	tggaagtaca	2160
gtagcgtaca	aagaaccagt	tgataactaa	acaccaggag	agaaaaacgc	tattgttgtt	2220
gtgacctatc	cagataagtc	aacagatgaa	gttcctgtaa	aagttacagt	ggttgaccca	2280
cgtacagacg	cagagaaaaa	tgatccagca	ggtaaagatc	aaactgtcaa	agtggttgaa	2340
caaccagatc	cgacaaaatc	tcttgaagca	gtaccagctg	gaagtacagt	agcgtacaaa	2400
gaaccagttg	atactaagac	accaggagag	aaaaacgcta	ttgttgttgt	gacctatcca	2460
gataagtcaa	cagatgaagt	tctgttaaaa	ttacagttgg	ttgacccacg	tacagacgca	2520
gagaaaaatg	atccagcagg	ttaaagatcaa	actgtcacaag	tgggtgaaca	accagatccg	2580
acaaaatctc	ttgaagcagt	accagctgga	agtacagtag	cgtacaaaga	accagttgat	2640
actaagacac	caggagagaa	aaacgctgtt	gttgttgtga	cctatccaga	taagtcaaca	2700
gatgaagttc	ctgtaaaagt	tacagtgggt	gacccacgta	cagacgcaga	gaaaaatgat	2760
ccagcaggta	aagatcaaac	tgtcaaaagt	ggtgaacaac	cagatccgac	aaaatctctt	2820
gaagcagtac	cagctggaag	tacagtagcg	tacaaagaac	cagttgatag	taagacacca	2880
ggagagaaaa	acgctgttgt	tgttgtgacc	tatccagata	agtcaacaga	tgaagttcct	2940

gtaaaagtta	cagtgggtga	cccacgtaca	gacgcagaga	aaaatgatcc	agcagggtggg	3000
gaaacaacag	taccacaagg	cacaccgatc	agtgatgaag	aaattacagg	attagtgaag	3060
attccagaag	gatcaaacgg	cgtaccgaaa	gtagtaggag	accgtccgaa	tacagacgta	3120
ccaggagatt	ataaagtaac	ggtagaagta	acgtatccag	atggaacaaa	ggatacagta	3180
gcagtaacgg	ttcatgtgac	accaaaacca	gtaccggata	aagataaata	tgatccaaca	3240
ggtaaattctc	agcaagtcaa	cggtaaagga	aataaaactac	cagcaacagg	tgagagtgc	3300
actccattct	ttaatgttgc	agctttgaca	attatatcat	cagttgggtt	attatctgtt	3360
tctaagaaaa	aagaggatta	a				3381

SeqID 30

atgcagattc	tccaagacta	tgatggtaga	gcattaccca	agctagaaac	ggatcgactt	60
atcttgcgtc	agcgaacgg	gggggatgtc	ccagccatgt	ttgattacgt	ttgcttggaa	120
gaggttgcc	atccagcagg	gctcagccca	atagcatctt	tagaagatga	gtatgattat	180
tttgaaaatc	gctactatca	aaatctggaa	aaggcaaaat	taccatctgg	ttatggtatt	240
acggttaaag	gaagtgcacg	gattatcgga	tcctgcgcct	ttaaccatcg	cogtgaagac	300
gatgttttcg	agattggcta	tctgcttcac	cctgactact	ggggtcatgg	ctatatgaca	360
gaagctgtcg	ccgctttgat	tgaagtcggt	tttacccttc	tcaatctcca	caaaatcgaa	420
atccgctgct	atgactacaa	taagcaaaag	cagcgcgtgg	cagaaaaact	aggattcacc	480
cttgaagcaa	ccatccgtga	tcgtaaggat	aatcaaggca	atcgctgtgt	caatttgata	540
tatgggttgc	tgaggagtga	gtgggagtaa				570

SeqID 31

atgtcaaaag	aactatcacc	aaaatacaat	cctgccgagg	ttgaggaaag	ccgttatcaa	60
acttggcctt	accaagatgt	tttcaagcca	tcaggggata	ctgaggctaa	gccctattct	120
atcgtgatcc	caccacccaa	cgttacgggt	aaattacact	tgggtcacgc	ttgggataca	180
actctacaag	atatcattat	tcgtcaaaag	cgtatgcagg	gctttgatac	actctggcct	240
ccagggtatg	accacgctgg	tatagccact	caagctaagg	ttgaggagcg	ccttcgtgag	300
caagggtatt	cacgttatga	tcttggctcg	gaaaaattcc	tagataaaag	ttgggaatgg	360
aaagacgagt	atgcagcaac	tattaaatct	cagtggggga	aaatgggtct	ttcgggtgat	420
tatagccgtg	agcgttttac	ccttgatgat	ggactttcaa	aagcggtaag	aaaagtcttt	480
gttgatttgt	acaataaagg	ttggatctat	cggtgggaat	tcacatttaa	ctgggatcca	540
gcagctcgta	cagccctttc	agatattgaa	gttattcaca	aggatgttga	gggtgctttc	600
tatcatatga	attatatgct	ggaagatggc	tcacgcgccc	tagaagtagc	aacaactcgt	660
cctgagacta	tgtttgagga	tgtggctgta	gcggtaaaat	cagaagatcc	acgttacaaa	720
gatttgattg	gtcaaaatgt	tatccttcct	atcatcaata	aacctattcc	aatcatcgct	780
gatgaacacg	ctgactccaga	atttggaaca	gggtgtggtta	agattacgcc	ggctcacgac	840
cctaagtact	tcgtctgagg	tcaacgccac	aacttaccac	aagttaacgt	tatgaacgat	900
gatggtaact	tgaatgaact	tcgggatgaa	tttaattggt	tggatcggtt	cgaagctcgt	960
aaggcagtag	tcgctaaatt	agaatcggtt	ggaaacttag	taaaaattga	aaaaatgact	1020
cattctgttg	gtcattcaga	acgaacaggc	gttgtggttg	aaccacgttt	atctactcaa	1080
tggttcgtca	agatggatca	attggctaag	aatgccattg	ccaaccaaga	tacagaagac	1140
aaggtagagt	tttatccacc	acgatttaac	gatactttta	tgagctggat	ggaaaatgtc	1200
catgaactgg	ttatctctcg	tcaattatgg	tggggacacc	aaattcctgc	atgggtacaa	1260
gtcaatgggt	agatgtatgt	tggagaagat	gccccagagg	gtgacggatg	gacacaggat	1320
gaagacgttc	tagacacatg	gtttagtctc	gctttatggc	cgttttcaac	aatgggatgg	1380
ccagacaccg	aagcagctga	cttcaaacgc	tacttcccaa	catcaacctt	ggtaactgga	1440
tacgatatac	tcttctctcg	ggatcgcgc	atgattttcc	aatctcttga	atttacagga	1500
cgccaaccat	tctcaaatgt	tcttattcat	ggactcatcc	gtgatgaaga	aggacgtaaa	1560
atgtctaaat	cacttggcaa	cgggattgat	ccgatggatg	tcattgagaa	atatggtgog	1620
gatgcctctc	gttgggttct	ctcaaatgg	tcagcccctg	gtcaagatgt	gcgtttttca	1680
tacgaaaaaa	tggatgcttc	gtggaatttc	attaataaga	tttggaacat	ttcacgctat	1740
atccttatga	ataacgaagg	tttaacgttg	gatcaagcca	gagaaaatgt	ggaaaaagtt	1800
gttaatatgc	aagttggaaa	tgtaacagac	cgttggattc	tccacaattt	aatgagact	1860
gtgggtaaag	ttactgaaag	ccttgacaag	tttgaatttg	gtgttctggt	tcacatcctt	1920
tacaacttta	tctgggaaga	atttgctaatt	tgggtacgttg	agttaacaaa	agaggttctt	1980
tatagtgaac	atgaagatga	gaaagttggt	acacgttctg	ttcttcttta	taccttagat	2040
caaatcttgc	gtcttcttca	tccaatcatg	cattttgtga	cagaagaaat	ttttggacaa	2100
tacgcagaag	gatcaattgt	ccttgcaagt	tatccacaag	ttaacgcgac	atttgaaaat	2160
cagacagctc	acaaaggcgt	tgaaagcttg	aaagatttga	ttcgttcagt	gogaaatagc	2220
agagcagagg	tcaatgttgc	tccatctaaa	ccaatcacta	tcttgggtta	gacaagtgc	2280
agcgaactcg	aaagcttctt	caaagacaat	agtaactaca	tcaaacgctt	cacaaaccca	2340
gagaogctcg	aaatcagctc	agcgattact	gccccagaac	ttgccatgac	tagcattatc	2400
acaggtgcag	aaatcttctc	cccatttgc	gaacctctta	acgttgaaga	agagttggca	2460
cgacttgaaa	aagaacttgc	taaaatggca	aaagaactaa	atatggtcgg	caaaaaactc	2520
agcaacgagc	gctttgtagc	taacgcctaa	ccagaagtgc	tccaaaaaga	aaaagacaaa	2580

cagaccgact	accaaactaa	atacgacgca	actatagcac	gtattgaaga	gatgaaaaaa	2640
ttaaataatg	attga					2655

SeqID 32

atggttgagc	caattatttc	aatacaagga	cttcataaaa	gttttgggaa	aatgaggtt	60
ttaaaaggca	ttgacttgga	tattcatcaa	ggagaagtgg	tggttattat	tggcccttct	120
ggctctggta	agtcaacatt	tttaagaaca	atgaatctct	tgggaagtacc	aacaaaggga	180
acagtgactt	ttgaagggat	tgatataaca	gacaaaaaga	atgatatttt	taaaatgcgc	240
gaaaaaatgg	gcatggtttt	tcaacagttc	aatctatttc	ccaatatgac	tgtactagaa	300
aatattactt	tatcacctat	taagacaaaag	ggactttcta	agcttgatgc	tcagacaaaa	360
gcatacgagc	tacttgaaaa	agttggactc	aaagagaagg	ctaagtctta	tccagctagc	420
ttatctggag	ggcaacaaca	acgaattgct	attgcaagag	gtcttgcaat	gaatcctgat	480
gtccttcttt	ttgatgaacc	tacttcagct	cttgatcctg	aaatggtagg	tgaagtcttg	540
actgttatgc	aagatttagc	taaatctggt	atgacgatgg	ttattgtcac	tcatgaaatg	600
ggttttgcac	gtgaagtagc	ggatcgtgtc	atttttatgg	atgcaggcat	tattgttgag	660
caagggaccc	ctaaggaagt	atttgagcag	acaaaagaaa	tccgcacaag	agatttctta	720
agtaaagtat	tataa					735

SeqID 33

atgaattata	aagagattta	tcaagagtgg	ttagaaaacg	actcactcgg	taaagatatt	60
aagtcagatt	tagaagctat	taaaggcgat	gaatctgaaa	ttcaggatcg	tttttcaaaa	120
acattagaat	ttggaacggc	gggattgaga	ggtaaaacttg	gagcaggaac	caatcgtatg	180
aatacttata	tgggtggggaa	agcagcacaa	gcattagcta	atacgattat	tgatcatggc	240
cctgaagcta	ttgcacgtgg	aattgcagtt	agttatgatg	tccgttatca	atctaaggaa	300
tttgcagaat	taacttgttc	cattatggca	gcaaagtgtg	ttaagtctta	tatttataaa	360
gggattcgcc	caacaccaat	gtgctcata	gctattcgtg	ctctaggatg	tgtttcgggt	420
gtgatggtta	ctgctagtca	taatcctcaa	gcttataatg	gttataaggc	atattggaaa	480
gaaggatctc	agatttttaga	tgatattgct	gatcaaattg	ccaatcata	ggatgctata	540
accgattatc	agcaaattag	gcaaataccc	tttgaagagg	ctctggcaag	tggtttggca	600
agttatatgg	atgagagtat	tgaagaagca	tataaaaaag	aagtgccttg	tttaaccatt	660
aatgatacta	acattgataa	gtcagtcoga	gtagttttata	ctccttttaa	tggcgttagga	720
aatttacctg	tgcgcgaagt	tttaagacgc	cgtggttttg	aaaatgttta	tgtgggtacct	780
ggtcaggaaa	tgcccgatcc	tgattttaca	acggttggct	atccaaaccc	tgaagttcct	840
aaagcatttg	cctattcaga	atctctagga	aagtcagttg	atgcagatat	cttacttgcc	900
acagatccag	attgtgaccg	agtagcattg	gaagtcaaag	atagtaaggg	agaatatatt	960
ttcttaaatg	gtaataagat	aggggcactt	ctttcctatt	atattttttc	acaacgatgt	1020
gccttaggga	atttgccaca	tcacccgtga	ttggtaaaat	ccattgtaac	tgggtgatcta	1080
tcaaaagtta	ttgcagataa	atataatatt	gaaactgttg	aaactttaac	cggattttaa	1140
aatatttggt	gaaaagctaa	tgaatatgat	atctcaaagg	ataaaaactta	tctctttggc	1200
tatgaagaaa	ttgcttggtt	ttgctatggc	gtgtatgtag	gtgataaaga	tgctgtgagt	1260
gcttcaatga	tggtagtaga	aatgactgcc	tattataaag	aacgagggca	aacactttta	1320
gacgttttgc	aaaccattta	cgatgaattt	ggctattaca	acgagcgcca	attttctctt	1380
gagttagagg	gtgctgaggg	gcaagaacgt	attagtcgta	ttatggagga	tttttagacag	1440
gacccaatat	tacaagtagg	tgagatgaga	ttggagaatt	ctattgattt	caaggatggt	1500
tataaggatt	ttccaaagca	aaattgttta	aaatattatt	ttaatgaggg	ttcatgggtat	1560
gctttaaggg	cgtcagggac	ggaaccctaag	ataaaatggt	acctttatac	gattgggtgt	1620
acagaagcag	atagtttatc	gaaacttaat	gcaattgagt	cggcttgctg	tgctaaaatg	1680
aatagtacta	aataa					1695

SeqID 34

atgtatagag	aaattaccgc	tgtcgaacac	gatcgctttg	tgagcgaatc	caaccaaaaca	60
aacctacttc	aactcttctaa	ttggcccaaa	gtaaaagaca	actggggtag	tcaattactt	120
ggcttttttg	acgggtgaaac	ccaaattggc	agcgctagta	ttctcatcaa	atcacttcct	180
cttggtcttct	ccatgctata	tattccgcgt	ggaccaatca	tggattactc	caatctagat	240
attgtaacta	aggtccttaa	ggaccttaaa	gcttttggca	aaaaacaaag	agctctcttt	300
atcaagtgtg	atcctctcat	ctatttataa	atgggtcaatg	ccaaagattt	tgaaaattcg	360
cccgatgaaa	aagaagggtt	aatcgccatt	gatcattttac	agcgtgcagg	tgctgattgg	420
actggtcggg	caacagattt	agctcatact	atccaaaccac	gttttcaggc	aaacctatat	480
gctaatacaat	ttggacttga	taaaatgtct	aaaaaaactc	gtcaagctat	tcgaacttcc	540
aaaaataagg	gagtagatat	acaatttggg	agccatgaac	tacttgaaga	ttttgcagag	600
ttgatgaaaa	aaacggaaga	ccgtaaaggg	ataaatctta	gagggaattga	ctactaccac	660
aaactccttg	atacgtatcc	taataactca	tacatcacaa	tggcttcgct	agatgttgca	720
aaacgatttag	aaaaaataga	aaaagaatgt	cagatagccc	aatctgaaag	aataaaatca	780
cttgaactta	atcgtgagaa	aaaagttaaa	caacaccaag	gtacgattga	tcgattaaat	840
aaagaaattg	attttctcaa	agaagctcaa	aaagcctatg	accgagacat	tattccattg	900

gctgcaaccc	tcactctaga	atttggtaat	acatcagaaa	atattttatgc	tggtatggac	960
gattacttta	aatcttattc	tgctcctatt	tacacttggt	ttgaaacagc	tcaaagggtc	1020
tttgaaacgtg	gaaatattttg	gcaaaatatg	ggggggattg	agaatgactt	atctggtggt	1080
ttatatcatt	ttaagtctaa	gttcgaacca	atcattgagg	aattttattg	agaatttaac	1140
attccagtga	acagattgct	ttataaagcc	tctaattatg	tctatgcctt	acgcaaaaaa	1200
cgtaaatagct	ag					1212

SeqID 35

atggcttgta	caacaatatt	ggttggtaaa	aaggcttctt	atgatgggtc	gactatgatc	60
gctagaacgg	aagactctgt	taatggcgat	ttcacaccca	aaaaattaaa	ggtaatgaca	120
tctaaagatc	aaccgcgtca	ttacaaatca	gtttttatcaa	attttgaagt	agatttacca	180
gataaacccac	ttccttatac	ttcagtagcg	gacgcattgg	gaaaagatgg	tatatgggg	240
gaagccggta	ttaacagtaa	aaatgtagcg	atgagtgtca	cagaaactat	tacaacgaat	300
tcccgcgttt	tgggtgcaga	tcctttgggt	tcagatggta	taggggaaga	ggatatactc	360
acttttagtgc	ttccctatat	tcagtcagcg	cgagaagggtg	tggagcggtt	aggtgctatt	420
ttggaaaaat	atggaaacct	tgaatcaaat	ggatttgctt	tttcagatac	cgaagaaata	480
tggtgggttag	aaacaattgg	tgggcatcat	tggattgtct	gtcgcgtacc	tgatgatgtt	540
tatgttacta	atcctaacca	actaggaatt	gatcattttg	aatttaataa	ctgtgatgac	600
tacatgtgct	ctagtgattt	gaaagagttt	atcgaacaat	accattttaga	tttgacctat	660
tctaattgagc	atttcaatcc	tcgatatgct	tttggtagcc	aacgtgataa	agatcgtcat	720
tacaacacac	caagaagttg	ggcaatgcag	cgttttttaa	atcctgaaat	tgaacaggat	780
ccacgtagct	tgtttattcc	ctgggtgtcaa	aagccttacc	gaaaaattac	tggtgaggat	840
attaaatatg	tggttagtga	tcattatcaa	gacagtgtgt	atgaccata	tggaaccgaa	900
ggggatgcgg	taagtaggag	agcttttctg	tcagttggta	tcaaccgaac	tagtcaaacg	960
tctattctac	aattacgacc	aaataaatca	cttgaaacga	caggtgttca	atggttatct	1020
tatggctcta	tgccattttg	aaccatgggt	ccgttgttta	cacaagttga	gactgtacca	1080
aactatTTTT	cgaatacaac	caaggatgct	tcaacagata	atTTTTattg	gaccaatcgt	1140
taatttgagc	ctctagcaga	cccacacttt	tatcaacatg	aagctgatat	tgaagctat	1200
atcgagagaa	cgatggctca	aggacatgca	catattaacg	gtgttgatag	agaagttgct	1260
gagaataaag	agattgattt	tcaacagaaa	aatcaagaaa	tgagtgacta	tatccaaaaa	1320
gaaagccaag	aattgttaaa	tcgtattcta	tttgatgcaa	gtaatttaat	gacaaatcgc	1380
ttttcaatgg	gagattaa					1398

SeqID 36

atgagaaaaga	aattttctttt	attgatgagc	ttttagtcta	tgtttgagc	ttggcaactt	60
gttcaagtta	aacaagtttg	ggctgatagt	aaacttaaa	tggttaacaac	tttttaccac	120
gtttatgagt	ttacaaaaaa	tgctggttgg	gataaagctg	atgtatctat	gttaattaaa	180
gcaggtacag	aaccgcgtga	ttttgaacca	tcaactaaaa	acatcgctgc	catccaagat	240
tcaaatgctt	ttgtttacat	ggatgataac	atggaaaact	gggctccaaa	agtagctaa	300
tcagttaaat	ccaaaaaagt	aacaactatt	aaaggtagct	gcgatatgtt	acttactaaa	360
ggcgtcgaag	aagaagggtga	agaacatgaa	ggacatggct	atgaaggga	tcacatgaa	420
cttgacccac	acgtatgggt	gtctccagaa	cgtgcgattt	ctgttgtaga	aaacatccgt	480
aataaatTTG	tcaaagctta	tccaaaagat	gcagcttcat	ttacaaaaaa	tgcatagctt	540
tacattgcaa	aattaaaaga	gcttgacaaa	gaatacaaaa	atggtttgtc	aaatgctaaa	600
caaaagagtt	ttgtgactca	acacgcagcg	tttggttaca	tggcgcttga	ttacggttta	660
aatcaagttc	caattgctgg	tcttactcca	gatgcagaac	cttcatcaaa	acgttttaggc	720
gaattagcta	aatacatcaa	gaaatataac	atcaactaca	tttattttga	agaaaatgct	780
tcaataaaag	ttgctaaaaa	tttagcagat	gaagttggcg	tgaaaacagc	tggtgcttagt	840
ccacttgaag	gactttctaa	aaaagaaatg	gcagctggcg	aagattactt	ctcagttatg	900
agacgtaatt	tgaaagttct	taaaaagaca	acagatgttg	caggtaaaga	agtagctcct	960
gaagaagata	aaactaaaaa	agttgaaaca	ggttacttta	aaactaaaaga	tggttaagac	1020
cgtaaattga	cagattactc	tggttaattgg	caatcagtat	atcctcttct	tcaagatggg	1080
acacttgatc	cagtttggga	ttacaaagct	aaatctaaaa	aagatatgac	tgctgcagag	1140
tacaaaaaat	atttatcagc	aggtttacaag	actgacgtag	aatcaatcaa	gattgatggt	1200
aaaaaacatc	aaatgacctt	tgtagctaat	gtaaaatcac	aaacattttac	atacaaatat	1260
gcagggttaca	aaatcttaac	ttataaaaaa	ggtaatcgtg	gagtacgtta	tctctttgaa	1320
gctaaagaaa	aagatgctgg	tcaattcaaa	tatatccaat	ttagtgaaca	tggtattaaa	1380
ccgaataaag	ctgaacactt	ccatatcttc	tgggggttcag	aaagccaaga	aaaattattt	1440
gaggaaatgg	aaaactggcc	aacatacttc	ccagctaaaa	tgtctggacg	tgaagttgcc	1500
caagacctta	tgtctcatta	a				1521

SeqID 37

atgaaattat	cgaagaagtt	attgttttctg	gctgctgttt	taacaatggg	ggcgggggtca	60
actgttgaac	cagtagctca	gtttgcgact	ggaatgagta	ttgtaagagc	tgacagaagt	120
tcacaagaac	gccagcgaa	aacaacagta	aatatctata	aattacaagc	tgatagttat	180

aaatcggaaa	ttactttctaa	tgggtgggtatc	gagaataaag	acggcgaagt	aatatcctaac	240
tatgctaacc	ttgggtgacaa	tgtaaaagggt	ttgcaagggtg	tacagtttaa	acgtttataaa	300
gtcaagacgg	atattttctgt	tgatgaattg	aaaaaattga	caacagttga	agcagcagat	360
gcaaaaagttg	gaacgattct	tgaagaagggt	gtcagttctac	ctcaaaaaac	taatgctcaa	420
ggttttggctg	tcgatgctct	ggattcaaaa	agtaattgtga	gatacttgta	tgtagaagat	480
ttaaagaatt	caccttcaaa	cattaccaaa	gcttatgctg	taccgtttgt	gttggaaatta	540
ccagttgcta	actctacagg	tacagggtttc	ctttctgaaa	ttaatattta	ccctaaaaac	600
gttgttaactg	atgaaccaaa	aacagataaa	gatgttaaaa	aattagggtca	ggacgatgca	660
ggttatacga	ttgggtgaaga	attcaaatgg	ttcttgaaat	ctacaatccc	tgccaatttta	720
ggtgactatg	aaaaatttga	aattactgat	aaattttgcag	atggccttgac	ttataaatct	780
gttggaaaaa	tcaagattgg	ttcgaaaaca	ctgaatagag	atgagcacta	cactattgat	840
gaaccaacag	ttgataacca	aaatacatta	aaaattacgt	ttaaaccaga	gaaattttaa	900
gaaaattgctg	agctacttaa	aggaatgacc	cttggttaaaa	atcaagatgc	tcttgataaa	960
gctactgcaa	atacagatga	tgcggcattt	ttggaaattc	cagttgcatc	aactattaat	1020
gaaaaagcag	ttttaggaaa	agcaattgaa	aatacttttg	aacttcaata	tgaccatact	1080
cctgataaag	ctgacaatcc	aaaaccatct	aatcctccaa	gaaaaccaga	agttcatact	1140
gggtgggaaac	gattttgtaa	gaaagactca	acagaaacac	aaacactagg	tgggtgctgag	1200
tttgatttgt	tggcttctga	tgggacagca	gtaaaatgga	cagatgctct	tattaaagcg	1260
aatactaata	aaaactatat	tgctggagaa	gctgttactg	ggcaaccaat	caaattgaaa	1320
tcacatacag	acggtacgtt	tgagattaaa	ggttttggctt	atgcagttga	tgcaaatgca	1380
gagggtagac	cagtaactta	caaattaaaa	gaaacaaaag	caccagaagg	ttatgtaatc	1440
cctgataaag	aaatcgagtt	tacagtatca	caaacatctt	ataatacaaa	accaactgac	1500
atcacggttg	atagtctgga	tgcacacact	gatacaatta	aaaacaacaa	acgtccttca	1560
atccctaata	ctgggtggat	tggtagcgct	atctttgtcg	ctatcggtgc	tgcgggtgatg	1620
gcttttgctg	ttaaggggat	gaagcgctcg	acaaaagata	actaa		1665

SeqID 38

atgaaaaaga	gacaaaaaat	atggagagggg	ttatcagtta	ctttactaat	cctgtcccaa	60
attccatttg	gtatatttgt	acaagggtgaa	acccaagata	ccaatcaagc	acttggaaaa	120
gtaattgtta	aaaaaacggg	agacaatgct	acaccattag	gcaaagcgac	ttttgtgtta	180
aaaaatgaca	atgataagtc	agaaacaagt	cacgaaacgg	tagaggggttc	tggagaagca	240
acctttgaaa	acataaaacc	tggagactac	acattaagag	aagaaacagc	accaattgggt	300
tataaaaaaa	ctgataaaac	ctgggaaagtt	aaagttgcag	ataacggagc	aacaataatc	360
gagggtagtg	atgcagataa	agcagagaaa	cgaaaagaag	ttttgaatgc	ccaatatcca	420
aaatcagcta	tttatgagga	tacaaaagaa	aattacccat	tagttaatgt	agagggttcc	480
aaagtgtggtg	aaacaatacaa	agcattgaaat	ccaataaatg	gaaaagatgg	tcgaagagag	540
attgctgaag	gttggttatc	aaaaaaaaatt	acaggggtca	atgatctcga	taagaataaa	600
tataaaattg	aattaactgt	tgagggtaaa	accactgttg	aaacgaaaga	acttaatcaa	660
ccactagatg	tcgttgtgct	attagataat	tcaaatagta	tgaataatga	aagagccaat	720
aattctcaaa	gagcattaaa	agctggggaa	gcagttgaaa	agctgattga	taaaattaca	780
tcaataaaag	acaatagagt	agctcttgtg	acatatgcct	caaccatttt	tgatgggtact	840
gaagcgacgg	tatcaaaggg	agttgcccgt	caaaatggta	aagcgctgaa	tgataggtga	900
tcatgggatt	atcataaaac	tactttttaca	gcaactacac	ataattacag	ttattttaaat	960
ttaacaaatg	atgctaacga	agttaatatt	ctaaagtcaa	gaattccaaa	ggaagcggag	1020
catataaatg	gggatcgac	gctctatcaa	tttgggtcga	catttactca	aaaagctcta	1080
atgaaagcaa	atgaaatttt	agagacacaa	agttctaattg	ctagaaaaaa	acttattttt	1140
cacgtaactg	atgggtgtccc	tacgatgtct	tatgccataa	attttaatcc	ttatatatca	1200
acatcttacc	aaaaccagtt	taattctttt	ttaaataaaa	taccagatag	aagtgggtatt	1260
ctccaagagg	attttataat	caatgggtgat	gattatcaaa	tagtaaaagg	agatggagag	1320
agtttttaaac	tgttttcgga	tagaaaagtt	cctgttaactg	gaggaacgac	acaagcagct	1380
tatcgagtac	cgcaaaatca	actctctgta	atgagtaatg	agggatatgc	aattaatagt	1440
ggatatattt	atctctattg	gagagattac	aactgggtct	atccatttga	tcctaagaca	1500
aagaaagttt	ctgcaacgaa	acaaatcaaa	actcatgggtg	agccaacaac	attatacttt	1560
aatggaaaata	taagacctaa	aggttatgac	atttttactg	ttgggatttg	tgtaaacgga	1620
gatccgtggtg	caactcctct	tgaagctgag	aaattttatg	aatcaatatc	aagtaaaaca	1680
gaaaaattata	ctaattgttg	tgatacaaat	aaaatttatg	atgagctaaa	taaatacttt	1740
aaaacaattg	ttgaggaaaa	acattctatt	gttgatggaa	atgtgactga	tcctatggga	1800
gagatgattg	aattccaatt	aaaaaatgg	caaagtttta	cacatgatga	ttacgttttg	1860
gttggaaaatg	atggcagtca	attaaaaaat	gggtgtggctc	ttgggtggacc	aaacagtgat	1920
gggggaattt	taaaagatgt	tacagtgaact	tatgataaga	catctcaaac	catcaaaatc	1980
aatcatttga	acttaggaag	tggacaaaaa	gtagttctta	cctatgatgt	acgttttaaa	2040
gataactata	taagtacaac	attttacaat	acaaataatc	gtacaacgct	aagtcgaag	2100
agtgaaaaag	aaccaaatac	tattcgtgat	ttcccaattc	ccaaaattcg	tgatgttcgt	2160
gagtttccgg	tactaaccat	cagtaatcag	aagaaaatgg	gtgaggttga	atttattaaa	2220
gttaataaag	acaaacattc	agaatcgctt	ttgggagcta	agtttcaact	tcagatagaa	2280

aaagattttt	ctgggtataa	gcaatttggt	ccagagggaa	gtgatgttac	aacaaagaat	2340
gatggtaaaa	tttattttta	agcacttcaa	gatggtaact	ataaattata	tgaaatttca	2400
agtccagatg	gctatataga	gggtaaaacg	aaacctgttg	tgacattttac	aattcaaaat	2460
ggagaagtta	cgaacctgaa	agcagatcca	aatgctaata	aaaatcaaat	cgggtatctt	2520
gaaggaaatg	gtaaacatct	tattaccaac	actcccaaac	gccaccagg	tgtttttccct	2580
aaaacagggg	gaattgggtac	aattgtctat	atattagttg	gttctacttt	tatgatactt	2640
accatttggt	ctttccgtcg	taaacaattg	taa			2673

SeqID 39

ggagcaaaaa	aggcaggggtg	gactgaatac	gctaggatgt	tagaagtcag	agagcaggtt	60
gaccatgtga	tgattccaaa	aatcaatcag	gatttaccac	tctacgctgg	tccagaagag	120
gacaatctgc	aacggggagt	tggtcatcta	gaagggataa	gtttgccgat	tgagggggct	180
tctacacatg	cggctcttgag	cgggtcaaaga	ggatatgccag	ctgctcggtt	gtttgccgat	240
ttggataaga	tgaaaaaagg	tgattatttt	tatgttacca	atctgaaaga	aaccttggtt	300
tatcaagtgg	atcgtatcat	ggtgattgaa	cctagccaat	tggtatgccg	gagcattgaa	360
gaggataaa	attatgtttac	ccttctgacc	tgtacacctt	atatgggctc	tttgtcaact	420
gtaatgggtg	acttatcatt	aacaacgaga	gagaatcagc	ttgggttctct	ctcttttttg	480
atgttcaaag	cgatgagaat	tttgctttta	aaatttttaa	agttgcaaaa	gccaaaggct	540
tgctcgctga	tgctcttgat	aagcttggtg	gtcgtctcta	atttggcatt	ggaaagggat	600
agctga						606

SeqID 40

atgtcggatg	ttgtcgaaaa	acaaacagct	aaatcgttta	taatgaacgt	attaaatggt	60
ttagcttttag	ggactgttat	tgtcttgata	ccaggagcaa	tccttgagga	attaatgaaa	120
gctttactgc	caatgtggag	cggatttgca	actttaatcg	ctgcaacagc	agttgcaaca	180
agtatgatgg	ggcttggtat	tggtattatg	gttggtctca	attttaaatt	taatcccat	240
caatcagcat	cactaggatt	agcggttatg	tttgcagggtg	gagctgcaac	cttctttaa	300
ggcgtatatta	tgctaaaagg	aacaggcgat	atcataata	tggaattac	tgctgcctta	360
ggtgtccttt	tgatccaatt	tttatctgac	aagacgaaat	cattcacttt	gattgtcatt	420
ccaacagtaa	cactcttact	agttggagga	gtaggatcatg	tgttattacc	ttatgtcaaa	480
atgattacca	ccatgatttg	acaagggatt	gcttcattac	ttggtttaca	acctgttttg	540
atgtcaattt	taattgcgat	gattttctgt	ttcttgatcg	tatctccaat	cacaacagtt	600
gggatttgctt	tggcaattag	tttgtccgga	attggttctg	gtgctgctaa	tttaggtatc	660
tgtgtctgcta	gttttgggct	ttgtatggct	gggtgggtcag	tcaattctaa	ggggacagcc	720
ttagcgcgatg	ttttagggtc	tcctaagatt	tcgatggcta	atgtattagc	aaaaccgaag	780
attatgctac	ctatgatata	ttcagcagca	atactaggaa	ttctcggagc	tctctttaat	840
attcaaggaa	caccagctag	tgcaaggttt	ggtatcagtg	gtttgattgg	accgattaat	900
gctcttaatt	tagcaaaagg	tggtatgtca	gttatgaata	tgttattgat	aattataata	960
tttgttgcctg	caccaattat	attgaatttt	atttttaatt	acctctttat	aaaagtactt	1020
aaaattattg	atccaatgga	ctataaatta	gatattttaa			1059

SeqID 41

atggctagac	ccttagtaga	acaaacagca	gatcgtctat	tgcatTTaat	tttagaaaga	60
gaataccctg	ttgggtgctaa	gctccccaat	gaatatgaat	tagcgggaaga	tctagatgtt	120
ggctcgacga	caatccgaga	agcagtcaga	agtttagcaa	cgcgtaatat	tttagaagtc	180
agacagggct	ctggaacata	tattagttct	aaaaagggtg	tttctgagga	tcatttaggg	240
ttctctctaa	taaaggacac	agataggttg	acatcagatc	tctttgaact	acgcctttta	300
ttggaacctc	gaatagcgga	gctggttagct	tatagaatta	cagatgatca	gttacaatta	360
ctcgaaaagc	ttgttggaga	tattgaagat	gctgttcacg	caggcgatcc	gaaacattta	420
cttttagatg	tggaaatttca	ttccatgcta	gctaaataca	gtggtaatat	tgcaatggat	480
agccttttgc	cagtcacata	ccagtcaatt	catctgataa	atgcgaatta	tacaaatcgt	540
cagatgaagt	cggatagttt	agaagcacat	agagaaatta	tcaaagcaat	ccgagaaaaa	600
aatccagtag	ctgcacatga	tgctatgctt	atgcataatca	tgagtgttag	acgttcagca	660
ttgaaagctt	aa					672

SeqID 42

atgattaaga	aaaataaagt	tttttttagga	gttcttttag	tccttgttgt	tatccttgga	60
gggtggtgat	tattttacca	atcacaaatc	caaaagacaa	ctaataaage	gttagctatt	120
gcttataaag	atgctaaggt	ggctaagaag	gatgtcatat	atcaaaaaat	tgacaaagaa	180
tttgaaaact	ttagagggag	ctacgaaatt	gagttcaata	ccaaaagcgc	agaatacagc	240
tatcatgtag	atgctaagac	tggaacaaatc	cttgagcggg	acatggataa	taatggcttt	300
tcaaaatcga	cttctcagtc	aagttcatcg	tcaagtcaaa	aatctcataa	aataagtcaa	360
gaagaagcca	aaaagattgc	attttaaagat	gctaataatag	aggaatcaga	agtcagtaat	420
cttaagatca	aagaagaaat	tgaaaatgga	aaatcagttt	atgatattga	ctttgtggac	480
ctgaaaaata	aaaatgaagt	tgattatcaa	attgatgcag	aaactggaaa	aatcattgaa	540

cgttctagag atcatatgaa tgattaa

567

SeqID 43

ttgaatcgta	aaaaaaggta	tcgtctcact	gtaaaaaagc	aaaatgctag	catacctaga	60
cgattaaatc	ttctattttt	tattattggt	ttattattta	ctgttcta	tcttcgttta	120
gagcaaatgc	agattgggca	acaatcattt	tacatgaaaa	aactgacagc	tcttacgagt	180
tatacagtga	aagaatcaaa	agcgagaggt	cagatttttg	atgctaaggg	agtagtctta	240
gttgaaaatg	atgaacgtcc	tactgtggcg	ttttctagag	gaaacaatat	ttcatctcag	300
tctatcaaag	agtttagcgaa	taaattatca	cattacatta	ccttaaccga	agttgcttca	360
agcgatagag	caaagagaga	ttattattta	gcagataaag	ccaactacaa	aaaagtgtgt	420
gaaagtttac	cagattctaa	acgttacgat	aaatttggtta	accatctagc	cgaatcaacc	480
gtatatgcaa	atgcagttgc	tgacgttcca	gtgagcgcta	ttaactattc	tgaagatgag	540
ttaaaagtgg	ttgcttattt	taaccaaagt	aatgcgacac	caacgtttgg	ttcagtga	600
ttaagtacag	gcgaattaa	tgatgatcaa	atcaagaaac	tggatgctga	taagaaggaa	660
ctgttaggaa	tttctgtaac	aagtaattgg	catcgctcgt	aaaaaggaa	ttctttatcg	720
gatataattag	gtactatttc	tacagaaaag	gcaggtttac	caagagaaga	agttaaaaaa	780
tatttgaaaa	aaggctattc	actgaatgac	cgagtgggaa	cttcttacct	tgaaaaacaa	840
tatgaagatg	acttacaagg	aatcagacaa	attcgcaaag	tagttgttaa	taaaaaaggt	900
aaagtgtgtt	cagataatat	tacgcaagaa	ggtagctcag	gaagaaatct	taaattaacg	960
attgatctta	attacccaaa	caaagtagaa	agtatcttga	aacaatacta	tggcagtgaa	1020
ttatctagtg	gacgcgctag	tttttccgaa	gggatgtatg	cagttgctat	agaaccttca	1080
actggtaaa	tgtagcaaat	ggctggctcg	aaaaatgatc	atgggaattt	agttgatgac	1140
agcctaggca	ctattgctaa	gaatttccag	ccaggatctg	ttgtgaaagg	tcgcagcgta	1200
tcacacagat	gggaaaataa	agttctttag	ggaaatgaag	tgctttatga	ccaagaaatt	1260
gctaataatac	ggctcatggt	tacacgaggt	ttgactccaa	tatctgcggc	acaagcgcta	1320
gagtattcat	ctaatactta	tatggttcaa	gtagcacttc	gtttaatggg	acaagactat	1380
aatacaggag	atgctttaac	tgatcgaggg	tatcaagaag	caatggctaa	actaaggaaa	1440
acttacggcg	aatatgggtt	aggggtttct	acaggattag	atttacctga	atcagaagggt	1500
tatgtacctg	gaaaatacac	cttaggaaca	actctaattg	aatcgttcgg	tcagtatgat	1560
gcctatacac	caatgcaact	tggtcagtat	atctcaacta	ttgcgaataa	tgggaatcgt	1620
ttagcacctc	acgtggtttc	agatatctat	gaagggaaat	attctaataa	gttcgctcaa	1680
ttggttcggt	caatcacctc	taaaacacta	aataagatag	ctatctcaga	tcaagagtta	1740
gccattattc	aagaagggtt	ttataacggt	gtcaatagtg	gaagtggcta	tgrcaactggt	1800
acgtcaatga	gggggaatgt	gacaaccatt	agtggtaaaa	ctgggtaccgc	tgaaacattt	1860
gctaaaaatg	taaatggaca	aacagtttct	acctacaact	taaacgctat	tgcttacgat	1920
actaatcgta	aaatagcagt	agcggtaatg	tatccgcagt	ttacaactga	tacaacaaaa	1980
tcccatcaat	tagttgcacg	agatatgatt	gatcaatata	tttcacagtt	cacaggacaa	2040
taa						2043

SeqID 44

atgacgggtt	ttcctaaaca	ttttctatgg	ggaggtgcag	ttgctgcca	tcaggtagag	60
ggtgcattta	gaacagatgg	caaagggtta	tctgtacaag	atgtacttcc	aaatgggtgg	120
ttaggcgatt	tcaccgcca	acctactcca	gacaatttga	agctagaagc	aattgatttt	180
tatcataact	ataaaaatga	tataaaactg	tttgagaga	tgggctttta	agtttttaga	240
acctctattg	ctgggtctcg	aatttttcca	aatggctgat	atagtgcctc	aaacgaagct	300
ggcttacaat	tttatgataa	tttatttgat	gagttgctta	aatataatat	cgagcccttg	360
gttaccttat	ctcattatga	aacaccgctt	catcttgcaa	aaacttataa	tggttgggct	420
gatagacgtt	tgatagcatt	ttttgagaaa	tttgctcaaa	cagtcatgga	gcgttataaa	480
gataagggtga	aatattgggt	gactttta	gaagtgaatt	ctattttaca	tatgcctttc	540
accagtgggtg	ctattatgac	cgacaaatca	caactaagtc	ctcaggagct	ttatcaagct	600
attcatcatg	aattagtagc	atcggctaga	gtgacaaaat	tagggcgctc	tatcaatcct	660
aattttaaaa	ttggctgtat	gattctgggt	atgccagctt	atcctatgac	atctgatcca	720
agagatgtcc	tggctgcaag	acaatttgaa	caacataatc	tgctattttc	agatatacat	780
gtcagaggta	aatatccac	ttatattcag	tcctattttc	aaaataatgg	tattaaaaatt	840
aaatttgaa	aaggagatga	ggaagtattg	gcacaaaata	cagtagattt	tctatcgttt	900
agttactata	tgagcgtgac	acaagcttat	gactttgaaa	attatcaaa	tggtcagggg	960
aatatccttg	gaggcctaac	taatcctcat	ttaacaaact	cagaatgggg	atggcaaatc	1020
gatcccattg	ggctacgcct	agtcctaaat	cagtattatg	aacgttatca	gattccggtg	1080
tttattgtag	aaaatggatt	gggagcaaaa	gatcaattga	tagaaacact	agacggtgat	1140
tatactgtcg	aagatgatta	tcgtattgat	tatatgaatc	aacatttagt	tcaagttgct	1200
aaagctattg	aagatgggtg	tgaaataatg	ggatatacat	cttgggggtg	tattgattgt	1260
gtatccatgt	ctacagctca	actaagtaaa	cgttatgggt	taatatatgt	tgatcgaaat	1320
gatgatggaa	caggagctct	acaacgttac	aagaagaagt	catttggttg	gtacaaaaaa	1380
gtgattaaga	caaatggcca	atcattgttt	gaacatcata	acagataa		1428

SeqID 45

atggctactt	ttcaaattaa	agaaaaaatg	ttttctctag	gcggtaaatt	tactattaca	60
gaccagactg	ggcttccctg	ttatcacgtt	gaaggaaagt	tgttccctct	acctaagact	120
tttaaagtct	ttgacgaaga	ggggcatctg	attagtcaga	ttgagaagaa	ggttttaagt	180
tttttaccac	agtttaagt	gacattagcc	aatgggaatc	atctcacgat	taagaaagat	240
ttctcatttt	tgaacacctc	ttacaccatt	gaagaccttg	atatggaagt	taagggaagt	300
ttttgggata	tagattttcc	actcttaaaa	gacaatcaag	ttatagcaaa	catatctcaa	360
cagtgggttc	gtatgacttc	aacttatcag	gtagaagttt	acaatgaaac	ttacaacgat	420
ttgacaattt	cgcttgctat	agcgatcgac	tatgtcaaa	agttagaaaa	aaatgcacat	480
aactaa						486

SeqID 46

atgaaaaaaa	taacaacttt	aatcttagct	agtagcttat	tactagttgc	aacgacatcg	60
gttaaagctg	atgataactt	tgaatgccca	acgcgttatg	ttaaaatgag	tgaaaaatca	120
aaagcatttt	atcaaagact	acaagaaaaa	caacgtaagg	cacatactac	tgtgaagact	180
tttaataatt	cagaataaag	gcacaaacta	cctcttaaac	aagaaaaggc	tagaaatgat	240
atctacaatt	taggcattct	tatttctcag	gagtcataag	ggttcatcca	acgtattgat	300
aatgcctatt	ctttggaaaa	tgtctcagat	attgttaatt	aagctcaggc	tttgataaaa	360
cgtaactatg	atttatttga	aaaaatcaaa	tctacacgtg	ataaggttca	agtcttactt	420
gcacgcatc	aagataatac	agacttaaaa	aacttttatg	ctgagttaga	tgatatgtat	480
gaacatgttt	atctcaatga	aagtagagtg	gaggcgataa	acagaaatat	ccaaaaatat	540
aattag						546

SeqID 47

atgaaattaa	aaaaattctt	tgaggatttg	ctggctaaac	tagaatatag	acccattcaa	60
gtttttatgc	gtcattttca	aagtgcagag	atggacttat	cagccatagc	agttgcttat	120
tatctattag	tgacagcttt	tccattacta	gttattgctg	ctaataattt	tccttatttt	180
catattaatg	tgtcggattt	attgtcactt	atgcaaaaaa	atcttccgaa	aaatatttat	240
gaacctgcct	cacgcttagc	agtagatgct	ttttcgaaac	cgtctaccgg	cattttggga	300
ttcgcttcat	taacagcttt	ttggacaatg	tctaaaagtt	tgacctctct	tcaaaaagcc	360
attaataaag	catacgggtg	tgaccaaacac	agagactttg	tgattagtcg	tttagtgggt	420
gtggggactg	ggctgatcat	cctattttta	ctgacttttg	ttttaatttt	ttcaactttt	480
tcaaaaccag	ttttacagat	aattgtaaac	atgtatgatt	tgaggagatac	tctaaccggc	540
tggcttttaa	atcttgcaac	accagttaca	tttttgacta	tatttttagg	tattggaatt	600
ttatacttta	ttttacctaa	cgcacgaatt	agaaaagtac	gttatgtcat	tccagggaca	660
ttattttcaa	cgttgtttat	tggttttttt	agtaatttaa	ttagccaata	cgtcttaaat	720
agggttgaga	aaatggttaga	tattaaaaac	tctgttctcg	tcgttatctt	tatcttaaat	780
ctatgggtta	ttttcttagc	ccacattatg	atttttaggtg	caatactgaa	tgccagcggt	840
caagaaattg	cgacaggaaa	aattgaatca	aggcgtggag	atattatgtc	tcttatccaa	900
aaatccaaag	aagaaaaata	a				921

SeqID 48

atgaaattac	tttatactga	tattaatcat	gatatgacag	aaatcttagt	caatcaggcc	60
gcgcagtctg	ctgaagctgg	atggcgtatt	ttttatattg	ctccaaactc	tttatctttt	120
gaaaaagagc	gtgcagtatt	agagaacctt	cctcaagaag	cctctttttg	tattacaatt	180
actcgctttg	ctcaattggc	acgttatttt	actttaaac	agcctaatac	aaaagaaagt	240
ttaaacgata	ttggattagc	aatgatcttt	tatcgtgctt	tagcaagttt	tgaagatgga	300
caattaaaag	tttttggacg	attgaagcaa	gatgcttcct	ttatcagtca	attggtagac	360
ctatacaaa	aattgcagac	agcaaatctg	agtatttttag	atttaaaaata	tttacattct	420
cctgaaaaat	ttgaagattt	attagctatt	tttctagttg	tttcagatct	tttaagagaa	480
ggagaatacg	acaatcaatc	taaaattgcc	ttttttacag	aacaagtaag	gtcaggccag	540
ctagatgtgg	atttaaaaga	cactatcctt	atagtcgatg	gttttaccgg	tttctcagct	600
gaagaagaag	ctttaattaa	aagtctgagt	tcacgttgct	aagagattat	catcggagct	660
tatgctagcc	aaaaagcgta	taaggctaac	tttactaatg	gaaatattta	ttctgcaggg	720
gttgattttt	taagatatct	agcaacgaca	tttcaaacaa	aaccagaatt	tatcttgtct	780
aagtgaggaa	gtaagtctgg	ttttgaaatg	attctgaaaa	atatcgaagg	taaacatgat	840
tttacaataa	gtagtccatc	tttagacgac	actgctaaag	attgtataac	aatttgggag	900
tgcattaatc	aaaaagatga	agtggacat	gtggctagag	ctatacgtca	gaaactttat	960
cagggatata	gctacaaaga	tatttttagt	ttactaggag	atgtagatag	ttataaacta	1020
caattaagca	agattttttga	gcagtatgat	attccttatt	atttcggtaa	agctgaaaca	1080
atggctgcgc	acccttttagt	tcatttttatg	gattccttgt	ctcgaataaa	acgttatcga	1140
tttagagctg	aagatgtttt	aaatcttttt	aagacaggta	tttatggaga	gattagtcaa	1200
gatgatttag	atttttttga	ggcttatatc	tcatatcgag	acattaaagg	tcctaagaag	1260
ttctttacag	attttgttgt	gggggctaaa	aaatttgatt	tagggcgtct	taacactatt	1320
cgtcagtcct	tccttgctcc	actggaaagt	tttgttaaaa	cgaaaaaaca	agacgggtata	1380

aaaacactca	accaattcat	gtttttcctt	actcaggtag	gtttgagtga	caatttatcg	1440
cgattagttg	gtcaaatgtc	tgaaaatgaa	caagaaaaac	atcaagaagt	ttggaaaaaca	1500
tttacagata	tttttagagca	gtttcaaaca	atatttggtc	aagaaaaatt	aaatttagat	1560
gaatttttat	cgttattaaa	ttcaggtatg	atgcaagccg	agtatcgtat	ggtccctgct	1620
actgttgatg	tgggttactgt	taagtctttac	gacttggttag	aaccacatag	taatcaattt	1680
gtctatgccc	taggcattgac	acaatcacat	tttccaaaga	ttgctcaaaa	caaactcttta	1740
atatctgata	ttgaacgtca	gcttataaat	gatgccaatg	acactgatgg	tcattttgac	1800
attatgacgc	gagaaaatth	gaagaaaaac	cattttgctg	ctctctctct	ttttaatgct	1860
gctaaacaag	cattagtgtt	gactatacca	caattattga	atgagtctga	agatcagatg	1920
tcacatatatc	ttatogaact	aagagatata	ggtgttcctt	ttaatcataa	aggacgcca	1980
tcgtttaaag	aagaagctga	taataattggg	aattacaag	ctttattatc	gcgtgttggt	2040
gacttgatc	gctctgctat	tgacaaagag	atgactaaag	aagaacaaac	tttttggtca	2100
gttgctgttc	gttattttgog	tcgtcaatta	acttctaaag	ggattgagat	accaataatt	2160
acagatagtc	ttgatactgt	gacagtttca	tcagatgtga	tgaccagacg	cttcccagaa	2220
gatgaccac	ttaaattatc	ctcatctgct	ttgacaactt	tttataataa	tcaatataag	2280
tatttttttac	aatatgtgtt	aggtttggaa	gaacaagact	caattcatcc	agatatgcgg	2340
caccatggaa	cgtaccttca	tcgtgttttt	gaaattctga	tgaaaaacca	agggatagaa	2400
tcctttgaag	agaaactcaa	ctctgcaatt	aataaaaacca	atcaagaaga	tgttttcaaa	2460
tccttgatt	cagaagatgc	agaaagtcgt	tattcttttag	aaattttaga	agatatcgcg	2520
cgtgcaactg	caaccatatt	acgacaagat	agtcagatga	ctgttgaaag	tgaagaagaa	2580
cgatttgaac	taatgattga	taatactata	aaaattaacg	gtattattga	ccgtatcgat	2640
cgtttatctg	atgggttcttt	gggtgtcgtg	gactataaat	caagcgctca	aaaattcgat	2700
atccaaaaat	tttataacgg	tctaagtcca	caattagtta	cctacattga	tgctatcagt	2760
cgtgacaagg	aggttgaaca	aaaaccaccg	atttttggag	ctatgtattt	acatatgcaa	2820
gaacctaaac	aagactttgtc	taaaattaaa	aatttagatg	atttagttaac	aaaaaatcat	2880
caagcttttaa	cttataaagg	attatttttca	gaagctgaaa	aagaattttt	agcaaattggg	2940
aaataccatc	tcaaagattc	cctttatttca	gaggctgaaa	ttgctatttt	acaagcacat	3000
aaccaattgc	tttacaataa	agcatctgag	actattaagt	caggtaagtt	tttgcataat	3060
ccatatacag	aagatgctaa	aacagttgac	gggtgatcag	ttaagagtat	tacgggggttc	3120
gaggcggata	ggcatatggc	gcgtgccaga	gcgctttata	aattacctgc	taaggaaaaa	3180
ogtcaagggt	tcttaacatt	aatgcagcaa	gaggaggaaa	atgatgacct	ttaa	3234

SeqID 49

atgagcgaaa	ctaaagttat	ggctttgctg	gaagcgatta	atgtcgctat	gagcgaagaa	60
atgacgcaaa	atgaaaaagt	atttttaatg	ggtgaagatg	taggtgtata	tggaggagac	120
ttcggtagat	cagttgggtat	gttagaagag	tttgggtgcta	agcgcgttcg	cgacacacca	180
atctcagagg	ctgcgattgc	aggttcagct	atcgggtgctg	cacaaacagg	tttgcgtcct	240
atcgttgatt	tgacattcat	ggatttcgta	acaatcgcaa	tggatgctat	cgtttaaccac	300
gggtgctaaaa	cgaattatat	gtttgggtgga	gggtctatcaa	ctccagttac	tttccgtgtg	360
gcacaggggt	cagggtattgg	ttcgggtgca	caacactcac	aatcattaga	agcttggtta	420
acacacattc	cagggtctaaa	agttgttgca	cctgggtactg	ttaatgagtc	aaaagcactt	480
ttgaaatctt	ctattcttga	caataaccca	gttatcttct	tagagccaaa	agctctctat	540
ggtaagaaa	aagaagttaa	catggatcct	gatttctata	ttccacttgg	taaaggggat	600
atgaagcgtg	agggtaactga	cttaacaatt	gtttcttatg	gccgtatgct	tgagcgtgtt	660
atgcaagctg	ctgaagaagt	tgctgaggaa	ggtattaacg	ttgaggttgt	tgatccacgt	720
acacttattc	cgcttgataa	agaatttaatt	atcgattctg	ttaagaaaac	tggtaaatgt	780
attttggtta	acgatgctta	taaaactggg	ggtttccactg	gtgaaattgc	aactatgggt	840
gctgaaagtg	aagcatttga	ttaccttgat	catcctatcg	tgctgtctgc	aagtgaagat	900
gttccagtac	cgtattcacg	tgtacttgaa	caaggaatct	tacctgatgt	agcaaaaatt	960
aaagatgcta	tctacaaagt	agttaacaaa	ggttaataaa			999

SeqID 50

atggcttttg	atgtaattat	gocaaaaactt	gggggttgaca	tgcaagaagg	cgaaatcctt	60
gagtggaaaa	aaaatgaagg	tgacaccggt	aatgaagggtg	atgtccttct	tgaaatcatg	120
tctgataaaa	ccaatatgga	aattgaagca	gaagacactg	gtgtactttt	aaaaattgta	180
catcaggcag	gagatgttgt	tcccgtcact	gaagtgattg	cctatatcgg	agaagaagggt	240
gaagaagtag	gtacgtcatc	accttcagct	gatgcaacta	tcacagctga	agatgggtcaa	300
tcagtttctg	gacctgtctg	tccttcacaa	gagacagttg	cagcagcaac	tcctaaagaa	360
gaacttgacg	ctgatgagta	cgatatcgta	gtcgtagggtg	gtggacctgc	aggttattac	420
gcagcaatcc	gcgggtgctca	acttggaggga	aaaattgcca	ttgttgagaa	aactgaattt	480
gggtgtacgt	gtttgaaagt	tggttggtatc	cctacaaaaa	catatcttaa	aaatgctgaa	540
atcctagatg	gtttgaaagt	agcagctgga	cgtgggtatca	accttgcttc	aactaactat	600
gcaattgata	tgataaagac	tggttgcttt	aaaaattctg	tagttaagac	actgactggc	660
gggtgtacgtg	gtctcttgaa	agcgaacaaa	ggtgaaattt	tcaatggact	tggacaagta	720
aacctgata	agtcgttgtt	tattggcgat	aaagttatca	aaggctgtaa	cgtcgttctt	780

gcgactgggtt	ctaaggtatc	tcgtattaat	attccaggta	ttgaatcacc	attagtatta	840
acatcagatg	atattcctga	tttacgtgaa	attcctaagt	cacttgctgt	tatgggtggt	900
gggtgcgtag	gtattgagct	tgggtcttgta	tgggcttcat	atgggtgttg	cgtaactggt	960
attgaaatgg	ctgatcgcat	cattccagca	atggataaag	aagtatcgct	agaacttcaa	1020
aaaatccttg	ctaagaagg	aatgaagatt	aaaacatcag	ttgggtgtttc	tgaaattggt	1080
gaagccaata	atcaattaac	gcttaaat	aacaacggcg	aagaagttgt	tgctgataaa	1140
gctcttcttt	caattggacg	tgttccacaa	atgaatggtc	ttgaaaatct	tgagcctgaa	1200
ccttgagatgg	aacgtggacg	tattaaagtt	aatgcttatc	aagaaacttc	aattccaggt	1260
atctatgcac	caggtgatgt	taatggaact	cgtatgttag	ctcatgctgc	ataccgtatg	1320
gggtgaagtag	ctgctgaaaa	cgcactcggc	ggtaataaag	gtaaaacaca	tctagatttc	1380
actccagcag	ctgtttatac	tcatcctgaa	gtagcaatgg	tggggatgac	agaagagcaa	1440
gcacgtgaac	aatatgggtga	catattagtt	ggtaaaaaata	gctttacagg	caatgggtcgt	1500
gctatcgctt	caaacgaagc	acatgggtttt	gtaaaagtaa	ttgctgaacc	taagtataaa	1560
gagattcttt	gtgttcacat	tattgggtcca	gctgcagcgg	aattgattaa	tgaagcttct	1620
acgattatgg	aaaatgagtt	gactgtctat	gatgtgacac	aatctatcca	tggtcaccca	1680
acattctctg	aagttatgta	cgaagctttc	ttagatgttc	tcggtgaagc	tattcacaaac	1740
cctccaaaac	gcaataaa					1758

SeqID 51

atgggaaaat	attttggtag	agatgggtgtt	cgcgggtgaag	ctaattgttga	actgacgcca	60
gaattggctt	ttaaattagg	acgttttggga	ggatatgttc	taagtcaaca	cgaactgat	120
cgtccgagag	tttttgtagc	tcgtgatact	cgtatttctg	gtgaaatgct	ggaatctgct	180
ttgattgctg	gtctactttc	agtaggtatt	gaggtttata	aacttgggtg	tttagccact	240
cctggagtgt	cttaccttgt	ccgtacagaa	aaagctagt	caggggttat	gatttcagca	300
agccacaatc	cagcacttga	taatgggtatt	aagtctcttg	gtagtgatgg	ttttaaactt	360
gatgatgatc	gtgaattaga	aattgaagct	ttacttgatg	cgaaggaaga	cactttacca	420
cgtccatcag	cacaaggttt	aggtacttta	gtagattatc	ctgaaggact	tcggaaatat	480
gagaagttta	tggaatcaac	tgggtattgat	ttagaaggta	tgaaggttgc	gttggtatata	540
gcaaattggag	cagcaacagc	ctcagctcgg	aatatctttt	tagacttgaa	tgctgatata	600
agtgttattg	gtgatcaacc	agatggtttg	aatatcaatg	atgggtgttg	ttcgacacat	660
cctgagcaat	tacaaagttt	agttagagaa	aatggttccg	atatcggtct	agcttttgat	720
ggtgatagt	atcgtttgat	cgctgttgat	gaaaatggag	agattgtaga	tggtgataaa	780
attatgttta	tcattgggaa	atatctttct	gataaagggc	agcttgctca	gaatacaatc	840
gtaaacacgg	tctatgtcaa	tctcggcttt	cataaagcgc	tcgaccgtga	aggtattcat	900
aaagcgatta	ccgctgtagg	agaccgctac	gtggttgag	aaatgcgtaa	atcaggatat	960
aatcttggcg	gggagcaatc	aggccacggt	attatcatgg	attacaatac	tacaggggat	1020
ggacaattaa	cagccatcca	attgactaag	gtcatgaaag	aaactggtaa	gaaattatca	1080
gagttagcta	gtgaagtga	gatttatcct	caaaaattag	taaatattcg	tggtgaaaat	1140
aacatgaaag	ataaagcgat	ggaagttcct	gcaattgcgg	aaattattgc	taaaatggaa	1200
gaagagatgg	atggcaatgg	tcgtattcta	gtacgtccta	gtgggtactga	gcctcttctt	1260
agagttatgg	cagaagcgcc	aacaaatgaa	gcagttgatt	attatgttga	tactatcgca	1320
gatgtcgttc	gtacagaaat	tgggttagat	ttaa			1353

SeqID 52

atgaaaggctc	aaaaaattat	tgctctagct	ggtcttgtcc	tgctcatgcca	ttttgctctt	60
acggcatgtc	atactcaaga	acacaaaaat	tctcatcata	ttaaaacaaa	gcaggttgct	120
aagaaaaaag	ctaataaaaa	gaaagtctct	gttaagggaa	gtcataaaaa	acgcaagggt	180
gttgacgggg	ttgactttcc	aactgatgat	ggctttttac	tgactaaaga	ttcgaagatt	240
ttatctcatc	ccgattctgg	aatcgttgta	gcacatggaa	atcattctca	ttttattttt	300
tactctgatt	taaaagggtc	aaaatttagc	tatttaattc	ctaattgcaa	tgcaaaaact	360
aataaaaaag	aagcggtaag	aaactttaaa	gcaggggctg	tagctgttaa	tacattaaat	420
gatggctatg	tttttaatcc	cgcagatatt	gtttcagaag	atgctaattg	ctacgtggct	480
agacatggtg	atcattttcc	ctatattcca	aaagcaagtt	tatctcagca	aaagcaagta	540
caagcaagta	gagctgtttc	acgttttagg	aatcaaaaata	atagccatta	cagagttaat	600
agttctaaaa	ttgcagggct	tcaccaccca	acaagtgtatg	gtttcttatt	caatggacaa	660
ggaataaaaag	gcactacccc	aacaggtatt	ttagtagaac	atcataatca	tctgcatttt	720
attagttttg	ctgattttaag	aaaaggggga	tggggatcaa	ttgctgaccg	ttaccaacca	780
caaaagaaaag	ttgattctaa	aaaacagtca	ccatcaagta	aaaagccaag	aactgaaaat	840
actttaccta	aggacatcaa	agataagcta	gottacottg	ctcgtgaatt	acatttagat	900
atttcacgta	tcagatgcct	taaaacacta	aatgggtgaa	ttggatttga	ataccacat	960
gatgatcata	cacatgttat	tatggcctaa	gatattgtatc	taagtaagcc	aattccaaat	1020
ccacatcatg	atgacgaaga	tcacacacaa	ggctcatcacc	atgatgagtc	cgaccataag	1080
catgaagaac	acgagcacac	taagtcaaat	aaattatctg	atgaagatca	aaagaaatta	1140
atttattttag	cagagaagct	tggtttaaat	cctaatacaa	ttgaagtatt	aacgtcagag	1200
gatgggagta	tcattcttta	atatccacat	gatgaccact	cacacactat	agcaagtaag	1260

gatattgaaa	ttgggaagcc	tatcccagat	ggacaccacg	atcactctca	tgcaaaagat	1320
aaagttggta	tggaactct	aaaacaaatt	ggttttgatg	atgagattat	tcaggatatt	1380
ctgcatgcag	atgctccaac	accattccca	tccaatgaaa	ctaactctga	aaaaatgcgt	1440
cagtggcttg	caactgttac	taagattaac	attggacaaa	gaaccaatcc	attccagcgt	1500
tttgggtctat	cattgatgcc	taatattgaa	gttctaggaa	ttgggtttac	tccgattaat	1560
gatatgacgc	cagtttttga	attcaaaaaa	cttaaacagc	tttggatgac	aaatactggt	1620
attacagatt	attctttcct	tgataagatg	ccactattag	aaggattgga	tatttcacaa	1680
aacggtatta	aggatttatc	tttccttaca	aaatataaac	aattaagtct	tattgctgca	1740
gctaataatg	gcattacttc	gctaaaacca	ttggctgaat	taccaaaacct	tcaattctta	1800
gttttgagtc	ataaacaatat	ctctgacttg	acaccgttat	caaacttgac	aaaactccaa	1860
gaattgcacc	ttgatcataa	taatgtgaag	aattttaagt	cactttctgg	taaaaaagat	1920
ttgaaagttc	tagattttatc	aaacaataaa	tccgcagact	tatcgactct	aaaaacaact	1980
agtcttgaga	cgcttctttt	aaatgagacg	aatacaagca	atctaagttt	cttaaagcaa	2040
aatcctaagg	tatcttaatt	aacaattaat	aatgcgaat	tagcatcatt	agatgggtatt	2100
gaagagagcg	atgaaattgt	taaagtagaa	gctgaaggga	accaaattaa	gtcactagta	2160
ttgaaaaata	aacaagggttc	gttaaaatttc	ttgaatgtga	ctaataatca	gttaacatca	2220
cttgaagggtg	ttaataatta	tacttcactt	gagaccttaa	gtgtttctaa	aaataaactt	2280
gaatcttttag	atattaaaaac	acctaacaaa	acagttacaa	atcttgattt	tagccataac	2340
aatgttccaa	catcaccaatt	gaaattgaat	gaaaaaaata	ttcctgaagc	agtagctaag	2400
aattttccag	cagttgtaga	aggttcaatg	gttggaaatg	gtagtcttgc	tgaaaaagca	2460
gctatggctt	ctaaagagga	caaaaacagt	tcagataata	ctaataacca	aaaaaacact	2520
gaaaaatctg	ctcaagcgaa	tgctgatagt	aaaaaagaaa	acctataaac	acatgatgaa	2580
catcatgacc	atgaagaaac	agatcatgca	catgtaggtc	atcatcacca	ttaa	2634

SeqID 53

atgaataaac	gcgtaaaaat	cgttgcaaca	cttggctctg	cggtagaatt	ccgtgggtggt	60
aagaagtttg	gtgagtcctg	atactggggg	gaaagccttg	acgtagaagc	ttcagcagaa	120
aaaattgctc	aattgattaa	agaagggtgc	aacgttttcc	gtttcaactt	ctcacatgga	180
gatcatgctg	agcaaggagc	tcgtatggct	actgttcgta	aagcagaaga	gattgcagga	240
caaaaagttg	gcttccctct	tgatactaaa	ggacctgaaa	ttcgtacaga	actttttgaa	300
gatggttcag	atttccattc	atatacaaca	ggtacaaaat	tacgtgttgc	tactaagcaa	360
ggtatcaaat	caactccaga	agtgattgca	ttgaatgttg	ctgggtggact	tgacatcttt	420
gatgacgttg	aagttggtaa	gcaaactcct	gttgatgatg	gtaaaactagg	tcttactgtg	480
tttgcaaaag	ataaagacac	tcgtgaattt	gaagtgttg	ttgagaatga	tggccttatt	540
ggtaaacaaa	aagggtgtaaa	catcccttat	actaaaattc	ctttcccagc	acttgcagaa	600
cgcgataatg	ctgatatccg	ttttggactt	gagcaaggac	ttaaactttat	tgctatctca	660
tttgtagcgt	ctgctaaaga	tgtaaatgaa	gttcgtgcta	tttgtgaaga	aactggcaat	720
ggacatgtta	agttgttttc	taaaattgaa	aatcaacaag	gtatcgataa	tattgatgag	780
attatcgaag	cagcagatgg	tattatgatt	gctcgtggtg	atatgggtat	cgaagttcca	840
tttgaaatgg	ttccagttta	ccaaaaaatg	atcattacta	aagttaatgc	agctggtaaa	900
gcagttatta	cagcaacaaa	tatgcttgaa	acaattgactg	ataaaaccacg	tgcgactcgt	960
tcagaagtat	ctgatgtctt	caatgctgtt	attgatggta	ctgatgctac	aatgctttca	1020
ggtgagtcag	ctaatggtaa	ataccaggtt	gagtcagttc	gtacaatggc	tactattgat	1080
aaaaatgctc	aaacattact	caatgagtat	ggtcgttag	actcatctgc	attcccacgt	1140
aataacaaaa	ctgatgttat	tgcatctgcg	gttaaaagatg	caacacactc	aatggatatac	1200
aaacttggtt	tgacaattac	tgaacaggt	aatacagctc	gtgccatttc	taaattccgt	1260
ccagatgcag	acattttggc	tgttacattt	gatgaaaaag	tacaacgttc	attgatgatt	1320
aactgggggtg	ttatccctgt	ccttgcagac	aaaccagcat	ctacagatga	tatgtttgag	1380
gttgacgaac	gtgtagcact	tgaagcagga	cttggtgaat	caggcgataa	tatcgttatac	1440
gttgacgggtg	ttcctgtagg	tacagggtgga	actaacacaa	tgctgttctg	tactgttaaa	1500
ttaa						1503

SeqID 54

atgactgcaa	ctaaacaaca	taaaaaagtt	atcctcgttg	gtgatgggtgc	cgtagggttct	60
tcttacgctt	ttgcacttgt	taaccaaggt	attgcgcaag	agttagggtat	cattgaaatc	120
ccagctttat	ttgataaagc	tgttgggtgat	gctgaagatc	tttcacatgc	ccttgcattt	180
acatcaccta	aaaaaatcta	cgcagctact	tatgcagact	gocgagatgc	tgaccttggt	240
gtcattactg	ctggcgcacc	tcaaaaacca	ggtgaaactc	gacttgacct	tgttggtaaa	300
aacttagcaa	ttaacaaatc	aatcgtaact	caagttgttg	aatcagggtt	caacgggtatc	360
ttcttagtag	cggctaacc	tgtagatgta	cttacaattt	caacttggaa	attctcaggt	420
ttccctaagg	aacgcgttat	tggttcaggt	acttcacttg	actctgcacg	tttccgtcaa	480
gcttttagcag	ataaaattgg	tgttgatgct	cgttcagttc	acgcatacat	catgggtgaa	540
cacggtgact	cagaatttgc	cgtttggtca	catgctaacg	ttgctgggtgt	ccaacttgaa	600
caatgggttac	aagaaaatcg	cgatattgat	gaacaaggac	ttgttgattt	gtttatttca	660
gttcgtgacg	ctgcatactc	aatcatcaac	aaaaaagggtg	ctacatatta	cgggtattgct	720

gtcgcacttg	ctcgtattac	taaagctatc	cttgatgatg	aaaatgcagt	tcttccatta	780
tctgtatata	aagaaggcca	atacggatg	gttaaagatg	tctttatcgg	tcagcctgca	840
atcgtagggtg	cacatgggtat	cgttcgtcca	gttaatatcc	cattaaatga	tgctgaactt	900
caaaaaatgc	aagcctcagc	tgaacaatta	aaagatatta	ttgacgaagc	ttggaaaaac	960
ccagaattcc	aagaagcatc	aaaaaactaa				990

SeqID 55

atgcaagata	aaaatttagt	agatgttaat	ctaactagtg	aaatgaaaa	gagttttatc	60
gattacgcca	tgagtgtcat	tggtgctcgt	gcacttccag	atgttagaga	tggtttaaaa	120
cctgttccatc	gtcgtatttt	atatgggtatg	aatgaactag	gtgtgacacc	tgataaacct	180
cataagaaat	cagcacgtat	tactgggtgat	gttatgggta	aataccatcc	acatgggtgat	240
tcactctattt	acgaagcaat	gggtgcgtatg	gcacaatggg	ggatcatatcg	tcatatgctc	300
gttgatgggtc	atggaaactt	tggttcaatg	gatggggatg	gtgctgcgcg	acagcgttat	360
acagaagcac	gtatgagtaa	aattgctcctt	gagatgcttc	gtgatatcaa	taaaaataca	420
gttgatttttc	aagataacta	tgatggcagc	gaacgtgaac	ctcttggtttt	accagcgcgt	480
ttccctaatt	tattagtcaa	tggtgcaact	ggtattgctg	taggtatggc	aacaaatatt	540
ccaccacata	atctagggtga	gtctatagat	gctgtcaagt	tggttatgga	taacctgat	600
gttactacac	gggagttaat	ggaagttatt	cctgggtccag	attttccctac	tggtgccttg	660
gtgatgggac	gttcaggtat	tcaccgtgcc	tatgaaactg	gaaagggatc	aattgtctta	720
cgttcacgga	ctgaaattga	aacaacttca	aatgggaaag	agcgtattgt	tgtcacagag	780
tttccatac	gtgttaataa	aacaaaagta	cacgagcata	ttgtacgttt	agcacaagaa	840
aagcgtattg	aaggtattac	tgctgttcgt	gatgaatcaa	gtcgtgaagg	cgcttcgtttt	900
gttattgaag	ttcgtcgtga	tgcttcagca	aatgtgattt	taaataatct	tttcaaatta	960
actagcttgc	agacaaat	tagcttcaat	atgcttgcta	ttgaaaaagg	tgttccgaaa	1020
attttgtcat	tacgacaaat	cattgataac	tatattgaac	acaaaaagga	agttattgtc	1080
cgctgctact	agtttgacaa	agctaaagca	gaagctcgtg	ctcatatctt	agaaggttta	1140
cctgtggcgc	ttgatcactt	ggatgaagtt	atcacgatta	ttcgtaatag	tgagacagac	1200
accattgctc	aagcagagtt	gatgtcacgt	tttgaattat	cggagcgtca	gagtcaagca	1260
attttagata	tgctgtcttc	tcgtttaact	ggattagaac	gcgataaaat	ccaatcagaa	1320
tacaatgact	tgctagcttt	aattgctgat	ttagcagata	tcttagctaa	gcctgaacgt	1380
gttgttacca	ttataaaaaga	agagatggat	gagggttaag	gtaagtatgc	tgatgcccgt	1440
cgtacagaat	taatgattgg	tgaagtttta	tcacttgaag	atgaagacct	tattgaggaa	1500
gaagatgttc	ttattactct	ctcaaacaa	ggatatatca	agcgtctcgc	tcaagatgag	1560
tttagagcac	aaaaacgtgg	aggacgcggt	attcaaggga	ctggagttaa	taacgatgat	1620
tttggttcgtg	aattggtttc	aacaagtact	cacgatactg	tgcttttctt	tacaaattta	1680
gggcgtgtgt	atcgtttgaa	agcatatgaa	attccagaat	atggacgtac	agctaaaggc	1740
ctccctatcg	ttaacctttt	aaaacttgac	gaaggtgaaa	caattcaaac	aattattaat	1800
gctagaaaag	aagatgtcgc	taataaatat	ttctttttca	caactcagca	aggtatagtg	1860
aaacgtacaa	gtgtttctga	atttagtaac	attcgtcaaa	atggacttcg	tgctattaat	1920
ttgaaagaga	gttagcagtt	gattaacgtc	ctcttgattg	acgaaaatga	agatgttatt	1980
atcgggacac	gtacaggcta	ctctgttcgc	ttcaaaagtga	acgctgtacg	taatattggga	2040
cgcacagcga	ctggggtagc	aggcgttaat	cttcgtgaag	gtgataaagt	tgtgggagct	2100
tctcgtatcg	ttaatggaca	agaagtactg	atcatcactg	aaaaagggtta	tggcaagaga	2160
acagaagcct	cggaatatcc	tacaaagggg	cgtgggtggt	aaggaataaa	aaccgcta	2220
attactgcta	aaaatgggcc	attagcacgc	ttagtgaacg	ttaatggaaa	tgaggacatc	2280
atggtcatta	cagatacagg	cgttatttat	ggaaccaatg	ttgctaata	ttctcaact	2340
ggtcgttcta	ctatgggtgt	taaagtgatg	agaacttgatc	aagaagctaa	aatcgttact	2400
gttgcgctag	tggaacaaga	aattgaagat	aagtctaata	tagaggatac	aaaagaatag	2460

SeqID 56

atgacaatct	ttgatgaaag	agagttaaaa	gaacgattta	ctcatgaaaa	tagggttagt	60
ttttatgagt	ttgtggctaa	atatgatgct	caaagtgggtc	ctgtgatgaa	agcaaagggc	120
tatcgatgta	ttcattcaat	ggagcgtaca	gtgggttttta	cttttgggga	attcacgatt	180
aggcgacgtc	gggtggcaaaa	aggagaacat	tgggtgggtgc	cagttgatga	aaagctagga	240
ctgaaaaaga	atgttcgcta	ctctttagaa	ttcatgtatc	aaattgctag	tttagcaacc	300
atgatgcctt	atgaaaaagt	gattaaaggtt	gttcagatga	tgtattgtat	tgtgattacc	360
aaacctactg	ttgtgaaggc	cgtaagattt	agtcgtgaat	tgcttaaaaga	aaaggaagcg	420
tatcgttttt	ttgatgaaga	tataccagta	gataaagaac	cagttgatat	gatttatctt	480
gaaggagatg	gagtcattgt	caaagctcga	gaagaaggat	tagataatcg	caatgttgat	540
ttgtctcatt	tcgtggttca	tacgggtagt	cagaaaagtag	gaagcaatcg	ctttgtctta	600
caaaataaaa	aagagtttgt	gtcccttgat	aatcgtcaaa	cgcgtcaaaa	gattttggac	660
tacctttaca	atcattttta	cattgccccca	aacaccttgc	ttattaccaa	ttcagatggg	720
ggccatggct	ataccccata	tgttttttaa	gagattgcga	aagcactcaa	agtgaagcaa	780
cacgaacact	tttgggatag	gtatcatgtc	aatgaaaaga	tcaaaagttt	ttttaaactc	840
tatccagtgg	aactgatgac	tggcgctttt	cagagcatta	aacagcatga	taaagaaaag	900

cttagaactg	ttttggatac	gacagaagca	ttgatactga	tggagaaga	aatggaaggg	960
tttaaccagt	tcaaacgaaa	gttgtaaacc	aattttcaat	atactaaatc	agctgaattg	1020
agaggtttca	gtcgtgcagg	aataggtgtt	atggagtcac	aacatcgaaa	aattacctat	1080
cggatgaaaa	agcgcgggat	gtattggaca	attcagggag	ctgagacgat	gagtcattta	1140
attgtcctat	cgtatgaagg	acagctaaga	gatctcttct	ttggttcttg	gcgtgaagac	1200
tatcagaaat	atcaagagct	agaaaacctt	agtgcgggaa	aaatcaaaca	tgaacagaat	1260
aaaatcaata	agagatatga	tctccagaca	cttggtcggc	ttaggtacgg	taggcacgt	1320
aatttatag						1329

SeqID 57

atggcatatt	tatcaaaatt	atccgatttg	gatccatcgt	tgatggatgc	ggattctgaa	60
caaatttata	ttcctaaggt	cttgtttgag	cataatgact	ttaaaggctt	gacctacaaa	120
gagattttat	tatatctttt	tttgtttaaat	cgtttaagag	agccattaga	ttttattcaa	180
aaaggctatg	atgataatga	agatacctat	gttcacttta	aggtcgaaga	tttatgtgaa	240
ctactcaacc	agagtaagac	aaccgttatt	tccttgaaga	aaagggttagc	tcaatatggg	300
ttgatagaag	aagtgaagc	aggtagtcac	cagccgaatc	gtattttatt	aacagataaa	360
ttagttccat	atattaaggg	gtaa				384

SeqID 58

atgacagata	atcgctttgc	ccaattaaaa	gaaaactttg	aaaagggatc	tcctaaaagg	60
cgagttccaa	cgtctcggcc	aatcgagct	caaaaagcgc	ctgagagcta	taaaaaaag	120
ggacggtatc	catttttcgt	ccaccaagat	gtgcgttatg	ataaattaga	agcattagta	180
gcttatcatg	gagctaagtc	tgcatcagat	tatctggaga	ggttgattgt	tcaggaatgg	240
gaaaagatgc	agcgggaagc	taagaacaaa	gaaaaataa			279

SeqID 59

atgttttagtt	ggttggaagc	tctttattac	actctgatac	aactggcaaa	agtgaaccgg	60
ttgaatgctc	ttttcttagt	tagcgttggt	ggttatcttt	gttaccaggg	aataaaactc	120
gtcagaaaaa	ccataagaaa	cttttttcag	ctgatgaagg	gtttcatagg	tgatagagag	180
aacatcaaga	aatgcatcaa	aaacaagaaa	gaggcactag	tccattcttg	gaaacatcgt	240
caagatattg	attggaaatc	aactggaaaa	gataagagta	aacagttatg	gaatcttatg	300
aagcgacttg	cgacagttgc	tccttcattt	ttgttcttat	tattgggaaa	tgttctcttt	360
cgtctcattt	atcaactgcc	ttttgtaaag	caagacagaa	agcgatttga	caaggaaatg	420
aagcccttgc	tctacttcaa	gaactatcgt	agttttgtgt	tcatgggaat	aggtttcagt	480
ttcatagcgt	ttattctcac	aaactatttt	gtgacggttt	taagggtgc	tattcgtttt	540
ctatatttct	caatcatgac	gttaagagat	aatagccaag	tcgttagctt	taacgttgat	600
agtttgctca	tccagaattt	attcaatgct	agggtatattg	tgatagctcc	cattctagca	660
gtgccaatct	ttctcattgg	tttagtcgta	gcttggcggt	ctgcttgggt	taactttgaa	720
cagtcaccgtg	attataatca	taatgaagaa	ggggatgac	gctttgogac	tgtcaaagaa	780
atccaccagc	aatataagaa	agttccta	aaaaacggaaa	cttatccagg	tgaaggaggt	840
gtgcccgctt	ttcatgaaac	aagaaagaat	ttgacaggct	taacgcttaa	atctcaaattg	900
ctttggcaaa	accgtacctt	tagtcgctat	ttaacgaatg	cggaaggat	tttagggctc	960
ttatcgacgc	cttcaggaga	ttattacatc	gatgatagca	ccacaaactt	gatcaccatg	1020
gggattactc	ggtcaggtaa	gggagaagct	catattgccc	ctattattga	tattaatagc	1080
cgtgcggaaa	ttcaaccgtc	actgattatt	gcagacccta	aaggggaaca	ttaccagtc	1140
tcttataaaa	ccatgcgtcg	gcgtggctat	gatgttaatg	tcctttcttt	ccaaaacatg	1200
gattgggtcca	tgtcctataa	cccttttagct	cttgcgattg	cagcagctaa	gaagggttac	1260
tatgaaatga	cacagacaag	ggttaatgct	gttgcagaag	ccatttatcg	taaaacgaaa	1320
cctggtagcg	gtaatggcaa	tgcaaaaatac	tgggaagata	cctccatttc	cctctttaat	1380
gccattgcta	tggcctta	ggaccgtgct	aatgaaacog	tcaggaatgg	tgaaaccgat	1440
gcttgggata	ccgttacagt	tcgtaacatt	gccaaagttt	tgactgactt	gggttctgaa	1500
gaagtctttg	tcaatgattt	tggagagatt	gttgagaatc	ctgataagaa	ccaacaagt	1560
aagaagaaat	ctaaaatcac	ggttttacttt	gataacttgc	gtaaaatcaa	tcaagaacaa	1620
ttttccaaat	ttagagatat	ggctgatttt	aacttttaggt	cttctgactt	cgcttcagaa	1680
gaaactaagg	gaaatgtctt	ctctagcatg	atgtcaggta	ttactttatt	cttgcaagat	1740
aatattgcta	aactaacctc	taaaaactct	attgacctag	aatcggttgg	tttcccacgt	1800
cgcttgtcta	tcaagtttcg	ttctagttcc	aatgtcgtta	tgcgtaacga	atacactcat	1860
aagacggcta	aggttaccat	tactagtcaa	gctgtttggg	gtaaaaccac	taaacaagtt	1920
atccacgtag	atgctgcaac	agctctgatt	gatggtgaag	gctatctaac	ctatgtgatt	1980
gaaccccgagc	ttcttgatca	attcttgggt	acaattgact	ttaatcacga	aaacaatggg	2040
ggttcagcta	ttcgtcacaa	aaactttccaa	ttctcagctg	agaaagtcta	taagaaacgt	2100
ggtaacgtta	ttacgttgga	tgactacacg	aaaaaaccag	ttttggatca	tatcaaagtt	2160
actgttctca	acaagcaaga	tgataacctt	ctccagaaag	aagatattga	cctgatttat	2220
tcagataatc	ctaaagtgat	ttacttgggt	acacctccaa	ataggactga	atataatagt	2280
attgtatctc	tgttttttga	tcaattgttt	aatgccaa	atgagtttagc	tctgtcaaat	2340

ggtcgcaagt	gtgtcaatcg	aattcttcat	atcctcgatg	aattcacaaa	cattccagct	2400
attcctcaca	tggataccaa	gatttccatt	ggtcttggtc	aaaatattct	ctactatctc	2460
tggattcaga	acttgaaaca	gttagtcagt	gaatatggcg	agaatacagc	ggaaaccatt	2520
cgggagaact	gttctttgaa	agtttatatc	aaatctactg	ccccagcgac	caacgagtac	2580
ttcagtaaag	agttggggac	tgggaccatt	acacgtcgca	gaaggtcaag	taatattcta	2640
gatgaagcta	atccaaatgt	ttccattgaa	aatcctagac	aggaactctt	aacaccgaca	2700
cagctctcga	aactccaaga	aggggaagcg	gttattttgc	gtgggtgttaa	aggtcgagac	2760
aatgcaggtc	ggaaaatcac	aacggatccg	attttcttgc	atgagaaaac	gagccttcct	2820
tatcgctaca	tgttcttaca	agaagaatth	gaccagtcga	tggctttggc	agatattcca	2880
gtggaaagtg	ggcatagggg	ccttgacctg	caagatatag	cagtaggggc	acaaagcact	2940
tttaataaga	ttattgattg	gcggtgggt	ctaactgacc	gtatgagaac	aaatgggaag	3000
atacctcaat	tagcatcaag	aaaacaaacg	attaaagctc	taagtcaatc	tcaatttact	3060
tctccagcag	acctaacaca	agctgtgatt	gcagaggtat	ttgatgagga	agatgatgac	3120
gatcttttct	ttgtggatga	tgtcatgtaa				3150

SeqID 60

atgaattcta	acacaaaagg	tcacggattt	ttccgcaagt	caaaagcata	cggttagta	60
tgtgctattg	cattagcagg	tgcattttaca	ttagctacta	gtcaagtgtc	tgctgatcaa	120
gtttacaactc	aagcaacaac	tcaaacagta	acgcaaaaac	aagcagaaaac	agtaaacata	180
actcaacttg	ataaagcagt	agctacagct	aaaaaagcag	ctgtagctgt	tacaaccaca	240
cctgcagtta	atcatgcgac	aactactgat	gcacaagctg	atttagctaa	tcaaacacaa	300
gctgttaaag	atgttactgc	aaaagcacaa	gctaatacac	aagctattaa	agatgctact	360
gctgaaaatg	caaaaattga	tgttgaaaac	aaagcagagg	cagagcgtgt	tgcaaaaagaa	420
aacaaggaag	gtcaagcagc	cgtagatgca	cgtaacaaag	caggtcaagc	agccgtagat	480
gcacgtaata	aagcgaaaca	gcaagcgcaa	gacgatcaaa	aagcaaaaat	tgatgctgaa	540
aacaaagcag	agtctcaacg	tgtaagtccg	ttaaattgcac	aaaataaagc	aaaaattgac	600
gcagaaaata	aagatgcgca	agctaaagca	aattgcgacta	atgcacaatt	acaaaaagat	660
tatcaagcta	aattagcgga	aatcaaatca	gttgaagctt	ataatgcagg	tgtacgtcaa	720
cgtaataaag	atgcacaagc	taaagcagat	gcgactaacg	cacagttaca	aaaagactat	780
caagctaaat	tagcacttta	taatcaagct	ctaaaagcta	aagcagaagc	agataaacag	840
tctattaata	atgttgcttt	tgatatcaaa	gctcaagcta	aaggtgttga	taacgctgaa	900
tatggaaact	caatcatgac	tgcaaaaact	aaacctgacg	gaagtctcga	gtttaaccat	960
gatatgatcg	atggtgtgaa	gacaatcggc	tatgggaaat	tgacaggtaa	agttaatcat	1020
cattatgttg	ctaacaagga	tggtctctgtg	acagcatttg	ttgattctgt	cactctttac	1080
aagtacgagt	atcgtaaatgt	tgctcaaaat	gctgctgtta	accaaataat	tgtatttaga	1140
gttttaacaa	aagatggtcg	tcctattttt	gaaaaagctc	ataatggtaa	caaaactttt	1200
gcagaaaactt	taaaacaaaac	tttacaactc	aatctttaa	atgagcttaa	accacatgct	1260
tcagcggtta	acgtcgaagt	ctttaagatt	catgatgact	gggtacatga	cacacatggg	1320
tctgctttag	tgtcttatgt	taataataat	gatgctgttc	ctaattgtgt	catcccagaa	1380
cggccaactc	caccaaaagc	agtgaaaagt	acacctgaag	cagaaaaaac	agtacctgaa	1440
aagccagttg	agcctaaatt	ggtaacgcct	acattaaaaa	cttatactcc	agtcaaattt	1500
attccgcgag	aatacaaac	agaaccaatc	acccctgaga	cgtttacccc	tgagaaattt	1560
actccagctc	aaccaaaagt	gaaaccacat	gtgtctatct	ctgaaaagat	taactactca	1620
gttagtgctt	atcctgtttt	agttccagct	gctaatacct	caaaagctgt	cattgatgaa	1680
gcaggtcaat	ctgttaattg	taaaaccgta	ttaccaaatg	caacattaga	ctatgttgct	1740
aaacaaaact	ttagtcaata	caaaggtatt	aaagcttctg	cagaagcgat	cgcaaaagg	1800
tttgcatattg	tagatcaacc	aaatgaagcg	ttagctgaat	tgactgttaa	gtctatcaaa	1860
gcatctaattg	gtgatgatgt	atcaagcttg	ttagaaatgc	gtcatgtttt	atcaaaagat	1920
acttttagacc	aaaaaacttc	atctcttatt	aaagaggcag	gaattagtcc	agttgggtgag	1980
ttttacatgt	ggactgcaaa	agatccacaa	gctttttata	aagcttatgt	tcaaaaagga	2040
ctagatatca	cttataatct	atccttttaa	atcaaagcta	actttactaa	aggtcaaact	2100
aaaaatgggtg	ttgcacagat	tgattttggg	aatggatata	caggtaatat	tgtagtcaat	2160
gatgttactg	ttccagaagt	acataaggat	atacttgata	aagaggatgg	taaatcaatt	2220
aataatagta	cggtttaagtt	aggtgatgaa	gtgacctaca	aacttgaagg	atgggttgta	2280
ccagcaaacc	gtgggttacga	tctttttgaa	tacaaatttg	tggatcaatt	acaacacaca	2340
catgatcttt	acttacgtga	taaagtggtc	gctaaagttg	atgtgacatt	aaaagatggt	2400
acagtcatta	aaaaagggac	taatttagga	gagtacacag	aaacagttta	caacaaaacg	2460
acaggtcatt	atgagcttgc	ctttaaaaaa	gagtttttag	ctaagggttc	tcgtgaatca	2520
gaatttggtg	catagatttt	tattgtagtt	aaacgtatta	aggcaggtga	tggtttcaat	2580
actgctgatt	tatatgttaa	tggatataaa	gttaagtcag	aagcagttgt	gactcatact	2640
actgagaaat	caaaaccagt	tgaaccacaa	aaagcaactc	caaaagctcc	agctaaagga	2700
ctgccatcaa	ctgggtgaagc	tagtatgacg	ccacttactg	caattggagc	aattatctta	2760
tcagctctag	gcctcgcag	ctttaaaaaa	cgtcaaaaat	aa		2802

SeqID 61

atgaaacaaa	taaaaattat	cacaggactt	acagtcgcaa	cactatccgc	agtggtaggg	60
aatgtatacg	cagaagatat	cacaccgaca	gcaccagtta	atgagccaca	agtttcaagc	120
gaaaccgcaa	aaacgcctca	agttacagaa	agtcaagtta	atagcgcaaa	agttactgcc	180
gatcaagcaa	taagtgatgt	taataaccaa	caaattgtag	ttgatgaggc	tcaaaagcag	240
aaagatcaat	cacaacaaaa	tcttgtaaaa	gccacatcaa	cagtaactga	agctgaaaaa	300
gtcgctgctg	aggcaacacc	tgaagttggt	aaagaagcta	ttaaagctgt	cactgaagca	360
aaggaagctg	ttacggatgc	tgaagctaata	gtagtcgatg	cacaaaagac	gggaacaaaa	420
gctaatacaag	aagtacaatc	gcaagctaag	actgttgatg	aaaatgttaa	agttgtttgct	480
gataaagaat	ccgaagtga	acaagcagag	ggtgttgtaa	ctacagctca	agaagctatt	540
gatagcaaaa	ccgctaacac	taatgcatca	gaagcagaaa	aagcagtgac	tgagaagcaa	600
acaaagcttg	aaactgctga	aacaaatctt	acagaggcac	aaaaacaaga	tgccaaaatc	660
gctgaagaaa	aacgacttgc	agaacaagaa	gttgtaata	aacaattagc	tgtgacagat	720
acacaaatc	ttttgaagaa	gcttgttact	gagattaata	acgagaaagt	aagcactagt	780
ttagaaaaac	aagcctatatt	taaccaacgt	gacggttcat	ggcggggcta	ttatggcaat	840
tatacttttg	ccgctactgg	ctgtgtacca	agtagtttag	caatgggtatt	tacggagtta	900
gctagacgcc	aaattactcc	aactgaaatc	gccaattatc	tttggaacaa	ttcaaatgag	960
tttaataaaa	actatgggtg	aacaagtggc	aaagggtttag	tacaagctac	taaacatttc	1020
ggttttgtac	caactcattt	agcatctcaa	tctgctattg	tggaagcctt	acaggcagga	1080
caccattgtc	tagcagctgt	ccaacaagat	aaattttctc	cttgggggtat	caattacagc	1140
catgagattg	tcttacgtgg	ttactcaaat	ggcaataactt	atgtttacga	tccttataat	1200
cgagctaaca	ttgggtggta	ccctgttgct	aatttatgga	atgaacaaag	tagagacgca	1260
attgacacat	ctagtgtagg	cgtaccattt	ttcaaaaatta	caacacaaaa	aatggcccaa	1320
ttagaagctc	agaaagcaca	agttcaatct	tctctaaata	cagctaaaaa	tcagtttagct	1380
aaaacacaag	acgtattaag	aacactagaa	gcaacacctc	ttaaaacacc	agaagcacaa	1440
gctaagctta	atcaagccaa	agaagctcta	gctcttgcac	aagcagacta	tactaaagcg	1500
caagaagctg	ttaaagttagc	tagtcaagac	ttagctgtta	aagaagaaac	acttaaaaat	1560
gctcaggctg	atattattaac	gaaacaaaca	gccttgaaag	atgctcaaac	tgttctcgtg	1620
gctagtcaag	ttaaattagc	tgatcttaaa	gcaacttttag	ctactgttga	aaataacggt	1680
aagaaagctc	aagctacttt	aacagatgcc	aaagcaattg	ttggtcaaaa	acaagcaaaa	1740
ttacttgctt	tacaaaatgc	ccctaaaatt	ctagcagatg	ctcaagctaa	acttgtaact	1800
gctaaaaatg	attttagctaa	taaaatggct	attttagatg	aagcagtcgc	aaaactaaaa	1860
tccttacaag	ccgttcaagc	cgaagcccaa	aaacaatacc	atgttggtttt	tgaagcctat	1920
aaagcagtac	gagatgccaa	agaacaagct	aaaacttgacg	aaagctataa	ccatattatc	1980
gcacgaggcg	gtgaggctat	cccagttggt	gacgaaacag	ataaaaataac	tggatatgta	2040
gatggttagc	agaaagcagt	tgctaatagaa	gtgactcttg	ccttaactag	taacgggtgca	2100
ccccttgaaa	gtccagttaa	taaagaaaac	caaaacgtaa	caaaatcatc	tcaagcttta	2160
ccacatactg	gtgaagctgg	attatccatt	ttatcagtat	taggtgtagg	tcttatctca	2220
acttttagggc	ttactagttt	gaaaaaacgt	cgccacatt	aa		2262

SeqID 62

gtgagattaa	cccacgtgag	tttgtggatg	ccatcaaaga	gaagttggcc	gctcaaattg	60
cagttgttaa	ggaaaggagt	gattgagttg	gaagatgaac	tgaagacccc	ttatcttgat	120
caatacacag	acaatttaac	ggctaaagtc	actaaaaaat	cggtatgacta	ccaagtttat	180
ggacgaaaca	aggaggttca	atccgtcatc	atctctcttc	tcagacgaac	caaaaataac	240
cctattttag	taggagaagc	aggggttggt	aaatcagcca	ttgtggaagg	tataacgctt	300
gctatcttac	gtggccaagt	tcctgaacct	ttaaaagggtt	taacgggttcg	ttccctggag	360
ttgtctagtt	tgatgagtga	agatgacgaa	ggcttttatg	ctaagtttaa	gaagattatt	420
gaagagatgg	ttgctacacg	tggtcataat	cttctctttg	tagatgaatt	tcatacgatt	480
attggtgcgg	gtagccagaa	tggtcaagcc	cttgatgcag	gaaatgtgat	taaacctgtc	540
ttagcacgtg	gtgatattca	gctgattgga	gcaaccacct	tagatgagtt	ccatgagtat	600
attgaaacag	atagaccctt	ggaacgtcgg	atgcagcctg	ttatggttga	agagccaacg	660
atttcacaag	ctattaccat	tattgaacaa	gctaaagcca	tttatgagaa	gtttcatggg	720
attcaaattt	cctcagatgc	tgtgcatcaa	gcaatccgtt	tatctgttcg	ctatttgaca	780
gatcgattct	tgccggataa	ggcctttgat	ttgatcgatg	aagcggcgac	gattgcttca	840
gttgaaggga	aaagtaagggt	gacagaaaaa	gatattgctc	aagtttttaa	agataaaacg	900
ggaattccag	tcactactat	cctaaagggg	gatcaagagc	ggtttagagg	tttcaaagaa	960
aggctgatga	atcgagtcaa	aggtcaagaa	gatgccattg	aggccgttgt	agatgcggta	1020
acgattgctc	aagctgggtt	acaaaatgaa	aaaaggccgc	ttgcatcatt	ccttttctct	1080
ggaccaactg	gcgttgggaa	aacagaatta	gccaaagcaa	ttgcagaagc	actttttgat	1140
gatgaagctg	ccatgattcg	ttttgatatg	tctgagtaca	aacaaaaaga	agatgtgact	1200
aaactcatcg	gcaatcgtgc	gacaagaata	aaaggacaat	tgactgaagg	agtaaaacag	1260
aagccttatt	gtgtcctggt	actagatgag	attgaaaaag	cacacagtga	ggtaatggat	1320
cttttcttgc	aagtgtctaga	tgatggctcg	ttaacagata	gttcgggtcg	tttgatttagc	1380
tttaaaaaaca	ccattgtgat	tatgaccacc	aatattggcg	ctaaaaaaat	catcaataag	1440
tgggagttga	aaggaaactt	taaagattta	accgatcgag	atcggaaaca	atttgaaaaag	1500

tcgatggaca	gtgagcttca	aaatgagttt	cgtccagaat	ttctcaatag	gattgaaaat	1560
aagctcatct	tcaacctttt	agaacgtgat	gtgattgaaa	aaattgcaga	aaaaaatcta	1620
tctgagattg	cggataggat	gaagcgccaa	aatttaacac	tgtcatatga	gcctagtctg	1680
attcagtatc	tctctgatgt	tggtactgat	gtgaaaaatg	gcgcacgtcc	cttagaacga	1740
ctgatgaaac	gaaaagtgt	ggcaccatt	tctgtaaaaa	gcttacagtt	agataagtca	1800
aagcaaggct	ataacgttca	tctctgggtt	gagggacggg	ctccagacgg	caatcatcgt	1860
caagaacaac	gtcaaattca	catggagata	gagggagaaa	gagataaactt	ttttagctga	1920

SeqID 63

atggcagaag	aaaatgcaca	acagccatct	ttacgtggaa	aaagccgtcg	agaacgtggt	60
gaatttgctc	gttcccgtga	tatttttagat	gtggcccatg	aattgaatat	ggaacttttt	120
cgagatggca	aaaattatcg	ttggaaagag	cacgattcta	tggttaattac	acctgcaact	180
aatcagtggg	actggttttc	acaacgtcaa	ggaggtgatg	tgattgcgct	tgtagagacg	240
ataaaagaaa	tcggcttcaa	tcaagcattt	gaatacctga	atgaagggtac	atttaaagaa	300
tttactgtgg	tcaatcaagt	aaaagaacct	ttttcttatt	atttagaacc	ttacgaacag	360
ctttttgttg	aagcaagacg	ttatttgaaa	gagaatcgtg	gcttatcaga	tgacactatt	420
gatttttttt	atgataaagg	agtacttgct	caagccaatg	ccaaggtagg	tgatatgatt	480
gagcctgttt	tggtgtttta	aaacttggat	aagaacggcc	aagtggttgg	cgctgctcta	540
caaggcttag	tagctgcccc	cgataaatat	ttcggtcggg	gttacctcaa	acaaatcatg	600
aaaaattccc	aaccttacaa	cggcatgcat	gttgatatgt	gcacaccaaa	ccgcctagtc	660
tttgcgaaa	gtagtattga	tcttatgagt	tactatgaaa	tcacaaaaga	tagcttatca	720
gatgttcgtt	tagtttccct	agaaggcttg	aaaacaggaa	caataggaag	gcatctcatc	780
caattaagag	ctgaaatgga	acgtcgtccc	ctctcctcca	gttggactga	tgaaataactt	840
gctcagggat	tagatgaggc	tgtaaagcaa	ggctatttca	aagatggtaa	gaacagtcac	900
ctccttacgc	tagctgtaga	taatgatgta	aaaggtaaac	aattgattga	agagttaaaa	960
gataagagca	tcccagtcac	tgatgccact	cctcctaaag	cagaagggtca	atctaaaatg	1020
gattggaatg	cctattttgca	ggaaaccaag	gctacttttt	ctactgaaaa	atatcaagaa	1080
aagattgata	acctaatatc	agatgttatt	ttaggtgatg	aaacttatta	tctttggcat	1140
gatgatgagt	tggtaaattt	aggagcagga	gactctatta	tacaggcggt	tcatcatcag	1200
ctggaagaca	gacgttatgt	tattaatcag	gcagaacttt	acgttgaaga	gtccagtaat	1260
gatggggcta	ctggctatct	atcaattgaa	ggacatgtat	tagataaagg	tggtattagt	1320
gactatttat	ctgatcaagc	tttaacagat	gcggaaaaag	tagcattctt	agaaaacttta	1380
cagacagaac	taccagatat	ttgggacgag	attatgacaa	ggtctttgaa	1440	
gaagttgtcg	ttaaatatgg	actcagagaa	aaactatcgg	acataattca	ggaacaagag	1500
ttggatttag	accttttagt	tgttccagaa	gcaaaagaaa	agtcccttga	aatgaatcaa	1560
gagactaaca	ctggcggcga	actattttaat	cgcaattcca	gttttttagg	agaagattct	1620
ccggggacag	caccgcagcc	cgttgagcca	actgctcaac	ctgattttcc	taccaatggt	1680
cgcttacatt	ttaccactga	tgatggaaat	atgtcaaata	aagcatttag	gaaaaacatg	1740
cgaaccttga	atttatatgc	taatacgatg	agagattcgg	cacaatggta	cttatcagaa	1800
atagccgata	ctacaatgat	ttatgtttat	aaaactcctc	atgaagaggg	agtacagggt	1860
cttagtgtgc	attttggtta	aaagaattgg	atgcacttaa	caggagtga	accagtatat	1920
gaaaattggg	tagattcact	ttctgaacaa	tttattgatg	atattgctaa	tagtaaggga	1980
catttttaaaa	atctaaagtt	tgcactaggg	actcctgata	agttaaagg	tcttaactta	2040
cttcctgaaa	ttattgaatc	agataccttt	gtattttaatg	atttatcatc	tgttcaaaaag	2100
ttaaataaat	ttgattttatc	acaggcgctt	aatcctgaag	atagcgattt	actttttgcta	2160
tttagagatg	aggggccttca	tcaagtgcct	gcttcgttga	tgaggataaa	gggcgattta	2220
gaagaagat	tatctcatat	agatagtggt	acagtggttag	gagtttaccg	agaaaagaaat	2280
ggccaacttg	agcaagtttc	tgtcaatgag	gagtatgtca	aagatagtgg	tcaagaaatg	2340
ctatctattt	tacagaataa	gcactatgaa	gaggctcttg	atagtgggtca	agaaatgggt	2400
caaacggatg	gtttttcagc	cgaagatttc	acaaaagttt	tggatgctgt	ctatcatggt	2460
ggtgttccag	atgatttagc	acgtgttcca	gaaggagtct	tacctgtttg	gcaaaaatat	2520
cttgagggtat	cagaagagaa	tcaatgggac	ttagaacaaa	tgattgatta	tgcggataag	2580
aacagtcttt	tagtaaaaga	ttctgccttc	tataaagagt	ggaaaagagga	tatgatctat	2640
aaaaatgact	atcatgttcg	cttacaattt	gctgagaatt	gggataatgg	cgttgaactg	2700
cctttccgta	cagaacaatt	gattgattac	aaaacgtttg	tcacaggact	ttatgaagct	2760
aatcaagctc	atcatcaacg	cagacaagaa	agtcagcttc	cttatacaaa	aacagagttt	2820
gacattttatg	ctcctggcgg	acagctcatt	aaagataatg	tccattatgc	tattggagat	2880
gaaacaagac	ctgtttcaca	actcatgggg	ttaggttatc	gtcgccctacc	tggttatcag	2940
gaattagctc	tgatagataa	cagtattctt	tctcagctgg	aaaataagga	gctaaatcaa	3000
gaaattgctt	ctgaagctaa	tgaacattcc	ttaaattcac	aagaaatacc	taaagaagat	3060
aactatccaa	gagaagcttt	cacttctcct	aaacaagaca	tcaaaaaggg	gctagctcaa	3120
cgagtagaag	agatttgtggc	agaagatgct	actaagattt	tagtatcttc	cattcctcaa	3180
gttcaagaga	atztatcagt	cgaaggaaac	ttggtcggta	ctccacaagc	ggataatcgg	3240
atgctatata	ctaacctaga	agattttggc	caagattatc	aattagagct	tgcagtttat	3300
agtccaaaac	gggttgactt	tttagaagat	gtgcaggctc	cgtggacctt	ggccctaatt	3360

agaaaaagaaa	aaaagatagg	ttatatttagcg	tatggtagtg	attggggcaaa	agaatttcag	3420
attgaagaag	agctagaaca	tttagctgca	caaattggag	acgaaaaagt	accagagggga	3480
ctctataaac	aagctgaagt	agagggtttt	atagctagtc	atcagggaaa	tgaaagcctt	3540
caggaaccaa	tacctactat	tgtagctgaa	ccgtttgact	ataccagtg	ctccgcctat	3600
gagatcagcg	aacacgcttt	ccaaaagatt	cgtgagtaca	cacaatcccc	tgaggacttg	3660
cttgagtaca	tggatttcat	gagtaagttc	ccacaacttt	cacctcgaaa	tgctcgctctt	3720
atccatgaac	aatggcgctgg	cgcaaattgca	gtcgcaactt	acgaacaatg	gaaagccatg	3780
ggagaagctc	taggtattaa	accagacgat	gttggtccaaa	caaaagcaac	ttatgttaat	3840
aagcggacag	gagagacgaa	ggaagtcgtt	catcaagggg	tatctgttaa	gactggcgaa	3900
aaatcgaaaa	ttacgctctt	tagaccgcta	atgggttaaaa	tgatcccagt	tcttgatgag	3960
aatggtcaac	agctgaaaaa	tgataaagg	aatccaaagt	ataagaagct	atcagaagcg	4020
tcacttcaag	agaaagcttt	agtaaaagac	ggtaaaacttc	cagttcgtca	atttcaggag	4080
agagattcaa	aaactgggtca	accaagggtt	acgactttaca	aagtttttga	gttggtcacia	4140
actactctga	agccaggaag	ctatcctaag	gtctatgccaa	accgtcattt	caactttaat	4200
gtggataaa	tcaagactaa	agagggtatta	gaaggggttt	gtgactatgc	ggaaaagatt	4260
gggttagcc	taatgaaaga	tgatgctcat	gttttggata	atgccaaagg	agctttttat	4320
tcagaagaac	agctgattct	tattaatcct	aataatacac	ctggagaaaa	aattgcaact	4380
accattcatg	agttagcaca	tgcaaccctt	cataatccta	agttggaaaa	acagtataaa	4440
gagttgccga	aaggacaaaa	agaatttgaa	gctgagatga	ccagttactt	gttggtcaaaa	4500
cactttggcc	tagatacgtc	tgaaaaggga	atccattata	tggaagttg	gacagataat	4560
ctaaaagcgt	tagaggataa	acaattggca	gctctctga	aacgagttca	tcaaacgggt	4620
tcgaaaaatgt	tgaaagcaagt	tgaaaaatat	acgaaccctc	accagctagg	aagggggaaa	4680
gaacacggtc	taaattttcc	taaagcccca	accaaagggg	ctagtcgtta	a	4731

SeqID 64

atggatgtat	cgtctagtcc	gaatattaca	tttatgctgc	aatacacaga	ggctaattcct	60
caatatgtgg	actatactaa	cagagaagag	gctgtcaaaa	ttgatgaaga	attgtcctta	120
gaaacgaaca	ggcaaagtat	tgaaggatta	actgaagacg	agttgactcg	tattcaggaa	180
gctgtccctg	aaacgcagtt	gaatttttagg	gaatacattg	attatatgaa	ccgctcgtat	240
gcaactgaag	aacaatctaa	agaactaaca	gctatcttta	ctcaagaagc	agattatctt	300
cagaaactac	gattaatcga	tctaaaaaat	aagttggaat	cagcttatca	aaatggttca	360
cttctctggc	aaggagttat	ttegtttgat	aatgcttttc	ttgcggaaca	gggattgtat	420
gatgttgcca	ctggtcaagt	tgatcaaaaa	gcgattaagg	cagtgatgcg	tgatatgatg	480
ccaacactta	tccagaaaga	gggcctttct	gattctgctt	tttgggtggg	gaatatccat	540
ctgaatacag	ataatatcca	tatccatttt	gggctttctg	aagttgaatc	taaccgtgag	600
aaaatattct	atcagccacg	tggacgtatg	gagtacaaag	gtaactttct	tcagaaaaac	660
atcaaccggg	ttaaaagtgg	tgtgtatcat	ggattgctga	aagaagaaac	aagatccaat	720
cttctcagaa	agaacagat	tttagcta	ctcaaagcgg	acttcataac	atctattttac	780
cagaaggaca	agattacttc	ttcagctgaa	aaaaattttt	tggaacaagc	ctacaatcat	840
ttgcccgtaa	ataagaagtg	gcgctatggt	tctaattgcca	gagatttttg	ggttagtaag	900
ttctttcttg	atcgctat	agatttcctat	ttaacaatg	aaggtagtgc	tgcttatcaa	960
gaatttttga	aagagactag	agattttctt	cagacttatg	aaggggttta	ttcagctgaa	1020
aaaaataaaa	tctatgaaaa	actacgtaaa	gttgatgggc	aaacgatcag	aacgcttgca	1080
gaatcaaaag	gatatgattt	agaacatcat	ttggcacgtc	gtgtaatgga	tttaagagag	1140
cgttttagcca	ataatatctt	acgttcgttt	agagaagctg	caccccaaat	tcaagacgtt	1200
cagctggaaa	aaaattttaga	gagtttttct	gttttgaacc	agaagaaaaa	tttagaaca	1260
catcctgaag	caagtgtggt	aaaaagtcag	aaagcttgcc	agaagttagg	ctactttgtg	1320
aaggctggag	agcagccact	tgaaattata	aggccagtct	ataaatctta	tgataagcat	1380
ggtaaaaggta	taggacggcc	agaatttgta	tcagatactg	tttatgatat	tagtcagcta	1440
acagaaaata	ttcagctgaa	aagtctaacc	ttgaaagacc	tctctctgtt	ttcttctaac	1500
gagttaaaag	agttagtaga	tgctgctaag	ttaaagacta	atccaacaga	gagagaacgc	1560
cgtgaattag	gtacctatcg	ttatgogttg	aaacttagca	tattagaatc	tagtcagaag	1620
gaattgcagg	ttcgtcaaaa	gctactagaa	caggtacagc	cactagcgtc	tgatcaacca	1680
tttttagatt	tttaagaaaca	gttaatagct	caggaattac	aagctatagc	gctacaattg	1740
actcctaatt	acaagctatc	agaagatgat	aaagccttga	aaaatcgatt	gaagaggcag	1800
tttgaagata	gtgttgccgt	acctgtttca	aaagctactc	ctggtgccat	acaacttcct	1860
attaggcaac	tttggactga	gotaggattg	gttcatcaca	ttcaagatga	aaacattcta	1920
acgcttctga	aagggacatc	aacgacgaaa	caagcttata	tagaagaact	tcagactcat	1980
atctctat	ttcagttgaa	atatcagatt	aacaatagaa	acaagcagat	aagccagtta	2040
tcggatgaag	caacaataaa	ggagatgag	atagctaagt	ctaaagggtt	ctctgagcta	2100
aaacgtctat	atgatacatt	acagccatct	gatgatggtc	aaaatcagat	tagtcaagct	2160
gtttctaaac	aattacaaga	acgaaaagtt	atcaaaaaag	ctcaattaca	acagacgcag	2220
agaagcggaa	aatcaatac	agacttcatg	cgacaattga	cagcttctct	taatcgttca	2280
caacaagcaa	gtaaaaaagc	attgatggaa	cgtgcacgta	gtgatgaacg	tgaggaacaa	2340
gaagaacgta	ggcaagctca	acgttaa				2367

SeqID 65

atgaagaaga	ataaattttct	attagtcagc	attgtatttta	tcatcattttt	tgtggtacag	60
ccacaaaatt	ttcaatcttt	aaaaaatata	tttactcaaa	atgatatagc	tagtcaattg	120
aatatatcaa	gttcacctga	agaaaaaaat	gatggccttag	gaacggccta	tcaaacgcaa	180
aatgaagatt	tgaaatctaa	aagttttgat	ggtcaacatc	aagtcatagt	ggttaatgaa	240
aaagcacaat	ttacggcaga	agagttgagc	atgagaaatg	gttcattggga	aaaatacgat	300
aacctagatt	ttttaaatcg	tggtgggggtc	gcagaagcta	tgttaggaaa	agagttaatg	360
ccaaaagagg	cacgtcagga	cattttcttca	gtcaaaccaa	ctggctggaa	aaataaaaaa	420
attaccttca	atggaaagca	agattatctc	tataatcggt	ctcacttaat	tggattttcag	480
ttaagtgggtg	agaatgccaa	tgtgaaaaat	ctcttttacag	gaacacgtgc	ccttaatgca	540
aactttaacg	atgataaatc	gtccatgggtg	tactatgaaa	atgaggctgc	aaactacatt	600
aagaaaacaa	atcatcatgt	tcgttatcga	gtgacccccc	ttttcaaaaa	tgtggagtta	660
gtagctcgtg	gcgtacgtat	agaagcaca	agtattgaag	atgagaccat	ctcatttgat	720
gtctatatatt	ttaatgggca	accaggatat	gacattgatt	atttgacggg	atcatctgaa	780
aaaataaatga	ttacaaaatg	a				801

SeqID 66

gtgactaaag	aaattaaaaat	tagatccatt	ccagaaaaaa	catgggcaca	gctacatatg	60
atttcggaag	aatatgagta	tccgtctttt	aatgaatttta	tgcttgctca	attgcaacgg	120
attgtcgaaa	atgggtggtc	tgatttatat	gataataaat	ttgcggaaac	cttggcagtt	180
attaaagaac	aacaagcaca	aatattggat	cagctcctaa	aaaacgaaat	caagttactg	240
gcttatcatg	caaagcaaga	tatagtggaa	gagctaacaa	cggactgggt	acgattttatg	300
gatgatgttg	atgcgctggc	tgcggaaga	ggagcaggag	gacgttga		348

SeqID 67

ttgtttatatt	atttttattta	cttgataaaa	gtaattggaa	atggccttaa	attatcactg	60
attttgtggtt	taaattggct	catcaaaaata	gtattc aaag	gacaatttta	tcttttctca	120
gctgtctttt	gtggcttggt	gacctactat	atgccacaag	atattcaatt	atttacagtg	180
agagtttttag	agctaactcat	catgctaaaa	gtgataatag	atgttaccoca	tacagctctt	240
tcaagagatt	ttaaaccggat	gaaaacgcct	cttttttttag	gagtgatgta	cgtctctctt	300
ctagctggta	acagtttatat	taaagcacat	cttttgacag	aagttatggt	taatcatctt	360
attttcgtttt	ggcttatcag	cctgtttttt	gccactcttg	taatagtatt	tcagcccaga	420
ttattttaagc	attatctggt	aaaaaaaagtc	attgataagg	aatacttggg	tatccgaaaa	480
ttcacagact	ctcttctctc	agaaatcaat	ttgtacaagg	atgcggacga	agaagatgcg	540
gacaaacgga	tgcgactgat	caaccagaat	gtcatcaaac	acccctatca	agaagttggt	600
gaactgagct	ttttgaatag	agaagtgata	acagctattg	gctataaagc	cgttccattt	660
gaaaaagaaa	ctgaacgtac	ttttatagac	gatgatacca	tctattatcc	cattttttacg	720
gttcaccctt	tcagaaattt	ggaagggaaa	tcagattttt	atcacatact	aatgaaactt	780
aaactcagtc	gaaaagcggc	ctttacaaaa	aatggtgagc	gattattaat	tagagatttt	840
ttaa						843

SeqID 68

atgattagaa	atgaatttta	taatcagtta	atcaatagtg	agccaatagg	ttttattgat	60
cctttcactg	acttaggaga	atttgattct	attcagatga	agttcaaaca	acctgttaga	120
aatctggtaa	ataagtaact	tggtaaacct	tataacttta	gttggaacaa	taagattgaa	180
cagatgagag	tgcttatata	taaatatcag	aaaagcttga	agctagaaga	tgaagaacaa	240
gaggttcata	accgagttaa	aaataaaaaag	tctaaaaaat	atgttcatga	aatcggtaca	300
acatatattga	agttaggatt	cagggtttaaa	gaaattgaag	caagggtatc	cctattcaat	360
actogtcttc	gtcgggaactg	gaaaagaagc	gactatgtga	caactgataa	ccctgaattc	420
tatttgaaga	aggatctaca	gaatgggttat	tgttctccaa	attcattttct	tcctcggagt	480
atgaaaaataa	actaa					495

SeqID 69

atgaacgaaa	tcaaatgcc	tcattgtgga	acagcttttg	ccatcaacga	gtctgaatac	60
catcaattac	tagaacaat	tcgtggagat	gcttttgaca	aagaagtaag	tgaacgggtg	120
gaaaaagaa	gtctaataat	aggggagcaa	gcaaaaaatc	aattacagga	agttgttgta	180
gaaaaagaca	aggagatagc	taaacttcag	tacaaagtca	aacaatttct	tatagaaaaa	240
gacaatcttc	tcaaaagaca	tgagtaccaa	ctcgtctgagc	aattaaatca	aaaagacatg	300
atgcttcgcg	accttgaaaa	ccaaatcgat	agactacgtt	tagagcatga	aaatagcttg	360
caagaggcgc	taacaaaagt	cgaacgagaa	agagatgcaa	tacaaaatca	gttgacacatt	420
caagaaaaag	aaaaagattt	agcttttagct	tcagtataaa	gtgattatga	agtacaacta	480
aaggcagcca	atgaacaagt	agaattctat	aaaaacttca	aagctcaaca	gtctactaaa	540
gcagtaggag	aaagtttaga	acattatgct	gaaacagaat	ttaataaagt	gcgacatttg	600
gccittccta	atgcttattt	tgagaaggac	aatacattat	caagtcgtgg	ctcaaagggg	660

gactttatct	atcgagaaaa	ggatgaaaaat	gaccttgagt	ttttaagtat	catgtttgaa	720
atgaaaaatg	agtctgatga	tactatcaag	aagcataaaa	atgaagattt	tttcaaagaa	780
ttagataaag	atcgctgtga	aaaatcttgc	gaatacgcag	ttttagtaac	tatgcttgaa	840
gcagacaatg	actattataa	tactggaatt	gttgatgtta	gtcacaataa	ccctaaaatg	900
tacgtttatac	gtccacaatt	ttttatccaa	ttaattggta	ttctaagaaa	tgcagcactc	960
aataccttaa	aataataaaca	agagcttgct	ttgatgaaag	aacaaaatat	tgacatcaca	1020
cattttgaag	aagatttaga	tattttccaa	aatgcatttg	ctaaaaatta	taattctgca	1080
agcaaaaatt	tccagaaagc	aatcgatgaa	atagataaat	ctattaaacg	tatggaagct	1140
gttaaggctg	ctttaacaac	gtctgaaaat	caactacgtc	ttgcaaataa	taaattagac	1200
gatgtttctg	tcaagaaatt	aacaagaaaa	aatccaacaa	tgaaagcaaa	attcgatgct	1260
ctaaaagact	aa					1272

SeqID 70

atgaatcatt	ttgaactatt	taagcttaaa	aaagctggac	taacaaatct	taatatcaac	60
aattattatca	actatctcaa	aaagaatagt	ttaacttctc	tatctgttcg	caatatggcc	120
gtagtatcaa	aatgtaaaaa	tcctactttc	tttatagaaa	attataaaca	gctagacctt	180
aaaaaacttc	gacaagaatt	caaaaaatth	ccagttctat	cgatttttgg	ttctaactat	240
ccttttagagt	taaaagaaat	atataatcca	ccagttctac	ttttttatca	gggtaatat	300
gaactttctat	ctaaacctaa	attagctgta	gtggggggcaa	gacaggcatc	tcagatagg	360
tgtcagtcgt	ttaaaaagat	tatcaaggag	actaacaatc	aatttgttat	cgtaagtgg	420
ttagcgcgtg	gcattgatag	agcagcacat	gttagtgctt	taaaaaatgg	cggcagtagt	480
atagctgtta	tccgggagtg	tttagatgtt	tattatccaa	cggagaataa	gaaacttcaa	540
gaatatatgt	catataatca	tctcgtatta	tcagaatatt	ttaccggaga	acaacccttg	600
aaatttcatt	tcccgaacg	taaccgtatt	attgcagggc	tgtgtcaagg	tattgtgggt	660
gccgaagcta	agatgagatc	tgggaagttta	attacctgtg	aaagagcatt	agaagaggga	720
cgagaagttt	ttgccattcc	cggaaatatt	atcgatggca	aatcagatgg	atgccaccat	780
cttatccaag	aaggagctaa	atgcattatt	tcaggaaaag	atatcctttc	tgaatatcag	840
tag						843

SeqID 71

atgactgaac	gaacattcga	agatattgaa	cttgacttaa	agttattcca	aataaagctt	60
gataatgctg	agaatagtaa	aaggctctta	caaaaattga	aaaacgacgt	catggagtta	120
caaataagag	tactagaatc	attaaaaact	ggtagatgct	atttaacaga	atcagaagaa	180
ttagaagaga	ataatgactt	tattctaacc	gtaaatagtg	aaacactaag	tttatcctat	240
gacaatagga	taaaacttagt	ttctaagag	attatggatt	atgaaaatgc	attagataag	300
ttgtattatg	aaaaacagag	tttgatgcaa	aaaagtaatg	aaagaaaagg	aggttaa	357

SeqID 72

ttgttcaata	aaataggttt	tagaacttgg	aaatcaggaa	agctttggct	ttatatggga	60
gtgctaggat	caactattat	tttaggatca	agtcctgtat	ctgctatgga	tagtgttgga	120
aatcaaaagtc	agggcaatgt	tttagagcgt	cgtcaacgtg	atgcagaaaa	cagaagccaa	180
ggcaatgttc	tagagcgtcg	tcaacgcgat	gcagaaaaaca	gaagccaagg	taatgttcta	240
gagcgtcgtc	aacgtgatgc	agaaaacaga	agccaaggta	atgttctaga	gcgtcgtcaa	300
cgtgatgcaag	aaaacagaag	ccaaggtaat	gttctagagc	gtcgtcaacg	cgatgttgag	360
aataagagcc	aaggcaatgt	tttagagcgt	cgtcaacgtg	atgcggaaaa	caagagccaa	420
ggcaatgttt	tagagcgtcg	tcaacgtgat	gcagaaaaaca	gaagccaagg	caatgtttta	480
gagcgtcgtc	aacgcgatgt	tgagaataag	agccaaggca	atgttttaga	gcgtcgtcaa	540
cgtgatgcaag	aaaacagaag	ccaaggtaat	gttctagagc	gtcgtcaacg	cgatgttgag	600
aataagagcc	aaggtaatgt	tctagagcgt	cgtcaacgcg	atgttgagaa	taagagccaa	660
ggcaatgttt	tagagcgtcg	tcaacgtgat	gcagaaaaaca	gaagccaagg	taatgttcta	720
gagcgtcgtc	aacgcgatgt	tgagaataag	agccaaggta	atgttctaga	gcgtcgtcaa	780
cgcgatgttg	agaataagag	ccaaggcaat	gttttagagc	gtcgtcaacg	tgatgcagaa	840
aacagaagcc	aaggcaatgt	tctagagcgt	cgtcaacgcg	atgcagaaaa	cagaagccaa	900
ggtaatgttc	tagagcgtcg	tcaacgtgat	gcggaaaaaa	agagccaagt	aggtcaactt	960
atagggaaaa	atccacttct	ttcaaaagtca	attatatcta	gagaaaaata	tcactctagt	1020
caaggtgact	ctaacaaaca	gtcatttctc	aaaaaagtat	ctcagggttac	taatgtagct	1080
aatagaccga	tgttaactaa	taattctaga	acaatttcag	tgataaataa	attacctaaa	1140
acaggtgatg	atcaaaatgt	cattttttaa	cttgtagggt	ttgggtttaa	tttgtttaaca	1200
agtcgctgcg	gtttgagacg	caatgaaaaat	ttaa			1233

SeqID 73

atgaaaagac	taacttatta	ttttaagggg	tatatcaaag	aaactatctt	tggacccttt	60
ttcaaattat	tagaagcctc	ttttgaactt	ttggtagcaa	togttattgc	aaaaatgatt	120
gacgagacca	ttccacgagg	ggatagaagt	agttttactgt	tgcaaatggg	attgattttc	180
tttttggctg	cgggtgggtgt	tgtagtagcg	ataactgtct	aatattattc	ttcaaaagcc	240

gcagttgggtt	atacgcagaca	attgcacagag	gatctctacc	aaaaagtcac	gtcactgggg	300
aaaaaagaca	gagatgaatt	gggaactgct	agtttgatta	ctcgtttaac	tgctgataca	360
tttcaaatcc	aaactgggtt	aaatcaattt	ttacgtttat	ttttgagggc	tccgattatt	420
gtttttgggtg	ccataattat	ggctttttcc	attagcccct	cattgactat	ttggttcttg	480
gtaatgggtg	tcacgtttat	tatcattggt	tttgtaatgt	ctcgactatt	aaatcctatt	540
taccttaaaa	tcagaacttc	aaccgattat	ttggtaaagt	tgactaggca	acaacttcaa	600
gggtgtacgag	ttatccgtgc	ctttaatcaa	gtagatagag	agagtgaagc	atttaattgat	660
atcaattatc	attatacgaa	tttacaatta	aaagcaggta	ggctttctag	tttagtaacg	720
cctctaaccat	ttctagttgt	taatatcact	ttggttgtga	ttatttggcg	tggttaattta	780
aatatagcta	atcatctttt	atcacaagga	atggttggtg	ctttaattaa	ttacttattg	840
caaattcttg	ttgaattggt	aaaaatgaca	atggttggtg	catcactgaa	ccaaagttat	900
atcagtgccta	agcgaattat	agccgttttt	gaaagaccgt	ctgaaataat	tgatgacaaa	960
cttgagccaa	aatatctgaa	taaggcttta	gaagtacaag	aaatggcatt	ttcttatcca	1020
aattcttctg	aaaaagcttt	atctgatatt	actttttcta	tgaatgtagg	agaaacttta	1080
gggataattg	gtggaacttg	ctctgggaaa	tcaaccttgg	ttaatctact	gcttcatatt	1140
tataaagtgc	aagaagggga	tattgatata	tatcatcagg	gaaaaagtcc	agatacaatt	1200
tcaaattggc	gtaccctggt	aagagtgtgt	cctcaaaatg	ctcagttggt	taaaggaact	1260
attcgttcta	acctttcttt	gggacttggg	aaagtttagt	aggaaaaact	ttggactgct	1320
ttagaaatag	cacaagctag	tgattttgta	aaagaaaaag	atgggtcaact	tgatgccctt	1380
gtagagagtt	ttggtagaaa	tttctctggt	ggtcaaaagg	aaaggttgac	gattgcaaga	1440
gcttttagttc	aagataagat	accatttttg	attttagacg	atgcaacatc	tgcatgggat	1500
tatttaacag	aagctcgttt	atttaaagcc	ataactaaac	atttcaacca	aactaatctt	1560
attattgtat	cacagagaat	taatagtata	caaaatgcag	atagaatctt	actccttgat	1620
aaggggaaac	aagttgggtt	tgataatcat	caatctttat	tagctcataa	caaagtttat	1680
aagtcatttt	accattcaca	aaattttaag	gaggaggagt	aa		1722

SeqID 74

atgaaattta	atgagcaaag	taactcgcaa	gcagcacttc	taggcttgca	acacctgtta	60
gctatgtatg	caggatccat	tcttgtacct	atcatgattg	ctagtgcctc	tggttataat	120
gctgagcaac	taacttatct	tattgcgaca	gatattttta	tgtgtgggat	tgccacctta	180
ttacaattac	aattaagtaa	gcacttttga	gtgggtcttc	cagttgtatt	agggtgtgcc	240
tttcagtcctg	tagctccttt	atcaattatt	ggtgcacaac	aaggttcagg	ctatatgttt	300
ggagctttta	ttgcttcagg	aatatatgtc	gttttagttg	ctggcatttt	ttctaaagtt	360
gcaaatttct	ttcctccaat	tgtaacagga	tcagttatta	ctacaattgg	tttgacatta	420
ataccagttg	cgatgggaaa	tatgggtgat	aatgcaaaag	aaccgagctt	acaatcttta	480
actttatcac	tggtaacgat	tggtgttggt	ttattaatta	atattttcgc	aaaaggcttt	540
ttgaagtcaa	tttcaatcct	tattggactc	atatcaggta	caattcttgc	agcatttatg	600
ggcttagttg	atgcttctgt	ggtagcagaa	gcaccacttg	tacatattcc	gaagccattt	660
tattttggag	ctcctagatt	tgaattttact	tctattttaa	tgatgtgtat	tattgcaaca	720
gtttctatgg	tagaatcaac	aggtgtttac	ctttgcgttt	cagatattac	aaacgataaa	780
ttagacagta	agagacttcg	taatggttac	cgttcagaag	gattggcagt	attacttggc	840
ggcttattta	atacctttcc	atataccggt	ttttctcaaa	atgtgggact	ggtacagata	900
tctgggatac	gtacgcgtaa	gccgatatat	tttacagctc	tcttcttagt	tatacttggc	960
ttgttaccta	aatttggcgc	aatggctcaa	atgattccaa	gtccagttct	tggtgggtgct	1020
atgttagttt	tatttgggtat	ggtagcactt	caagggatga	aaatgcttaa	tcaggttgat	1080
tttgagcata	atgagcataa	ctttatcatt	gcagccgat	caattgcagc	aggagtagg	1140
tttaattgga	caaactctct	cattagctct	ctcaataact	tacaaatgtt	tttgacaaat	1200
ggtattgtta	tctcaaccct	gacagctgtt	gttttaaaata	tcattttgaa	tggtattgcct	1260
aaaaaattaa	tatga					1275

SeqID 75

atggctaata	catacgattt	aatttcacag	cgtattgaag	cacaacgaca	gaaactcatc	60
gctatagata	ttgtggccgt	tgcgagctca	ctaggactta	acttgaaaca	aggttcagg	120
ggacatctct	attgggatga	acatgatagt	tttcatattt	accccaaac	taacaccttt	180
cgttggtggt	caagaagcat	ggggaccaat	accattgatt	tagtccaagt	catccaagaa	240
gagctaacag	gaaagaaacc	tagctttoga	gaaactgtca	actttttaga	aacagggcaa	300
tttgaatcgg	ttacggtaac	accagtcggt	agagaaccct	ttaagcacta	cctcgctcct	360
tatgaacatc	acaattttga	cttagggcga	cagtatctta	aagaagaacg	agggctatct	420
gatgagacca	ttgattttgc	tttggcatca	ggtagtatga	gctctgcgac	attgaaaaag	480
ggtgattatt	ttgaacctgt	tattatcttt	aaaagttttg	cggaagacgg	ccgaatgatc	540
ggcgtagcc	ttcaggggat	cgttgaaaat	aaagtccagc	atcctgaacg	tgcccgctctc	600
aaacaaatca	tgaagcattc	agacggtcta	gcaggttttc	atgttgacgt	tggaacacct	660
aaacgtctcg	tgttttcgga	agctcctatt	gacctctctc	cttattatga	attacataag	720
gagagtttac	agaatgtccg	cttagtcggt	atggatgggg	tcaaaaaagg	ggtgattagt	780
cgctatacgg	ctgattttatt	gacagatggc	cagtattctc	aaaccatgcc	cagagagtcg	840

attagaggag	cgatagatgc	cattaaccaa	acgactagaa	tccttaaaaa	caatcccaat	900
atgattacca	ttgccgttga	taatgacgag	gcaggccgaa	actttattaa	ggagttacag	960
gaagatggca	ttccaattaa	cgtagacctc	ccaccacgga	aagaacacca	gagtaaaatg	1020
gatttgaata	attatctgaa	acaaaagaaa	ggattactaa	aaatgccaca	aacagaaggc	1080
acacaaaaag	ccccagaaca	agttctggag	catgaaaaaa	tggataggag	ccaaattagt	1140
tccgggtctt	tagaggacga	ccctcaaggc	agtgcacaa	ctgtatccaa	aagggatacc	1200
tttgagcaag	ctgtttaccag	ccaccgcact	ttctcctatc	ctttactaca	gttttagcaca	1260
gaagaagcct	ttgtgtcaaa	cgtttagagat	ggctaccaca	tcgcaagtga	ggaggatatt	1320
cggaatctca	attactatgc	ccctagtctc	caacaaacgg	ctaactggta	tcgggataat	1380
ctggcagacc	gtcaagtgc	ttatatgtta	aaaggggata	aggagataaa	ggcgcttcag	1440
gtcagttttg	ccaaggataa	gtttgcccac	ttaaccggta	ttcgtccgat	tggaaaaggg	1500
ttgtcagctg	aaaaactggt	agatgatttt	gcgaaaggtc	gaggttccta	tcctaactcg	1560
accttatcaa	atgggttttaa	tgacaagata	caagttttgc	caatgattca	agaactatct	1620
caatccaagt	cttttgtctt	tacagattta	gagggaagttc	aaaaaatgag	aaacttaaa	1680
gccagtcacg	cgattcaatc	caataatcgg	agtttagtcg	tcgcttttaa	aactattgat	1740
gatgtcacct	ttccttcgtc	cctcctaaga	ggaaaaaaga	atctaaatga	tgatctgatt	1800
caaaaggcga	aagaaaatga	agttctaggt	gtactcagtg	agaaagatgg	gaacatcacg	1860
gtgctgtccg	ttaacgataa	gtacatccaa	gatgggtggg	aagccttaaa	agatatgatt	1920
aaaaatggcg	aacttgaacc	actccaaatg	gagacgatac	agcgacatgt	tcctcatgag	1980
aatgcctatc	ctaaggattc	tgacggtgat	ggcttaaccg	atgatgaaga	aatcgctcta	2040
ggcaccaatc	ccttttagttc	tgatagtgat	gggtgatggga	ctccagataa	tgtcgaaaag	2100
gcaaattggaa	cagacccac	caatgcttct	gataatgagg	tgacaaggca	acaagaagcc	2160
aataaacgtg	acttcacttt	gtcagaaatg	attaaagcca	aaaataccgc	agcgctgaat	2220
caacacttac	aagacggcat	caaacagtat	tttgatagtg	atacctataa	gcaataacctg	2280
gaagggatgg	cccacttcaa	taactacttc	ccacgaaata	ttcaattgat	tatgtcacaa	2340
tttcagaag	catcgatggg	tgcgtctttc	caagagtggga	ggaagcgaaa	tggttcggtt	2400
aaaaaagggtg	agaaggccat	ctatatccaa	gcccctgttt	ctgttatgaa	aaaagatgag	2460
aatgggaaac	ctatccttaa	tcctgaaacg	ggagaaaagg	agaccatcac	ttacttttaa	2520
cctgtccctg	tctttgacat	taaacaggtc	tctccccaag	aaggaaaaga	actcaatctc	2580
cctaaagcca	tgggaactat	tccagaacaa	ttggataaag	aatactacca	aaatgtctat	2640
cgtagcttaa	gagatatttc	tcagaataac	aataaggttc	ccattcgatt	tagagaactt	2700
ggacaagaag	atgggttcta	tagtccacag	acaaatgaaa	ttgttattaa	gaaagggatg	2760
tcttatgaac	gaacctgtgc	aacgctgatt	catgaaattg	ctcattcgga	attacacaac	2820
aaacaaaagtt	tgacgggaacg	cctttgatgg	aaactaacaa	gaagtaccaa	agaacttcaa	2880
gcggaatcca	ttgcttatgt	tgtatccagt	catctaggtt	ttgataccag	tcaagagtca	2940
tttccttatt	tagcgtcttg	gtcaaaaagaa	aaagacgggc	ttgccaaactt	aacagcacaa	3000
ttggaaatcg	tgcaagaaga	agccaaaaac	ttaatggaac	ggattgatca	acagttaagt	3060
caatatcaaa	cagtaacact	gaataaagaa	acccaacaat	tgactaaaca	agaaatgaaa	3120
aagcagactc	atccctttta	tcaaagttta	gcagccgcta	aaacatcaag	agcacaagtc	3180
accactcagg	agaagggaagc	aagcgtaaaa	aaagacaatc	gacctacgat	gccgtag	3237

SeqID 76

atgaattcac	aagaaacaaa	agggtcacgga	tttttttagaa	aatcaaaagc	atatggttta	60
gtatgtggga	ttgcaactagc	agggtgcattt	acattagcta	ctagtcaagt	gtctgctgat	120
caagttacaa	ctcaagcaac	aactcaaaca	gtaacgcaaa	atcaagcaga	aacagtaaca	180
tcaactcaac	ttgataaagc	agtagataca	gctaaaaaag	cagctgtagc	tgttacaaac	240
acaacagcag	ttaatcatgc	gacaactact	gatgcacaag	ctgatttagc	taatcaaaac	300
caagctgtta	aagatgttac	tgcaaaaagca	caagctaata	cacaagctat	taaagatgct	360
actgctgaaa	atgcaaaaat	tgatgctgaa	aacaaagcag	aggcagagcg	tgttgcaaaa	420
gctaataaag	cagggtcaagc	agaagtagat	gctcgttaata	aagcagggtca	agcagccgtt	480
gatgcacgta	ataaaagcaaa	acagcaagcg	caagacgatc	aaaaagcaaa	aattgatgct	540
gaaaacaaa	cagagtctca	acgtgtaagt	cagttaaatg	cacaaaataa	agcaaaaatt	600
gacgcagaaa	ataaagatgc	gcaagctaaa	gcagatgcga	ctaattgcaca	attacaaaaa	660
gactatcaaa	caaagtttagc	aaacattaaa	tctgttgaag	cttataatgc	agggtgtacgt	720
caacgtaata	aagatgcaca	agctaaagca	gatgogacta	acgcacagtt	acaaaaagac	780
tatcaagcta	aattagcact	ttataatcaa	gctctaaaag	ctaaagcaga	agcagataaa	840
cagtctatta	ataatgtttg	ttttgacatt	aaagcccaag	ctaaagggtg	tgataacgct	900
gaatatggaa	actcaatcat	gactgcaaaa	actaaaacctg	acggaagttt	cgagtttaac	960
cacgatatga	tcgatgggtg	gaagacaatc	ggcttatggta	agcttacagg	taaagttaat	1020
catcattatg	ttgctaacaa	ggatggctct	gtgacagcat	ttgttgattc	tgtcactctt	1080
tacaagtacg	agtatcgtaa	tgttgctcaa	aatgctgctg	ttaaccaaaa	tattgtattt	1140
agagttttta	caaaagatgg	tcgtcctatt	tttgaaaaag	ctcataatgg	taacaaaact	1200
tttgacagaaa	ctttaaacaa	aactttacaa	ctcaatctta	aatatgagct	taaaccacat	1260
gcttccagcg	gtaacgtcga	agtcttttaag	attcatgatg	actgggtaca	tgacacacat	1320
gggtctgctt	tagtgtctta	tgttaataat	aatgatgctg	ttcctaattg	ggcatccca	1380

gaacagccaa	ctccaccaa	accagaaaa	gttacacctg	aagcagaaaa	accagtacct	1440
gaaaagccag	ttgagcctaa	attggtaacg	cctgttttaa	aaacttatac	tccagtcaaa	1500
tttattccgc	gagaatacaa	accagtccca	agtacccttg	agacgtttac	ccctgagaaa	1560
tttactccag	ctcaaccaa	agtgaacct	catgtgtctg	tacctgaaaa	aattaactat	1620
aaagtagcgg	tgcattccag	acagatacca	aaggccacac	caactaagaa	agttctagat	1680
gaaaacgggc	aatctattaa	cggtaaactt	gtattaccaa	atgcaacatt	agactatggt	1740
gctaaacaaa	acttttagtca	atacaaaggt	attaaagctt	ctgcagaagc	tatcgcaaaa	1800
ggttttgcat	ttgtagatca	accaaagtaa	gcgttagctg	aattgactgt	taagtctatc	1860
aaagcatcta	atgggtgatga	tgtatcaagc	ttgttagaaa	tgcgtcatgt	tttatcaaaa	1920
gatacttttag	acaaaaaact	tcaatctctt	attaaagagg	caggaattag	tccagttggt	1980
gagttttaca	tgtggactgc	aaaagatcca	caagcttttt	ataaagctta	tgttcaaaaa	2040
ggcttagata	ttacttataa	cttatcattt	aaagttaaaa	aagagtttac	taaagggtcaa	2100
atcaaaaatg	gtgttgccaca	gattgatttt	gggaatggat	atacaggtaa	tattgtagtc	2160
aatgatattga	caactccaga	agtcacataa	gacgtgttag	acaaagaaga	cggcaagtct	2220
attaacaatg	gtactgtcaa	actcggtagc	gaagtcactt	acaagcttga	aggatgggtt	2280
gtaccagcga	accgtgggta	cgatcttttt	gaatacaaat	ttgtagatca	cttacaacac	2340
acacacgata	tttacctaaa	agataaagta	gtcgctaaag	tagcaattac	acttaagat	2400
ggcactgtaa	ttccaaaagg	gacaaatcta	gttcaatata	ctgagactgt	ctataataag	2460
gaaacagggtc	gctatgagtt	agcctttaag	gcagacttcc	tcgcacaagt	ttcacgttct	2520
agtgcctttg	gggcagatga	ctttatttga	gttaaacgta	tcaaagcggg	tgatgtttac	2580
aataccgcag	acttctttgt	caatggcaat	aaggtaaaaa	ctgaaactgt	ggtaacacat	2640
actctgaga	aaccaaaaacc	agttatgccg	caaaaagtaa	ctcctaaagc	accagcttta	2700
ccatccacag	gagagcaagg	ggtatctgtc	ctaacagtac	ttggtgccgc	cttactctca	2760
ctcttaggcc	ttgtaggggt	taaaaagcgt	caacagtaa			2799

SeqID 77

atgaatcaga	taaaaaattat	cacaggactt	acagtcgcaa	cactatccgc	agtggtaggg	60
aatgtatacg	cagaagatat	cacaccgaca	gcaccagtta	atgaaccaca	agtatcaagc	120
gaaaccgcaa	aaacgcctca	agttacagaa	agtcaagtta	acagcgcgaaa	agttactgcc	180
gatcaagcaa	caagtgatgt	taatgcacaa	aaaaatgtag	ttaataatgc	tcaaaatcaa	240
aaaaatcaag	cacaacaaaa	acttggttaac	gcaactacaa	cgtaaataatga	aacacaaaaa	300
ttagtgcgaag	aatctaccaa	tcaaaatcaa	gtacaacaaa	cagttgattc	cgcaaagcaa	360
aggttgtcgc	agacagaagc	taatcaaaaa	attactcaaa	ctgaacaagt	caaagctcaa	420
aatcaagtta	atgcacaaca	aacagttgtt	gttaacaatg	agcatgatgt	tgcaactaag	480
acagctgatg	ttaaacgaagc	tcaagcatca	gtcgatacag	ctaaagatgc	tttgactaat	540
actatagtta	atagtgtatt	aaataaagca	cagtcaaacg	tcacaactaa	gacagctgat	600
gttaaaaactg	cgacagatgc	acttacaaaa	gcacaagcga	ctgataaaac	acttactaat	660
caaaaagcaa	aagcacaaca	aatagttgat	tcagcaaaac	aaaacttatc	tgctaaagat	720
acacagcttt	cacaagctaa	tgctgaggtc	aatcatcaca	agtttaaaac	ggctctaggg	780
caaagtcatt	attacaatca	acgtgataat	gcttgggctg	gggtatatgg	agggcataca	840
tttgcttcaa	ctggatgtgt	cccatcagca	ttagcaatgg	tttactctga	tttatcaaat	900
cggacaataa	cgccgagaga	gatagctgat	tacttataca	acaacacaga	tgaattcaat	960
aaacgtttcg	gtggcacaag	tgggaaggt	attatttctg	ctactaaagc	gtttgggttat	1020
gttgtgactc	atgttgctag	caaaaatgct	ataactgaag	cattaaaagc	aggtcatcat	1080
gttgttgctg	ctgtacaaaa	taataaattc	agtcctctgg	ggcctcaata	cagtcacgaa	1140
attgtattga	gaggtagtct	taatggcaat	acgtatgttt	atgatccgta	taaccgtgat	1200
aacaatgggt	tttagcagtgt	tgaccgcatt	tggaatgaac	agtcacgaga	tagtattgat	1260
actgctgggt	taggtgtacc	gtttttcgca	attatgacta	aaaatatggc	taatgcttta	1320
actaagcagt	cacaagcttt	agcaagccaa	caagttgtct	aaaaacaatt	aatgatgca	1380
caagctaaag	caacaggtct	taatgcagta	actatgcaga	caccgattgc	acaagctaat	1440
ttgattaaag	cacagtcaaa	tttaaaagat	gctcaaaagc	gattagcaga	agcacaagca	1500
tcagtcaaaat	tagctaatca	agataatgtt	aaaaaacaag	ctgacttaac	aaaagcagag	1560
tctaaattaa	aagatgctca	aaagcaatta	gcagcagcac	aagctaaaatt	gacaacaagc	1620
aaaacaaaaa	ttaattcaatt	aaaacaagt	ttagcagaag	caagtcaaca	agtagcccaa	1680
gcaaatcaag	attacaagca	agctaaagat	aatctaacac	aaaaaactgc	ttatctaaca	1740
aatctacgca	atgcacaagc	taatttgatt	aaagcacagt	ctgatgtagc	acaagctaaa	1800
gataacttag	caaataagat	tgctaagtta	caaagagaag	tagcttattt	acaagagtta	1860
aaaactaaag	cagtagatgc	gcaatcacag	tatcaaaaag	ttttatcagc	ttataagtca	1920
gtttttatcag	ctaaagcaag	tttaaaatta	gcggaagaga	aagctcgact	tgataaaaaa	1980
ggtcacgaag	cagtagcagt	agttgacgaa	acaggttaaa	ttactagcta	tattacttct	2040
aaacacaaaa	tagaaatgaa	atctcttggt	gcaactaaga	caactgatgt	taaacaagta	2100
tcagttgcta	aagcaagcgt	gttgccaagt	actgggtgat	ttaaacaagt	atcagttgct	2160
cttctgggta	tgttattaac	gttctctgggt	tttttaggta	tacgtaaaaa	aagtaaaaaa	2220
gttattaatt	aa					2232

SeqID 78

atgatatcac	gtaaagtgtgc	gcttgtgacg	ggggcatctg	ctggtttttg	tgcagctatt	60
gttactaaat	tagtttcaga	tggttatagc	gttattgggt	gtgctcgtcg	aatggataaa	120
ttaaaatgct	ttggagaaaa	gttttcagag	ggttactttt	atccacttca	aatggatatt	180
acaagtagag	aatcgggttg	caaagcttta	gaaagtctgc	ctaaaaattt	gcaatcaatt	240
gatttgttgg	ttaataatgc	aggttttagc	cttggattgg	ataaatcata	tgaagctgat	300
tttgaagatt	ggatgactat	gattaatact	aacgttgtag	gattaattta	cttgacacga	360
tgcattttac	cgaaaatggt	agaagttaat	agagggttaa	ttatcaattt	gggatcaact	420
gcaggaaaca	ttccttatcc	aggagctaat	gtctatggcg	catcaaaagc	ttttgtaaaa	480
caattttctc	tcaacttgcg	tgccgattta	gctggaacta	aaatcagagt	tactaaccta	540
gaaccgggtt	tatgtgaagg	gacagaattt	tcaactgtac	gtttcaaagg	agatcataaa	600
agagttgaaa	aacttttatga	aggtgcgcac	gcaattcaag	cagaggatat	tgctaatacc	660
gtgtcatggg	ttgctagcca	accagaacac	attaatatta	atcgcataga	aataatgcca	720
gtcagtcaaa	cttatggacc	tcaacctgtt	tatcgtgatt	aa		762

SeqID 79

atgattttatt	tagacaatgc	tgctactacc	gctctaacc	catctgttat	tgagaaaatg	60
accaatgtca	tgacaagtaa	ctatggtaat	ccatctagta	tacatacctt	tgggctgcaa	120
gcaaatcaac	ttttacgtga	atgtcgacaa	attattgctg	aatatctaaa	tgtaatttca	180
cgtgaaatta	ttttcacttc	tgggggaact	gagagcaaca	atacagctat	caaaggggat	240
gctcttgcaa	atcagctaaa	aggtaaacat	attattacct	ctgaaattga	acatcattca	300
gtcctacata	ctatgactta	cttatcagag	cgatttgggt	ttgatattac	ttacttaaaa	360
ccaaaccatg	gacaaattac	tgcaaaagac	gttcaagaag	ctttacgaga	tgatactatt	420
atggtatctc	tcatgtttgc	taataatgaa	accggggact	ttttaccaat	tcaagagatt	480
ggtcagcttc	tcaggaacca	ccaagctgtt	tttcacgttg	atgccgttca	agtcttttagc	540
aaaatggaac	ttgatcctca	ttcttttagga	attgactttt	tagctgcttc	tgcccataaa	600
tttcacggtc	caaaaggtgt	tgggatactc	tactgtgctc	cccatcactt	tgatagtcta	660
cttcattggtg	gagaccaaga	ggaaaaaagg	cgtgcttcaa	ctgaaaatat	aattgggtatt	720
gctggaatgt	ctcaagctct	tactgatgct	acgactaaca	cccttaaaaa	ttggactcac	780
attagtcagc	tgagaacgac	cttttttagat	gctatttcag	accttgactt	ctatcttaat	840
aacgggtcaag	actgcttacc	tcatgtactt	aatatagggt	ttcctagaca	gaataatggc	900
ttgttattga	cacagttaga	tttagctgga	ttcgcagttt	caacaggttc	tgcatgtact	960
gcaggaacag	tcgaacctag	tcatgtctta	acaagcttgt	atggagccaa	ctcaccacgt	1020
ctaaatgaat	caatacgtat	tagtttttca	gaactaaata	cccaagaaga	aattcttgaa	1080
ttagctaaaa	ccttaagaaa	aattatagga	gattaa			1116

SeqID 80

atgtctagga	aaacatttta	acatatacta	tcgattggag	tttgcacgct	cgtactatcg	60
atgagtcctt	attacactga	aaaagcccac	gctattgctg	gtcctagtga	ccgccaatac	120
gtagaaaaac	caaatcctca	cattattgta	aatggtacag	gtactgatca	aaacgggaaat	180
agcattttac	cgcattacat	cgaagtcaat	gtaaagatgg	gacaaacttt	aagtaaaagaa	240
gaaattctag	attatattgc	tcgaaattta	aactctagtg	ttggaggaga	aagtaaaaaac	300
gttcaataca	gcaacatcga	gtttaaggaa	agtgcctatc	tgaagcgtca	attagatgat	360
ggcaagacag	aagaaatagc	aattgataac	gacggtgtta	ctgtaccta	agacggtcca	420
aacaaatttt	ggattgacgt	tccagtaact	tgtactgtta	ctcctatcgt	aacagaaaca	480
catgaagttc	gatgggggac	tccagtcgct	atatcacacc	gtatttactt	tgttgaagaa	540
tcttctggaa	aagttttaga	tgaatacaca	aatctacaca	ctgctgattc	ggaacttaac	600
ggttatcgtg	ttggagatta	tatcacagac	tatgcacttt	ctaagtctgc	ttacgaagct	660
tttttaaaat	ctcgtttaga	taaagaagg	tacaaaactt	aacatcgtat	tagcacgaat	720
gtacgacaaa	accttcaaat	tgataaattg	attttcaatt	atgactttta	tgaggaaaat	780
atttactacc	aaatcgggaa	tatccgtcca	ctattaagtc	gctcatcagc	tgaagtagaa	840
tctgacatca	ttacagaacg	ctactatggt	tctaaaaatg	ctaaaagttt	agcacgtaca	900
gaatcaacca	tttctgattaa	aatgggtgat	gccccaaactg	aacaaccgct	atttaaccac	960
acattaaactg	gttatcaatt	ggcaactgtc	tcccatgtct	ataacagact	ctttgaagaa	1020
aactttatcc	caactacaaa	atcaggagaa	agatatattta	ttcaaaatat	gaaaaaaaca	1080
gctgaacaag	aatatactgt	ttacctttca	gaaacacctt	attctaaaga	gaacgctccc	1140
gtaatttctt	atgatgcaag	acctgttgat	tgggattatc	actcaggcgc	ttcaggatca	1200
cttgaaaatc	agcctaacaat	ctatactgaa	gaagattcaa	ctgaattttt	gggtaataaa	1260
ccacaagcag	cttggttatcc	aaacaaacaa	tttgcttgcg	aaaatactga	ctctaaatac	1320
aactatagct	atttagaaaa	atag				1344

SeqID 81

atgaatcctt	taataattgg	aatgaatgat	aaacaagcag	aagcgggtaca	aacgacagac	60
ggaccgcttt	tgattatggc	aggagctggc	tctggaaaaa	cacgtgttct	gactcatcgt	120
attgcttatt	taatagatga	aaaatatggt	aatccttgga	atatttttagc	gattactttt	180

actaataaag	cagcgctga	aatgctgaa	cgtgctatcg	ccttgaatcc	agctacccaa	240
gatactttga	ttgcaacttt	tcatagtatg	tgtgttcgta	ttttacgtcg	tgaagctgat	300
tatattggat	ataatcgtaa	ctttacaatc	gttgatccag	gtgagcagcg	tacttttaatg	360
aagcgaatca	ttaagcaatt	aaattttggac	acaaaaaagt	ggaatgaacg	ttcaattttta	420
ggtacaatct	ctaattgctaa	aaatgacott	cttgatgaaa	ttgcatatga	gaagcaagcc	480
ggagatatgt	atacacaggt	aattgctaaa	tgctataaag	cttatcaaga	ggaattacgt	540
agaagtgagg	ccatggattt	cgatgacttg	attatgatga	cacttcgatt	atttgatcag	600
aataaagatg	ttttggccta	ttaccaacag	aggtatcaat	atatccatgt	agacgagtat	660
caagatacta	accacgctca	ataccaatta	gttaagttaa	tagcttcgcg	tttcaaaaat	720
atttgtgttg	ttggtgatgc	cgatcaatcc	atttacggat	ggcgtggagc	tgatatgcaa	780
aatattccttg	attttgaaaa	ggactatccg	caagccaaag	ttgtattatt	agaagaaaat	840
tatcgatcga	ctaagaaaat	acttcaagct	gctaataatg	tgattaatca	taataaaaaat	900
cgccgtccca	aaaaattatg	gactcaaaaat	gatgaagggt	agcaaattgt	atatcataga	960
gctaacaatg	agcaagaaga	agccgttttt	gtagcatcaa	ctattgataa	catcgttcga	1020
gaacaaggaa	aaaattttcaa	agatttttgc	gttctttatc	gtacgaatgc	gcaatctcgt	1080
actattgagg	aagcactttt	aaaatccaat	attccatata	caatggttgg	tggaaacaaa	1140
ttctatagtc	gtaaagaaat	tcgagatggt	attgcttata	tcaatatcct	tgcaataact	1200
tctgataata	tttcttttga	gctgattgta	aatgaaccta	aaagaggggt	tgggcccaggc	1260
acttttagaaa	aaatacggtc	atttgcctat	gaacagaaac	tgtctcttct	tgatgcctct	1320
tcaaatgtca	tgatgtcgcc	cttaaaaagg	aaggctgctc	aagctgtttg	ggatttagct	1380
aatctgattt	tgactctacg	tagtaagcta	gatagtttaa	ctgtaacgga	gattacagaa	1440
aacctactgg	ataagacagg	atatctagaa	gcacttcaag	ttcaaaatac	attagaaagt	1500
caagcgcgta	ttgaaaatat	tgaagaattc	ttgtcagtg	ctaaaaat	tgacgataac	1560
cctgagatta	cagtagaggg	tgaactgggt	ttagatcgtc	tatcgcgttt	tttaaatgat	1620
ttagcttttaa	tagcagatac	tgatgatagc	gccactgaaa	cggtgaggt	cacttttaatg	1680
acattacatg	ctgccaagg	tctagaattt	ccagttgttt	tcttaatcgg	tatggaagaa	1740
ggagtatttc	ctttatcgcg	tgcaatagag	gatgctgatg	aattagaaga	agagcgtcgt	1800
ttagcttatg	tggggtattc	gagagcagaa	caaatacttt	tctttacca	tgctaatacc	1860
cgtactttat	ttggtaaaac	tagttataat	agaccaaccc	gtttttatac	tgagattgat	1920
gatgagctga	tacaacatca	agggttgggt	cgaccagtta	attcttcatt	tgggtgtgaa	1980
tattcaaaaag	aacagcctac	acaatttgggt	caaggaatga	gtcttcaaca	agcgttccag	2040
gcacgtaaaa	gtaattcaca	acctcaagta	actgcccaac	tccaggctct	taacgcgaac	2100
aatagccatg	agacatcatg	ggagattggt	gatgttgcaa	ctcataaaaa	atgggggggac	2160
ggtacgggtg	ttgaagtttc	aggtagcgga	aagactcaag	agttaaaaat	aaattttcca	2220
ggtattgggt	taaagaaatt	attagcgagt	gtcgctccta	ttagtaaaaa	ggaaaactaa	2280

SeqID 82

atgaaattat	acgtttcaatt	aatggttatt	tttaacctttt	cattcgctgg	tgaggttcta	60
tctactatat	tcaacttacc	tgtaccaggt	agtattattg	gattaatatt	actattccta	120
gcgttaaaat	acaaaatcat	caggctcagg	catattgatg	ccgtggggaa	ttttctatta	180
gcaaatatga	ccatttttatt	tttaccacca	gcagttggac	tgatggagca	ctttcaagac	240
ataaaaccct	atcttttttg	gatagctatc	attatcttag	gagcgttatt	tctcaatatt	300
ctaactattg	gactgggtatc	ccaatggatc	aaaaagagat	atgaaggaga	ttatccagaa	360
attggaggta	aaaatggcaa	ctttaacgaa	taa			393

SeqID 83

atgatttttg	tcacagtggg	gacacatgaa	cagcagttca	accgtcttat	ttaaagaagt	60
gatagattaa	aaggggacagg	tgctattgat	caagaagtgt	tcattcaaac	gggttactca	120
gactttgaac	ctcagaattg	tcagtgggtca	aaattttctct	catatgatga	tatgaactct	180
tacatgaaag	aagctgagat	tgttatcaca	catggcgggtc	cagcgacgtt	tatgtcagtt	240
atttcttttag	ggaaattacc	agtcgttggt	cctaggagaa	agcagtttgg	tgaacatatc	300
aatgatcatc	aaatacaatt	ttttaaaaaa	attgccacc	tgatccctt	ggcttggatt	360
gaagatgtag	atggacttgc	ggaagtgttg	aaaagggaata	tagctacaga	aaaatatcag	420
ggaaataatg	atatgttttg	tcataaatta	gaaaaaatta	taggtgaaat	atga	474

SeqID 84

atgggtgatga	aaatcataga	gttaaaagaa	gcaaccgtac	aagtcagtaa	tggttttagca	60
gaaatgaaaa	cgatattaga	ccatgttaat	ttgagtattt	atgaacatga	cttcattaca	120
atattgggtg	gaaatggagc	tggaaaaatc	acgcttttta	atgtaattgc	aggtaacctg	180
atgttaaagc	gtggaaatat	ttacatcatg	ggacaagatg	ttactaattt	accagcagaa	240
aaacgagcta	aatattttatc	acgggtattt	caagatccga	aaatgggaac	agcacctagg	300
atgacagttg	ctgaaaattt	attagttgct	aaatttcgag	gtgaaaagag	accgttagtt	360
cctagaaaga	ttactaacta	taccgaagaa	tttcaaaaat	tgattgctag	aactggtaat	420
ggacttgatc	gccattttaga	gacacctaca	ggtttattat	caggtggaca	aagacaagca	480
cttagtttat	taatggcaac	tttgaaaaaa	ccaaatctgt	tattattgga	cgaacacaca	540

gcagcgcttg	atcctagaac	aagtgtttcg	cttatgggct	tgactgatga	gtttatcaaa	600
caagattcgt	tgactgcctt	aatgattaca	catcatatgg	aagatgctct	caaatatgga	660
aatcgtatat	tagtaatgaa	agatggcaag	attgtcagag	atttaaataca	ggcacaaaaa	720
aacaagatgg	ctatagctga	ctattatcaa	ttatttgatt	aa		762

SeqID 85

atggaaatca	aaaagaaaca	tcgattattg	ctttattcag	cccttatttt	aggaacaata	60
ttggtaaca	atagttacca	agctaaagct	gaagagctta	ccaaaactac	ctcaacgtcc	120
caaataagag	atactcaaac	taataatatt	gaagttctcc	agactgaaag	taccactgtc	180
aaagagacta	gcaccacaac	cacacaacaa	gatctgtcta	accccacagc	ttcaaccgca	240
actgcaacag	ccactcatag	cacaatgaaa	caagtagtag	ataatcaaac	tcaaaataag	300
gagctgggtga	aaaaaggaga	ttttaatcaa	actaacctcg	tatctggaag	ctgggtcacat	360
acaagcgcta	gggaattggtc	tgcttggaatt	gataaagaaa	atactgctga	taaatcacct	420
attatccaac	gtaccgaaca	aggccaagta	agcctatcca	gcgacaaagg	ctttagaggt	480
gctgtaacac	aaaaagtga	cattgatccc	actaaaaaat	atgaggtcaa	gtttgatatt	540
gaaacaagta	acaaggctgg	acaagctttc	cttcgtatta	tggagaaaaa	agacaacaat	600
acgcgacttt	ggctttctga	gatgaccagc	ggtactacta	acaaacatac	cttaacaaag	660
atatataacc	caaagttaaa	tgtctccgag	gtgacacttg	aactttatta	tgaaaaagga	720
actggttctg	ctacttttga	taatatatca	atgaaagcaa	aaggccctaa	agactcagag	780
catccacaac	ccgtcacaac	acaaattgaa	gaaagcggtta	atacggcttt	aaacaaaaat	840
tacgttttta	ataaagctga	ctaccaatac	actotaacca	atccgtctct	cgggaaaaat	900
gttggtggaa	tattgtatcc	aaacgctact	ggttcaacaa	ctgttaaaat	atctgataaa	960
tctggtaaaa	taattaaaga	agtaccgtta	tcagttacag	cttcaacaga	agataagttt	1020
acaaaactcc	tcgacaaatg	gaacgacgtg	actattggta	atcatgttta	cgataactaat	1080
gattcgaaca	tgcaaaagat	taatcagaaa	ttagatgaaa	ctaacgccaa	aaacatcaaa	1140
actatcaaac	tggaattctaa	tcacactttc	ctttggaaag	atttagataa	tctcaataat	1200
tcagcacagt	taaccgctac	ttatcgtcgt	ttggaagatt	tagctaataa	aatcaccaat	1260
cccactctta	ctattttaca	aatgaaaaaa	gctattcgta	ctgtaaaaga	gagtcgtggc	1320
tggcttcac	aaaactttcta	caatgttaat	aaagatatag	aaggctctgc	caattgggtgg	1380
gatttttga	tcgggtgtccc	tcgctcaatt	acagctaccc	tagctctcat	gaataactac	1440
ttcactgacg	ctgaaataaa	aacttatacc	gacccaattg	aacactttgt	tcctgatgca	1500
ggatattttc	gtaaaacgct	tgacaatcca	tttaaagccc	ttgggtggtaa	tctagtcgat	1560
atggggcgcg	ttaaaatcat	tgaaggttta	cttcgtaaaag	acaatactat	tatcgaaaaa	1620
acttctcatt	ctctaaaaaa	tctttttact	actgctacta	aagctgaagg	tttctatgct	1680
gacggttctt	acatcgacca	tacaaatggt	gcttatactg	gcgcctatgg	taatgttctg	1740
atagatgggt	tgacacaatt	gctgcctatc	attcaagaaa	ctgactataa	aatctcta	1800
caagaacttg	atatggttta	taaatggatt	aatcaatcat	ttttaccttt	aattgtaaaa	1860
ggtgagttaa	tggaatagag	tcgtggacgc	tcaattagta	gagaggcagc	ttcttcgcat	1920
gcggctgcag	ttgaagttct	cagaggtttc	ctcagattgg	ctaacatgtc	taatgaagag	1980
cgaactttag	acctcaaatc	aactattaaa	acgattatca	cttcaataaa	attctacaat	2040
gtcttcaata	acctcaaatc	gtattccgat	attgccaaaca	tgaataagat	gcttaatgac	2100
agtacagtcg	ctactaaacc	tttaaaaagt	aatttatcaa	cctttaatag	catggaccgc	2160
ttagcttatt	ataatgccga	gaaagacttt	ggtttcgcg	tttcattaca	ttctaaccgt	2220
accctcaact	atgaaggaat	gaatgatgaa	aatacacgtg	attggtatac	cggagatggg	2280
atgttctatc	tttataatag	tgatcaatc	cattatagta	atcatttttg	gccaacctgc	2340
aatccttata	aaatggctgg	aacaactgaa	aaagatgcta	agcgtgaaga	taccactaag	2400
gaattcatga	gcaaacatag	caaagacgct	aaagaaaaaa	ccggccaagt	tacaggaaca	2460
tctgactttg	ttggttccgt	caaacttaat	gatcactttg	ctcttgccgc	tatggatttt	2520
actaactggg	atcgcacctt	aacagcacaa	aaaggttggg	ttatcttaaa	tgataagatt	2580
gtcttttttag	gtagcaacat	caagaatact	aacggcattg	gaaatgtttc	tacaacaatt	2640
gatcaacgaa	aagacgattc	taaaacacct	tatactacat	acgtcaatgg	aaaaactatt	2700
gatttaaaaac	aagcaagttc	tcaacaattt	acagatacaa	aaagtgtctt	tttagaatca	2760
aaagaacctg	gtcgaatat	tggttatatc	ttcttttaaaa	atagcactat	tgatattgaa	2820
cgcaagagac	aaacagggtac	ttggaacagc	attaatcgta	cttctaaaaa	tacctcaatc	2880
gtagcaatc	cttttatcac	tataagccaa	aagcatgaca	acaaagggtga	tagctatggg	2940
tacatgatgg	ttccaaacat	tgatcgaca	agttttgata	aattagccaa	cagcaaagaa	3000
gtagaattac	tagaaaatag	ttcaaaaacaa	caagttatct	atgataaaaa	cagtcaaac	3060
tgggctgtta	tcaaacacga	taatcaagag	agtctcatta	acaatcaatt	caaaatgaat	3120
aaagcgggac	tttacctagt	acaaaaagtt	ggtaatgact	atcaaaatgt	ctattaccaa	3180
cctcaaacca	tgacaaaaac	agaccaatta	gctatcttaa			3219

SeqID 86

atgcattctt	tttctaatac	tggatatact	tatgataatg	cogtaactga	agcatttttc	60
aagtatttaa	agcatagaca	aatcaaccga	aaacattatc	aaaatatcaa	acaggttcaa	120
ttagactgct	ttgaatacat	tgagaatttt	tataacaatt	acaaccacaa	tacggcta	180

ctaggactaa cccctaataca gaaagaagaa aattatattta acgcaataaa ataa 234

SeqID 87

gtgaagaaaa	catatgggta	tatcggtca	gttgctgcca	ttttactagc	tactcatatt	60
ggaagttacc	aacttggtaa	gcatcatatg	ggtctagcaa	caaaggacaa	tcagattgcc	120
tatattgatg	acagcaaaag	taaggcaaaa	gccctaaaa	caaacaaaac	gatggatcaa	180
atcagtgtg	aagaaggcat	ctctgctgaa	cagatcgtag	tcaaaattac	tgaccaaggc	240
tatgtgacct	cacatgggtga	ccattatcat	ttttacaatg	ggaaagttcc	ttatgatgcg	300
attattagt	aagagttggt	gatgacggat	cctaattacc	gttttaaaaca	atcagacggt	360
atcaatgaaa	tcttagacgg	ttacgttatt	aaagtcaatg	gcaactatta	tgtttacctc	420
aagccaggta	gtaagcgcaa	aaacattcga	accaacaac	aaattgctga	gcaagtagcc	480
aaaggaacta	aagaagctaa	agaaaaaggt	ttagctcaag	tggcccatct	cagtaaagaa	540
gaagttgcgg	cagtcaatga	agcaaaaaga	caaggacgct	atactacaga	cgatggctat	600
atTTTTtagtc	cgacagatat	cattgatgat	ttaggagatg	cttatttagt	acctcatggt	660
aatcactatc	attatatccc	taaaaaggat	ttgtctccaa	gtgagctagc	tgctgcacaa	720
gcctactgga	gtcaaaaaca	aggtcgaggt	gctagaccgt	ctgattaccg	cccgacacca	780
gccccaggtc	gtaggaaagc	cccaattcct	gatgtgacgc	ctaaccctgg	acaaggatcat	840
cagccagata	acggtggcta	tcattccagcg	cctcctaggg	caaatgatgc	gtcacaacac	900
aaacaccaaa	gagatgagtt	taaaaggaaa	accttttaagg	aacttttaga	tcaactacac	960
cgtcttgatt	tgaaataccg	tcattgtgga	gaagatgggt	tgatttttga	accgactcaa	1020
gtgatcaaat	caaacgcttt	tgggtatgtg	gtgcctcatg	gagatcatta	tcattattatc	1080
ccaagaagtc	agttatcacc	tcttgaaatg	gaattagcag	atcgataactt	agctggccaa	1140
actgaggaca	atgactcagg	ttcagagcac	tcaaaaccat	cagataaaga	agtgacacat	1200
acctttcttg	gtcatcgcat	caaagcttac	ggaaaaggct	tagatggtaa	accatattgat	1260
acgagtgatg	cttattgtttt	tagtaaagaa	tccattcatt	cagtggataa	atcaggagtt	1320
acagctaaac	acggagatca	tttccactat	ataggatttg	gagaacttga	acaatatgag	1380
ttggatgagg	tcgctaactg	gggtgaaagca	aaaggctcaag	ctgatgagct	tgctgctgct	1440
ttggatcagg	aacaaggcaa	agaaaaacca	ctctttgaca	ctaaaaaagt	gagtcgcaaa	1500
gtaacaaaag	atggtaaagt	gggctatatg	atgccaaaag	atggttaagg	ctatttctat	1560
gctcgtgatc	aacttgattt	gactcagatt	gcctttgccg	aacaagaact	aatgcttaaa	1620
gataagaagc	attaccgtta	tgacattggt	gacacaggta	ttgagccacg	acttgctgta	1680
gatgtgtcaa	gtctgcogat	gcatgctggt	aatgctactt	acgatactgg	aagttcggtt	1740
gttatccac	atattgatca	tatccatgtc	gttcctgatt	catgggtgac	gcgcgatcag	1800
attgcaacag	tcaagtatgt	gatgcaacac	ccgaagttc	gtccggatgt	atggtctaag	1860
ccagggcag	aagagtcagg	ttcgggtcatt	ccaaatgtta	cgcctcttga	taaacgtgct	1920
ggatgccaa	actggcaaat	tatccattct	gctgaagaag	ttcaaaaagc	cctagcagaa	1980
ggtcgttttg	caacaccaga	cggttatatt	ttcgatccac	gagatgtttt	ggccaaagaa	2040
acttttgtat	ggaaagatgg	ctccttttagc	atcccaagag	cagatggcag	ttcattgaga	2100
accatttaata	aatctgatct	atcccaagct	gagtgccaac	aagctcaaga	gttattggca	2160
aagaaaaata	ctggtgatgc	tactgatacg	gataaaacca	aagaaaagca	acaggcagat	2220
aagagcaatg	aaaaccaaca	gccaagtga	gccagtaaag	aagaaaaaga	atcagatgac	2280
tttatagaca	gtttaccaga	ctatggtcta	gatagagcaa	ccctagaaga	tcatatcaat	2340
caattagcac	aaaaagctaa	tatcgatcct	aagtatctca	ttttccaacc	agaagggtgc	2400
caattttata	ataaaaaatg	tgaattggta	acttatgata	tcaagacact	tcaacaaata	2460
aacccttaa						2469

SeqID 88

atgaaaaaag	gtttttttct	catggctatg	gttgtgagtt	tagtaatgat	agcagggtgt	60
gataagtcag	caaaccccaa	acagcctacg	caaggcatgt	cagttgtaac	cagcttttac	120
ccaatgtatg	cgatgacaaa	agaagtatct	ggagacctca	atgatgtgag	gatgatccaa	180
tcagggtcag	gcattcatct	ctttgaaccg	tctgtaaatg	atgtggcagc	tatttatgac	240
gctgatttgt	ttgtttacca	ttcacatacc	ttagaagctt	gggcaaggga	tctagaccct	300
aattttaaaaa	aatcaaaagg	tgatgtgttt	gaagcgtcaa	aacctttgac	actagataga	360
gtcaaaagggc	tagaagatat	ggaagtcaca	caaggcattg	acctgctgac	actttatgac	420
ccacatacct	ggacggatcc	cgttttagct	ggtgaggaag	ctgttaatat	cgctaaagag	480
ctaggacggt	tggatcctaa	acacaaaagc	agttacacta	aaaaggctaa	ggctttcaaa	540
aaagaagcag	agcaactaac	tgaagaatac	actcaaaaat	ttaaaaagggt	gcgctcaaaa	600
acattcgtga	cgcaacacac	ggcattttct	tatctggcta	aacgattcgg	cttgaaacaa	660
cttgggtatct	cgggtatttc	tccagagcaa	gagccctctc	ctcgccaatt	gaaagaaatt	720
caagactttg	tcaaaagaata	caacgtcaag	actatttttg	cagaagacaa	cgtcaatccc	780
aaaattgctc	atgctattgc	gaaatcaaca	ggagctaaag	taaagacatt	aagtccactt	840
gaagctgctc	caagcggaaa	caagacatat	ctagaaaatc	ttagagcaaa	tttggaagtgc	900
ctctatcaac	agttgaagta	a				921

SeqID 89

ttgcgtaaaa	aacagaaact	accattttgat	aaactttgcc	ttgcgcttat	gtctacgagc	60
atcttgetca	atgcacaatc	agacatcaaa	gcaaatactg	tgacagaaga	cactcctgct	120
accgaacaaa	ccgtagaaac	tccacaacca	acagcggttt	ctgaggaagc	accatcatca	180
aaggaaacta	aaaccccaca	aactcctagt	gatgcaggag	aaacagtagc	agatgacgct	240
aatgatctag	ccccccaagc	tcctgctaaa	actgctgata	caccagcaac	ctcaaaagcg	300
actattaggg	atttgaacga	cccttctcag	gtcaaaaccc	tgacaggaaa	agcaggcaag	360
ggagctggga	ctgttgttgc	agtgattgat	gctgggtttg	ataaaaaatc	tgaagcgtgg	420
cgcttaacag	acaaagccaa	agcacgttac	caatcaaaag	aagatcttga	aaaagctaaa	480
aaagagcacg	gtattaccta	tggcgagtgg	gtcaatgata	aggttgctta	ctaccatgac	540
tatagtaaag	atggtaaaac	cgctgtcgat	caagagcacg	gcacacacgt	gtcaggaatc	600
ttgtcaggaa	atgctccatc	tgaacgaaa	gaaccttacc	gcctagaagg	tgcgatgcct	660
gaggctcaat	tgcttttggat	gcgtgtcgaa	attgtaaatg	gactagcaga	ctatgctcgt	720
aactacgctc	aagctatcag	agatgctatc	aacttgggag	ctaaggtgat	taatatgagc	780
tttggttaatg	ctgcactagc	ttacgccaac	cttcagacg	aaacccaaaa	agcctttgac	840
tatgccaaat	caaaagggtg	tagcattgtg	acctcagctg	gtaatgatag	tagctttggg	900
ggcaagaccc	gtctacctct	agcagatcat	cctgattatg	gggtggttgg	gacacctgca	960
gcggcagact	caacattgac	agttgcttct	tacagcccag	ataaacagct	cactgaaact	1020
gctacgggtc	aaacagccga	tcagcaagat	aaagaaatgc	ctgttctttc	aacaaaccgt	1080
tttgagccaa	acaaggctta	cgactatgct	tatgctaata	gagggacgaa	agaggatgat	1140
tttaaggatg	tcaaaggtaa	gattgccctt	attgaacgtg	gcgatattga	tttcaaagat	1200
aagattgcaa	aagctcaaaa	agctgggtgc	gtaggagtct	tgatctatga	caatcaggac	1260
aagggtcttc	cgattgaatt	gccaaatgtt	gatcagatgc	ctgcggcctt	tatcagtcga	1320
aaagatggtc	tcttattaaa	agacaatccc	caaaaaacca	tcaccttcaa	tgcgacacct	1380
aagggtattg	caacagcaag	tggcaccaaa	ctaagccgct	tctcaagctg	gggtctgaca	1440
gctgacggta	atattaagcc	agatattgca	gcacccggcc	aagataatttt	gtcatcagtg	1500
gctaacaaca	agtatgcca	actttctgga	actagtatgt	ctgcgccatt	agtagcgggt	1560
atcatgggac	tgttgcaaaa	gcagtatgag	acacagtatc	ctgatatgac	accatcagag	1620
cgtcttgatt	tagctaaaaa	agtattgatg	agctcagcaa	ctgccttata	tgatgaagat	1680
gaaaaagctt	atttttctcc	tcgccaacaa	ggagcaggag	cagtcgatgc	taaaaaagct	1740
tcagcagcaa	cgatgtatgt	gacagataag	gataatacct	caagcaaggt	tcacctgaac	1800
aatgtttctg	ataaatattg	agtaacagta	acagttcaca	acaaatctga	taaaacctca	1860
gagttgtatt	accaagcaac	tgttcaaaca	gataaagtag	atggaaaaca	ctttgccttg	1920
gctcctaag	caattgtatg	gacatcatgg	caaaaaatca	caattccagc	caatagcagc	1980
aaacaagtca	ccgttccaat	cgatgctagt	cgatttagca	aggacttgct	tgcccaaatg	2040
aaaaatggct	atlttcttaga	aggttttgtt	cgtttcaaac	aagatcctaa	aaaagaagag	2100
cttatgagca	ttccatata	tggttttccga	ggtgattttg	gcaatctgtc	agccttagaa	2160
aaaccaatct	atgatagcaa	agacggtagc	agctactatc	atgaagcaaa	tagtgatgcc	2220
aaagaccaat	tagatgggtg	tggattacag	ttttacgctc	tgaaaaataa	ctttacagca	2280
cttaccacag	agtetaaccc	gtggacgatt	attaaagctg	tcaaagaagg	ggttgaaaaa	2340
atagaggata	togaatcttc	agagatcaca	caaacatttt	ttgcaggtag	ttttgcaaaa	2400
caagacgatg	atagccacta	ctatatccac	cgtcacgcta	atggcaagcc	atatgctgcg	2460
atctctccaa	atggggacgg	taacagagat	tatgtccaat	tccaaggtac	tttcttgctg	2520
aatgtctaaa	accttgtggc	tgaagtcttg	gacaaagaag	gaaatgttgt	ttggacaagt	2580
gaggtaaccg	agcaagttgt	taaaaactac	aacaatgact	tggcaagcac	acttgggttc	2640
acccgttttg	aaaaaacgcg	ttgggacggg	aaagataaag	acggcaaaat	tgttgctaac	2700
ggaacctaca	ccctacgtgt	ccgctacact	ccgattagct	caggtgcaaa	agaacaacac	2760
actgattttg	atgtgatatt	agacaatacg	acacctgaag	tcgcaacatc	ggcaaacattc	2820
tcaacagaag	atcgtcgttt	gacacttgca	tctaaaccaa	aaaccagcca	accggtttac	2880
cgtgagcgta	ttgcttatat	ttacatggat	gaggatctgc	caacaacaga	gtatatattct	2940
ccaaatgaag	atggtaacct	tactcttcc	gaagaggctg	aaacaatgga	aggcgctact	3000
gttccattga	aaatgtcaga	ctttacttat	gttgttgaag	atatggctgg	taacatcact	3060
tatacaccag	tgactaaagt	attggagggc	cactctaata	agccagaaca	agacggttca	3120
gatcaagcac	cagacaaaaa	accagaagct	aaaccagaac	aagacggttc	aggtcaaaa	3180
ccagataaaa	aaacagaaac	taaaccagaa	aaagatagtt	caggtcaaac	accaggtaaa	3240
actcctcaaa	aagggtcaacc	ttctcgtact	ctagagaaac	gatcttctaa	gcgtgcttta	3300
gctacaaaag	catcaacaag	agatcagtta	ccaacgacta	atgacaagga	tacaaatcgt	3360
ttacatctcc	ttaagttagt	tatgaccact	ttcttcttgg	gattagtagc	tcataatattt	3420
aaaacaaaaa	gccaaaaaga	aactaaaaaa	tag			3453

SeqID 90

tttagtgtaa	cctattcaca	gtctgaacgt	acggttgttt	tctcttttgg	agaaataaca	60
tttagtagga	gtcgtggac	aaatggcttt	gaaactagaa	taccagtaga	tgagtgggta	120
ggtcttgaaa	aatataagag	atattcaata	gaattcttat	atcatgttgc	aaaattggct	180
acaatgatgc	cttatcgtca	agtttgcaaa	gtaatagata	gcactttgca	aacaatcata	240
acaaaagact	gtgtttttaa	agcagtaaaa	ttttagataa	aattgttaaa	agaaaaagaa	300

cgctatcggtt	tttattttgga	agagccaccc	gaacgtaaaa	aagtgaaaaa	actgtatggt	360
gaggggtgatg	gagtcgatgat	taaaagcaca	gattctagag	aggaaagaag	gtatttagat	420
ttaacacattt	ttgttattca	tacaggctca	aaaaaagttt	ctactaaaag	atatgaattg	480
caggacaagc	acgaaatatt	acagcttaat	tatgataaag	ctaaatataa	tcttttagat	540
tatattttata	ataactatga	agtagatgac	gatactatgt	taatcactaa	ctctgatatg	600
ggtaaagggt	atactagtag	agtttttaag	gaattaggaa	aagcaactta	ggtaaagaaa	660
catgagcatt	tttgggatat	ctatcatgtt	aaagaaaagt	taagttcata	ccttagaaaa	720
tatccaattg	aattaaccga	ttttgcttta	gatgcggtta	aaaaatataa	ttctgataag	780
cttgaattag	tttttgatac	tggtgaatca	ctgatttgtg	atgaacttga	agatcaagaa	840
tttcagaagt	ttaagaaaaa	agtattaaat	aatttcaaat	atataaaaac	agctcatctt	900
agaaatcttt	caaactcggtg	tattgggtatc	atggaaatcac	aacacagaaa	gataacgtat	960
agaatgaagc	gacgtggcat	gtattgggtca	aagtggggaa	tctccacaat	ggcaaatatg	1020
attatacttg	aaagagctaa	cgggtttacga	gaattattttt	tccggttcttg	gagaaaggtta	1080
tacagtgaag	ataaagaagg	ttcattttagt	gcagggcgac	tttttaaaaa	gacagatgaa	1140
ttagataaat	tttctaagcc	ccttctaaaa	aatggcagaa	aatggagtat	aacaggaatc	1200
aaaacaaaaat	ag					1212

SeqID 91

aaagcaagca	gcggtgatta	tggcacaaaa	agggaaataa	tcaactgctaa	taaggataaa	60
tacagcattt	caaagatgtg	tcgctggctg	aatatgccac	gctcaagtta	ttactatcaa	120
gccgtggagt	cagtatctaa	aacggagttt	gaagaaacta	ttaaaagaat	ttttctcgat	180
agcgagtcta	gatacggatc	cagaaaaatc	aaaatatgct	tgaataacga	aggtatcaca	240
ctttcacgtc	gtcggattcg	acgcattatg	aagcgactca	atgttggtttc	tgtttatcag	300
aaagccacct	tcaaaccaca	ttctagaggc	aagaatgaag	cccctattcc	caaccactta	360
gacaggcaat	ttaagcaaga	aagaccacta	caagccttag	tcaactgactt	aacctatggt	420
cgtgtaggca	atcgtttgggc	ttatgtttgc	ctcatcattg	acctatacaa	ccgtgaaatc	480
atcggcctgt	ctcttgggtg	gcacaagacc	gctgaactcg	ttaagcaagc	catacaaaagc	540
atcccttacg	ccctgaccaa	agtcaagatg	ttccattcag	atcgtggcaa	agagtttgat	600
aatcagttaa	ttgatgaaat	attggaagcc	tttggaaatca	cacgttgcgt	tagtcagggt	660
ggttgtcctt	atgacaatgc	cgtagctgaa	agtacgtatc	gtgctttcaa	aattgaattt	720
gtttatcaag	aaacctttca	atcgtctggaa	gaactagctc	ttaagactga	aaaggcaaca	780
cttttctgta	caacattttat	aaagtgttgc	cttttcaggt	ttttaccaat	gctataa	837

SeqID 92

atgaagacaa	gaaatcgtaa	aggtgggttat	ttagcgaata	ctgcaaatga	gtacatcgac	60
tctaaacagg	caattcattg	cttgagtgtta	gaacttgaac	cgcaaattag	gtttgaagag	120
ggtcagccta	ctggggagat	tatcgcttat	aaggcttggt	tctctcaaaa	agggcttccg	180
ccttttatgg	tgaagtttga	aatgaagtg	acactaccag	catatatggt	aatgggtgaa	240
tttgagaatc	ttcaagcttg	tgagggttggg	ttcaatgttt	atttcaaggc	agacaatctc	300
aaggaggtca	aataa					315

SeqID 93

ttgtccactt	ttgattcagt	tacaggaagg	accaatcact	tggaagctta	tgaagggctg	60
aacctttctg	aaaaatttgc	catttttaagt	cacttttgaca	aacttagaaa	tgagctgcag	120
acaccatcta	ttcagctagg	ggagtttgat	agggaaatgg	aagctttttc	aatcactttg	180
ggaaatgaac	tggttgggtta	tttagaggca	aatggcagcc	cctatgagtt	gaagcgagaa	240
ttgaatcagg	cggaaatgat	ggcagtcctt	gagcttagcc	gtcaactggg	tgcaaaattt	300
tctacaaaac	tagaggagct	gggaattgat	ttgggttcat	ttcaaccaga	ccaagtcaac	360
atcttatttg	atgccgttgg	togttttcgc	ttgaaaaatg	cggacattgc	tttattaggc	420
ggttatccaa	aagcgagtgt	ttcccagcta	gctcttgcga	cagaactcct	ccagatggga	480
ctaagtcatg	ataaggtaga	atttttctta	accagtcagc	ttcagttaga	ggatatgcga	540
caggctcgctt	ttgctttcct	acatgaaagc	ttgaccagag	aagaagcaga	gcaatttgaa	600
acagaccgct	ttcgtcatat	aagcttaaac	tttcgagaat	ggcgagaact	tctagaaaag	660
caagagccag	aaatgggtga	gatgtcagac	gtcagcccgc	ttgttcggga	agtcttgcat	720
cattatccac	ttggttcaag	ggtcacttat	aaaggacagg	agtttgagat	cttgtctatt	780
gaagctgcgg	acatggataa	tctgattcga	atagagcttc	aaaatgattt	ttcatatctc	840
attgaacaaa	atcccgttct	ctattttocaa	aacttggcag	aaatcaggca	agttcttcat	900
ttgtctcggt	cggaaaattgt	agaaaagagag	gaacaacctg	aggaagaatg	gactctcttt	960
togtttatgg	atgaggggac	agaggataac	gaaaaggaac	ctgagattgt	ttttgaatct	1020
accgataaag	ttgttacatt	agatagtcag	ccagcacaag	taagtgagac	tatatccgaa	1080
tcagttcctg	aaaccaaaga	ggtgattgaa	gcagaacaag	caatagcagt	tgatttttagc	1140
tttctgaag	atttgactaa	tttttaccct	aaaacagcta	gggataaagt	agtggcgaa	1200
ctcgtagcta	ttcgtcttgt	aaaagaatta	gaaagtgtca	atcaatcagc	aacaccta	1260
gaacaagaaa	ttcttgccaa	atatgtgggt	tgggggtggtc	ttgccaatga	attctttgat	1320
gagtacaatc	cgaagttttc	taaggaaaaga	gaggagtgtga	aaactctcgt	ttctgataaa	1380

gagtattccg	atatgaaaca	atcatctcta	acggcctact	atacggatcc	gcttttaatt	1440
cgtcagatgt	ggtctaagtt	agaacaagac	ggcttttagt	gtggaaaaat	attagaccca	1500
tcaatgggaa	cagggaaatt	ctttgcggct	atgccagctc	atttgaggga	aaagagttag	1560
ctgtgtgggg	ttgagttaga	tactatcaca	ggagcgatag	ctaagcagct	tcattcaaatt	1620
gtccatattg	aagtaaaggg	atgttgagacg	gttgctttta	atgataatag	ttttgatttg	1680
gttattttcaa	atgttccctt	tgccaatatc	cgtatcgcgg	ataatcagta	cgataagccc	1740
tatatgattc	atgactactt	tgtcaagaaa	tctcttgatt	tggtacatga	tggtgggcaa	1800
gtagccatta	tttcctccac	aggaaccatg	gacaaaacga	cagaaaaatat	tctccaagat	1860
attcgtgaga	cgacggattt	tcttggtggc	gtgcgtttgc	cagatacggc	ttttaaggcc	1920
attgcaggta	caagtgtgac	aacggatatg	cttttctttc	agaaacatct	gaacaaaggc	1980
tatcaagcag	atgacattgc	cttttcagggt	tctgttcggt	atgacaagga	cgagcgtatt	2040
tggctcaatc	cctactttga	tggggagtat	aatgcccagg	ttcttggaag	gtatgagatt	2100
aaaaacttta	acggtggaac	acttttcggtt	aaggaaacga	ctgataacct	gattgcgagt	2160
gttcgagaag	ccttgcaaca	tgtaaaagca	ccaaggggta	ttgataaaac	agaagtcagt	2220
attaactcgg	atgtgattgc	aagacagggtc	atagatacca	ccattccacc	tgaaattaga	2280
gaaaaccttg	aacaatatag	ctatgggttac	aaaggttcta	ccattttatta	tcgtgataat	2340
aaggggatcc	gtgttgaggac	aaaaacggag	gaaatttagct	attatgtgga	tgatgaggga	2400
aacttttcagg	cttggggagt	caagcattca	caaaaaacaga	ttgaccgttt	taataaactta	2460
gaagtcacag	atagcacagc	tcttgatggt	tatgtgactg	aagaacctgc	gaaacgtggg	2520
caattttaaag	gatattttcaa	aaaggcgggt	ttttatgaag	ctcctttgtc	tgaaaaagaa	2580
gtggcacgga	ttaaaggaat	ggtagatatt	cgcaatgcct	atcaagaggt	cattgctatt	2640
caacgcaatt	atgattacga	taagaatgag	tttaaccgct	tgtaggaaa	cctcaatcgc	2700
acctatgata	gctttgtcaa	acgctatggc	tttttgaaca	gtccagttaa	ccgaaattta	2760
tttgatagtg	atgataagta	ttcgctttta	gctagtctcg	aagatgaaag	tcttgaccca	2820
agtgggaaga	cggtcattta	tacgaagtca	ctggcttttg	aaaaagcctt	ggtccgtcct	2880
gaaaaaatgg	ttaaagaggt	gtcaaccgct	cttgatgcac	tcaactccag	tcttgccgat	2940
ggtcgtggag	ttgactttga	ttacatggct	tccatctatc	aaacagcatc	taaggcagct	3000
ttgattgagg	agctggggaga	tcagattata	ccagatccag	aaagttattt	aaaaggacag	3060
ctgacctatg	tatctcgcca	ggagttttta	tcaggagata	ttgtgacaaa	attagaagtt	3120
atggacttac	tgtaaagca	agacaatcat	gattttaact	gggcgcatta	tggtaatattg	3180
ttagaaagtg	ttcgtccagc	acgagtgatg	ttggcagata	ttgattatcg	aattggttca	3240
cgttggtatc	cttttagctgt	ttatggaaaa	tttgtccaag	aagcctttat	ggggaagaat	3300
tatgacttaa	gggtcacaga	agtgggaag	gtcctctctg	tcagcccgat	tgatgggacg	3360
atggaatttc	cggcacgggt	tgccctatacc	tactcaacag	cgacggatag	aagcctgggt	3420
gtagcaggct	cacgctatga	tagtggctcg	aaaatctttg	agaatctgct	taactccaat	3480
cagccaacca	tcacgaagca	gattcaagag	ggagataaga	aaaagaatgt	gacagatgtg	3540
gagaagacaa	ccgttctgcg	tgctaaagaa	gcacaaatcc	aagacctctt	tcaagatttt	3600
gtcgcaagct	atcctgaagc	ccaacagatg	attgaggata	cctataatag	tctctataat	3660
cgtaccgtct	ctaaagttta	tgatggcagc	cgtttgga	ttgatgggtt	ggctcaaaat	3720
atttcgcttc	gtcctcatca	aaaaaatgcc	attcagcgaa	tcgtggagga	aaaacgggct	3780
cttttagctc	atgaagtggg	ttcaggcaca	actttaacca	ttcttgaggc	aggcttttaa	3840
ctgaaagagt	taggtatggt	acataaaccg	ctttatgtgg	taccttctag	cttgaccgct	3900
cagtttggtc	aagaaatcat	gaagtctctc	ccaacgaaga	aagtctacgt	gacgacaaag	3960
aaagattttg	ccaaagctcg	gcgcaagcag	tttgtctcac	gtattattac	aggggattac	4020
gatgccattg	tcacggggga	ctcccagttt	gaaaaaatcc	ccatgagtc	ggaaaaacag	4080
gtgacttata	ttcaagataa	gttggaacaa	ttacgggaga	taaagcaagg	aagcgatagt	4140
gactacacag	tcaaagaagc	ggagcgttcg	attaaaaggt	tggaaaacca	attggaagaa	4200
ctccagaaac	tagatcgaga	tacctttatt	gaatttgaaa	atcttggcat	tgattttctc	4260
tttgtggacg	aagcccatca	tttcaaaaaat	attaggccga	ttactgggtc	gggaaatgta	4320
gcgggaatta	ccaacacgac	ttctaaaaaag	aacgtggata	tggaaatgaa	agttagacag	4380
attcaggcag	agtatggaga	tagaaatgtc	gtttttgcga	caggaacgcc	ggtgtctaatt	4440
tccattagt	aactctatac	tatgatgaac	tatattcagc	cagatgtcct	agaacgctac	4500
caagttttcta	acttttgactc	ctgggttgga	gcttttgcca	atatcgaaaa	ttcgatggag	4560
ctagcgccaa	caggagataa	gtatcaaccc	aagaaaacgg	ttaaaaagtt	tgtgaattcta	4620
cctgaactca	tgcggtttta	taaagaaacc	gctgatattc	aaacgtcaga	tatgttggat	4680
ttacctgtac	ctgaagccac	agtcattgcg	gtggaaagtg	aactcacaga	agctcagaaa	4740
aactaccttg	aagaattggt	ggaccgttca	gatgcgatta	aatcaggaag	cgttgaccct	4800
agtgtcgata	acatgttaaa	ggtgataggc	gaagccagaa	agctagccat	tgatatgcgt	4860
ttgattgacc	ctgcctatac	cttatctgac	aatcagaaga	ttatgcaagt	agtggataac	4920
gtggaacgga	ttacacgtga	gggcaaaagg	gataaggcta	cacagatgat	ttctctgac	4980
attggcacgc	ctaaaagtaa	agaagaagga	tttgatgtct	ataatgaatt	gaaagccctc	5040
ttagttgacc	gaggaattcc	aaaagaagaa	attgcctttg	tccatgaagc	taatacggat	5100
gagaagaaaa	attctttgtc	acgaaaggtc	aatagtgggg	aagtaaggat	tctcatggct	5160
tcaactgaaa	aaggaggaac	aggattaaac	gtgcaagcac	gcataagagc	tgttcaccat	5220
ttagacgttc	cttggcgctc	ctcagacatt	cagcaacgca	atggacgttt	gattagacaa	5280

ggaaatcaac	atcagaatgt	agagattttat	cattatatta	ccaaagggttc	atttgataac	5340
tatttggtgg	ctacacaaga	gaataagttg	cggttatatta	aacaaattat	gacttcaaaa	5400
gatcctgttc	ggtcagcaga	agatattgac	gagcaaacca	tgaccgcttc	agatttcaaa	5460
gcgttagcta	ctggcaatcc	ctatctcaaa	ctcaaaatgg	agtttagagaa	tgaattgacc	5520
gtcttagaaa	atcagaaaacg	tgcttttcaat	cgctccaaag	atgaatacag	gcacactatt	5580
tcctattgcg	agaaaaactt	acctgtttatg	gaaaaacgat	taaggcagta	tgacagagat	5640
attgagaaat	cacaagcaac	gaagaatcaa	gagtttatca	tgcggtttga	taaccagaca	5700
attgacaatc	gcagcgaagc	tggggatttat	ttacgaaaac	tcatcaccta	taatcgttcc	5760
gaaaccaaaag	aagtcagaac	cttagcgacc	tttagaggct	ttgagcttaa	aatggctaca	5820
cgaagtccctg	gtgaaccctt	gtctgacatg	gtgtctctaa	ctatttcagg	ggataaccag	5880
tattcagttt	cccttgattt	aaaatcagac	gtgggaaacga	ttcaacggat	taacaacgcc	5940
attgaccata	tcctagagga	taaggaaaag	acagaagaga	tgacaaacaa	cctcaaagat	6000
aagctagcag	tcgcaagagt	tgaagttgag	aaagtccttg	caaaggaaga	ggaatatcag	6060
ttggtaaagc	ccaagtatga	tgtacttgcc	ccattagtgg	aaagagaagc	agacttagaa	6120
gaaattgacg	tagcactttc	ccaatttagt	agctctgacc	catgcttgaa	aaaagatcaa	6180
cagttagtc	ttgacattta	a				6201

SeqID 94

atgaccacaa	aatgcaatca	tcatttttctc	atcaatcagg	agaaaggcga	aaagtatggt	60
tttcgtaaaa	gtaagcaata	tcgcacgctg	tgttcggttg	ctttaggaac	agtttgtgatg	120
gcattcgtag	ctttggccgg	accgatggtg	caggcggatg	aagtagggag	aactggtgcg	180
acaagtgtac	agacggaaac	gaatcctgca	acaaatttaa	aagaaaaatca	gccaagtccg	240
attgcggaac	aaaaagatat	tcttgacgca	accggtcaat	caactggaac	ggtgacagtc	300
actgttccac	atgataagg	gacacaagct	gtcgataagg	caaagaccga	aggaataaaa	360
gcagtacaag	acaagccgat	ggacttaggc	aatacagtat	ccgcagctga	aaccagccaa	420
caactcaaaa	aggcagaaga	agatgccaca	aaccaaacia	caactatttc	taaaactggt	480
gaaatctaca	agtctgataa	agcaacttat	gaagctgaaa	agaagtgggt	agagaagcgt	540
aatgaagagt	taactgctgc	ttatgataag	gcagaacaaa	cagggactgg	cttaaacctat	600
tcggttgata	cgactgtttc	agaattgaag	tcgcaagacc	aaaacgctca	tgtgaccgtg	660
aacacacaaa	cagtaaaatc	aggagatggg	acgagtgttt	caggctatca	ggagtacgtc	720
aagtctgttg	cggccattga	taagaagaat	aaagcgaact	tagctgatta	tcggactaag	780
aaacaagccg	cagacgctgt	tgtggctaag	aatcaactca	ttcaaaaaga	gaatgaagct	840
gggcttgcta	aggcaaaagc	agaaaatgaa	gcgattgaca	gacggaataa	agaagggcaa	900
aaagctgttg	atgaagcaaa	taaggctggg	caagccgag	tagagcaagc	gaaccaagaa	960
aaacaaaagc	aggccgcaaa	ccgtgtcttt	gaaattgcga	caattaccaa	acggaataaa	1020
gaaagagaag	aagtcgcaaa	gaaagaaaat	gcagcgattg	atgcttataa	tgcgaaagaa	1080
tggatccgct	ataagcggga	tttagcaaac	atctcaaaag	gggaggaagg	ctacatttca	1140
gaagcccttg	cgcaggctct	agattttaa	catggcgaac	cgcagggtcaa	acatggtgca	1200
gggtactcgaa	atccagatcg	aatcatttca	aaggagatg	ccatgttggg	tggctattct	1260
aacattcttg	attcaacggg	tttctttgtc	tacaatcact	ttaaaacagg	tgaaacgctg	1320
aactttacct	atcaaaaatct	gaagcatgca	cgttttgatg	ggaagaaaat	tacagccata	1380
acttatgata	ttaccaatct	ggtttcacca	actggaacca	atgcggtgca	gttagttggt	1440
ccaaacgacc	caacagaagg	ctttattgct	tatcgcaatg	atggcgctgg	aaattggcgg	1500
acagataaga	tggagttccg	tgtcaaagct	cggtatttct	tagaagacgg	ttcacaagtg	1560
acctttacta	aagaaaaacc	aggtgtcttt	acccactcgt	cactcaatca	taatgatatt	1620
gggcttgaat	atgttaaaga	ctcatcagg	aaatttgctc	ctattcatgg	ttcaagtgtg	1680
caagtaacca	atgagggtct	agccggttcg	ttaggttcaa	accgagcgag	tgacttgaag	1740
ttgccagaag	aatgggatac	gacttctagt	cgctatgctt	ataaaggagc	gattgtatca	1800
acagtcacat	cggggaatat	ttataccgta	acctttggcc	aaggagatat	gccaacccaa	1860
gtgggaggga	agacctattg	gtttgcttta	aatactttgc	cagtcgcaaa	aacagtgact	1920
ccctacaatc	caaagactca	tgtaaagcca	cagctggatc	cagttcctga	accgataaaa	1980
gttacaccag	aaacttatac	tcctaaaatc	tttactcctg	aaaaaccagt	aacctttact	2040
ccaaaatcag	tagaaaaagt	gccccaacct	agtttgacct	taacaaaagt	cacactacca	2100
acaaatctga	agctagaacc	attaccocaa	gctocacaaa	agccaaccgt	tcattaccac	2160
gattacctct	taaccacaac	acccgctatc	gcaaaaagaag	tgatgaatgt	tgacaaagtt	2220
aatcttcatg	gtaaacaggt	ggctaaggat	tccactgtta	tttatccctt	gacagtagat	2280
gttttatctc	caaatcgctt	caagataacc	agtcttatct	ttgaagatta	tctgcctgct	2340
ggttatgcgt	ttgatatgac	gaagacacaa	gcggagaata	gogactatga	cttaaccttt	2400
gataaaaata	agaactttgt	gaccttgaa	gcgaagata	gcttacttca	aacgttgaat	2460
aaagagttaa	acaagtctta	tcaactgtct	gctocaaaa	tttatggttc	agttcaaaat	2520
gatgggcca	cttattctaa	tagctataaa	ctccttatta	acaaggacac	cccaaacacc	2580
tatacgggta	tttcaaacgt	agttagaatt	cggaactccag	gagacgggtga	aacgaccagc	2640
cgaatccggc	ctaaaaagga	caatgaaaat	gcggacgggtg	tgttgataaa	tgatacgggt	2700
gttgctctta	gtacaaccaa	tcattaccgt	ttgacctggg	atttggtatca	gtacaagggg	2760
gatacttctt	caaaagatac	cattgcacga	ggattccttt	ttgtagatga	ctaccagaa	2820

gaagcacttg	acttggtaga	taaagggaca	gttatcacca	cccttgatgg	taaagctggt	2880
tcaggtattt	ctgtatcacg	ctatacatcc	cttgataaaag	cacccaaaaga	gctacaagat	2940
aaattagctc	gtgcgaacat	ttcgccaaaa	ggagcgttcc	aggtctttga	accggacaat	3000
catcaagcgt	tttacgatac	ttacgttaag	actgggcagt	cttttagccct	tctcacaaaa	3060
atgaaggtaa	aagatagttt	gtacggtcag	actgtcagat	acaaaaataa	agcctacca	3120
gttgatTTTT	gcaatggcta	tgaactaag	gaagtcgtca	atacagtcgt	tcatccagag	3180
cctaagaaac	aaaatctcaa	taaggacaag	gtggacatca	atggcaaaagc	gatgcttgct	3240
ggctcccaaa	acttctatac	gctttcttgg	gatttagatc	agtatcgtgg	cctacaagcg	3300
gataagagtc	agattgctca	aggcttttac	tttgtggacg	attatcccga	agatgttctt	3360
cttctcgaca	caaaagccat	tcaaattatg	acgaaagacg	ggaaagctgt	taaaggaatg	3420
gagataaaaa	cctatcatca	actctcagat	gctccaaagg	aattgcaggc	agctcttgcc	3480
aaacgtaata	tcacgccccaa	aggcgctttt	caagtcttta	tgcctaaaaga	tccacaagct	3540
ttttataaaag	cttatgtgac	aactgggtcaa	aacttgacta	ttgtgaatcc	gatgacggtt	3600
cgtgaagcag	tatacaactc	agggaagtct	tatgataatg	tggcctatca	agtggacttt	3660
ggacaggcct	atgaaacgaa	tatagtgacc	aatcacgtgc	caacagtaaa	cccgcataag	3720
tccaataacca	ataaagaagg	tgtgtcaata	gaaggtaaga	cagtccttcc	gaatacggtc	3780
aactactata	aaattgttct	agattatagt	cagtacaaga	atatgattgt	gacagatgat	3840
gtcctcgta	aagggtttta	tatggtggat	gattacccag	aagaagcact	tactcctcat	3900
ccagatggga	ctcaagtgat	ggatcagaac	gggaaatttg	tcagaggcct	gtctgttcga	3960
acttacgcaa	gtttggcaga	tgcaccgaaa	gcagtaacaag	aagcaatgaa	atctcgaaat	4020
ttcattccta	aaggagctat	tcaggtcttt	caggcagatg	acccaaaaac	tttctttgaa	4080
acttatgtga	aaacaggaca	aaaattgggt	gtgacaacac	cgatgacagt	gaagaatgaa	4140
cggattcaaa	caggcggtca	gtatgagaat	acagcttatc	agattgattt	tggcatcgct	4200
tatgtaacgg	aaacagttgt	gaataatgta	ccaaaattag	aacctcaaaa	agatgtgggtc	4260
attgacttat	ctcaaaaaga	taagagttta	aacggaaaag	caatcgcttt	ggatcagggtc	4320
tttaactacc	gcttggtagg	ttcacttatc	ccacgcaatc	gtgcgacagc	cttggtggaa	4380
tacagtttta	aagatgacta	cgatgaaaag	cacgatgaat	ataaagggtgt	ttataaagcc	4440
tatactttgc	gtgatgtaac	cttaaaagat	ggcacagtat	taaagcaggg	gacagaagtg	4500
acgaaataca	ccttacaagg	tgttgataag	gcataaaggaa	cgattgcgat	togttttgat	4560
acagcttttt	tggaaaatat	agctgatgaa	tcagagtttc	aggctgagct	ttatcttcag	4620
atgaaacgca	ttgcttcagg	tgatgttgaa	aatacagtta	ttcatagtgt	caatggttat	4680
aatattcgct	ctaacacggg	taagaccaca	accccaacaac	cagagtcacc	gactcctgat	4740
aaccaccgt	cacccaacc	gccagttcca	accacagaat	cccagttca	agctagtgtc	4800
ctaccaagta	caggggaaag	tcaatccctt	ttggcgctca	ttggaggagg	tctcctgctt	4860
ggcctcgctt	acggactttc	taaacgaaaa	aaggagaaaa	actaa		4905

SeqID 95

atggcaata	ataattttta	taatcgtgac	ccttttggaa	atatggatga	tatttttaat	60
tctctaattg	gaaatatggg	gggtataat	agtgagaata	aacgatactt	aatcaatgga	120
cggaagtta	ctcctgaaga	attcagtcac	tatcgtcaaa	ctggaaaact	cccgggtcaa	180
gagctaaata	accaaatac	tctacaacac	caagctctcg	cagatagtg	tttgactaaa	240
ttaggaaacta	atttaaccga	tcaagcacgt	cagcatttgc	tagatccagt	tattggaaga	300
aacaaagaaa	ttcaggaaac	tgcagaaatt	ctagctcgct	gtactaaaaa	taatcctggt	360
ctagttgggtg	atgcagggtg	tggtaaaaca	gctgttattg	aagggttggc	acaagcaatt	420
ataaatgggtg	atgtccctgc	tgtatcaaaa	aataaagaaa	tcatttcgat	agatatctct	480
agccttgaag	ctggcaccca	atataggggt	agttttgaag	aaaatattca	aaatatcata	540
aaagaagtta	aggaaacagg	aaatattatt	ctcttcttgg	atgaaataca	ccaaatatta	600
ggagccgggtt	caactgggtg	tgatagtggt	tctaaggggc	tcgcagatat	acttaagcct	660
gcactttcac	gtgggtgaatt	aacgggttata	gggtgcaacta	ctcaagatga	atatcgtaac	720
accattctca	agaatgctgc	cttagcacgc	cgctttaacg	aagttaaagt	caatgcacct	780
tctgcacaag	atactttcaa	tatccttatg	gggataagaa	acctctatga	gcaacatcat	840
aatgttggtt	tacctgactc	tgttttgaaa	gcagctgtag	atztatctat	tcaatacata	900
ccacaaagaa	gtctccctga	taaagcaatt	gaccttattg	atatgactgc	tgcacaccta	960
gctgcgcaac	atcccgtaac	tgaccttaaa	tccttagaaa	aagaaaatcg	tgcgcaaaga	1020
gacaaagcaag	aaaaagctgt	caatactgaa	gattttgaag	aagctcttaa	ggtcaagaca	1080
cgcattgaag	agttacaaaa	ccagattgat	aatcataccg	aaggacaaaa	agtcactgca	1140
actatcaatg	atatcgctat	gtcaattgag	cgtctaaactg	gagttcctgt	atcaaatatg	1200
ggtgctagtg	atattgaacg	cttaaaagaa	cttggcaatc	gtctaaaagg	taaagtcat	1260
ggtcaaaatg	atgctgttga	ggcagttgca	agagctattc	gccgaaatcg	tgctggtttc	1320
gatgatggta	atcgctccgat	tggtagcttt	ctatttcttg	gaccaactgg	agttggtaaa	1380
actgagctag	caaagcaatt	agcttttgat	atgttcggat	caaaggatgc	tatcgttaga	1440
cttgatatgt	ctgaatataa	tgatcgtaact	gcagttttota	agctaattgg	agcgactgct	1500
ggttacgttg	gttatgacga	caatagtaat	acactaacag	aacgtatccg	tcgaaatcct	1560
tattctattg	ttcttcttga	tgaatcgaa	aaagctgacc	cgaagttat	cacgcttctc	1620
cttcaagttc	tagatgatgg	tctgttaact	gatgggtcaag	gaaacactat	taacttttaa	1680

aatactgttta	tcattgcaac	ctcaaagtga	ggttttggaa	acgaagcatt	tacaggtgac	1740
agcgataaag	acttgaaaat	tatggaacga	atttctccat	atttccgtcc	agaattttcta	1800
aatcggtttca	atgggtgttat	tgaattctct	cacctaagca	aagatgactt	aaacgaaaatt	1860
gtagattttga	tgcttgatga	agttaaccaa	acaattggca	aaaaaggaat	tgaccttggtg	1920
gtagatgaaa	atggttaaata	acacttaatt	gacctgggtt	atgacgaagc	aatgggagta	1980
cgtccatttgc	gccgtgtcat	cgagcaagaa	attcgagatc	gcatcacaga	ctactatctc	2040
gatcatacag	atggttaaaca	cctaaaagct	aatttgcgaag	atggccaaat	cgtcattttct	2100
gaaagataa						2109

SeqID 96

atggggaagat	ttaaagaact	tttagagagt	aaaaaagctc	tcatectaca	cggtgccttg	60
gggaccgagc	ttgagagtag	aggttgtgat	gtttctggta	aactttggtc	agacaaatat	120
ctgattgagg	atccagcagc	tattcagacc	attcatgaag	attatattcg	tgctggcgct	180
gatattgtga	cgacatcaac	ttatcaggcg	actttacaag	ggctagctca	agttgggtgc	240
tctgaaagtc	aggcagaaga	cttgattcgc	ttgactgttc	agttggcaaa	agctgtgcgt	300
gagcaagttt	ggaaaaagttt	gacaaaaagaa	gaaaaatcag	aaagaatcta	tcctttgatt	360
tctggggatg	ttgggtcccta	cgctgccttt	ttggcggacg	gttctgagta	cacagggctc	420
tacgatattt	ataaggaagg	tctcaaaaat	ttccatcgcc	atcgtattga	gcttctttta	480
gatgaggggtg	ttgaccttct	ggcacttgaa	accattccaa	atgctcagga	ggctgaggct	540
cttattgagc	tacttgtcga	ggatttccct	caggttgagg	cttatatgtc	attcacctct	600
caagatggta	agaccatctc	agatggtagt	gctgttgccag	gcttggcgaa	agctattgat	660
gttaggccac	aggctcgtggc	gctgggcatt	aactgttcaa	gtccatcggt	agttgctgat	720
ttcttgcaag	caatagcaga	gcagacggac	aagcctcttg	tgacctatcc	aaactctgga	780
gagattttatg	atggggcaag	ccaatcttgg	caatctagcc	gagatcattc	acacacccta	840
cttgaaaata	caagtgactg	gcaaaaactt	ggcgcccaag	ttgtcggagg	ttgttgccga	900
actagaccag	ctgatattgc	tgacctctca	gaacatttga	cataa		945

SeqID 97

atgaaaatag	gaattgataa	gattgggtttt	gcaaccagtc	aatatgtcct	tgaaatgact	60
gatttggtcta	ttgctcgcca	agttgaccct	gaaaaattca	gcaagggatt	attgttagat	120
tcacttagta	ttacgccagt	tacagaagat	atcgttacac	ttgcagcctc	tgcaagtaata	180
gatatttttat	ctgatgagga	caaagaaact	attgatattg	tgattgtcgc	tacagaatca	240
agtatcgatc	agagtaaggc	ggcttctgtc	tatgtacatc	aactttttaga	gattcaacct	300
ttcgcaaggt	cattcgagat	gaaagaagca	tgctatagcg	caactgctgc	tcttgattac	360
gctaaattac	atgtagaaaa	acatccagat	tctaaagtat	tagtgatagc	ttcagatatt	420
gctaaatatg	gcattaaatc	tactggagaa	tccactcaag	gtgcaggcag	tatcgctatg	480
cttattagtc	aaaacccatc	cattctagag	ctaaaagagg	accgtctagc	gcaaaaccgt	540
gatattatgg	acttttggcg	accaaattat	tctgatgttc	cttatgttaa	tggcatgttt	600
tcaacaaaac	aatatctaga	tatgctaaaa	actacttgga	aagaatatca	aaaacgtttt	660
aatactagtc	taagtgaata	tgctgctttt	tgtttccata	tcccttttcc	aaaattagct	720
ttaaagggtc	ttaataaaat	tctagataat	aacctagatg	aacaaaagaa	agctgaacta	780
caagaaaatt	ttgagcactc	tattacttat	agtaagaaaa	ttggaaattg	ctatactggc	840
tcattgtatc	taggaacttct	atcgttacta	gaaaatagtc	aaaattttaa	agcaggtgat	900
caaattgcct	tcttttccata	cggtagcgga	gctgttgctg	aaatttttac	cggtcagtta	960
gtagacggct	acaaaaataa	acttcagagc	gatcgtatgg	atcaactcaa	taaacgtcaa	1020
aaaattacag	taactgagta	tgagaaactc	ttctttgaaa	aaacaatcct	agacgaaaat	1080
ggaaatgcca	acttcaacac	ctaccgtact	ggcacttttt	ctctagactc	tatttgcgaa	1140
catcaacgta	tctacaagaa	aattaataat	ttaa			1173

SeqID 98

atgaaaagtg	cttatatctt	ttttaatcca	aaatctggta	aagatgaaca	agcattggca	60
caagaagtaa	aatcttattt	aatagaacat	gattttcaag	acgattatgt	tcgtatcatt	120
acaccttcat	ctggttagga	agctgtcgcc	ttagcaaaaa	aagcatcaga	agaccataatc	180
gacttgggtta	ttccttttagg	gggagatggc	actattaata	aaatctgtgg	tggtgtctac	240
gctgggtggtg	cttatccctac	tatcggacta	gtacctgccc	ggaccgtcaa	taacttttca	300
aaagctttga	acatcccaca	agagaggaat	ctcgctcttg	aaaaccttct	aaacggctcat	360
gtaaagtcgg	tagatatctg	taaagttaac	gaogattaca	tgatttagcag	tttaacactt	420
gggctccttg	ctgatattgc	tgctaattgtc	acttctgaaa	tgaagcgtaa	attaggacct	480
tttgctttcg	taggtgatgc	ctaccgtata	ttaaagcgta	atcgatcata	ttctattact	540
cttgcttacg	ataataatgt	acggtcttta	cgcaagcggt	tactacttat	taccatgacc	600
aattcgattg	cgggtatgcc	agccttctct	ccagaagcaa	caattgatga	tggacttttt	660
agagtctaca	ctatggaaca	tattcacttc	ttcaaattat	tggtgcatct	aagacaattt	720
cgtaagggag	atttttagtca	agcaaaggag	ataaaacatt	ttcataccaa	taatctgact	780
atttcaactt	ttaaacgttaa	aaaatcagct	atccctaaag	ttcgtattga	tggcgatcca	840
ggtgaccaat	tgctgttaaa	agttgaagtc	atccctaaag	ccttaaagtt	tatcattcct	900

aactcattac cataa

915

SeqID 99

atgacaacat	ttactgctaa	atattattgac	caagagtggg	aagtcccagt	agaatcaggt	60
cgctaccata	tgattggttg	ggaattttgt	ccttatgcac	aacgtccgca	gattgcacgc	120
caactgcttg	gtttggataa	acatatttct	atcagttttg	tggtgatgt	tccaagtgat	180
ataggactta	tttttagcca	accagaacag	gttactggtg	ctaagtcgct	togtgatatt	240
tatcatttga	ctgacccgac	ctacaaaggt	ccttatacta	tcccaatttt	aattgacaag	300
actgataatc	gtattgtctg	taaggaatct	gcagatatgc	ttcgactttt	tactacagat	360
ttctctgatt	tgcacaaaga	ggatgctcct	gtccttttca	gccaaagaaac	tgcttcactt	420
attgataatg	atattaaaga	cattaataat	aacttccaaa	gcttaatgta	taagtttagct	480
tttcttgata	aacaagcaga	ttatgatact	tatagtaagg	aattcttcac	ttttctagat	540
caaaaagaac	acttactagg	acaacgtcct	ttcttgctcg	gagataatct	aagtgagggt	600
gatattcatt	tctttacacc	attagtcgag	tgggataattg	ctgggcgtga	tcttctacta	660
cttaactcaga	aagcgctaga	agactaccga	aataattttt	cttggggttaa	aactttatac	720
aatgacttta	atttaaaaaac	attaaccaat	ccacaatcca	taaaaataaa	ctattactta	780
ggcaaatattg	gaagagctgt	tcgtcatcat	accatcgtac	caacaggtcc	aaatatggta	840
aatgggaaa	aataa					855

SeqID 100

atgaaaaaga	aaattatttt	gaaaagtagt	gtccttggtt	tagtcgctgg	gacttctatt	60
atgtttccta	gcgcattcgc	tgaccaagtc	ggcgtccaaag	ttataggcgt	caatgacttt	120
catggtgcac	ttgacaatac	tggacagca	aatatgcttg	acggaaaagt	tactaatgct	180
ggcactgctg	ctcaattaga	tgcttatata	gatgatgctc	aaaaagattt	caaacaaact	240
aaccctaattg	gtgaaagcat	tagagttcaa	gctggtgata	tgggtggagc	aagtcacagct	300
aactcagggc	ttcttcaaga	tgaaccaacc	gttaaaacat	ttaatgcaat	gaatgttgag	360
tatggcacat	taggtaacca	tgaatttgat	gaaggtttgg	cagaatacaa	togtatcggt	420
actggaaagg	cccctgctcc	agattctaata	ataaataata	ttacgaaatc	ataccacacac	480
gaagctgcaa	aacaagaaat	tgtagtggca	aacgttattg	ataaagttaa	caaacaaatc	540
ccttacaatt	ggaaacctta	cgctattaaa	aatattcctg	taaataacaa	aagtgtgaac	600
gttggtcttta	tcggaatcgt	taccaaagac	atcccaaacc	ttgtcttacg	taaaaattat	660
gaacaatatg	aattttttaga	tgaagctgaa	acaatcgtaa	aatacgccaa	agaattacaa	720
gctaaaaatg	tcaaggctat	tgtagtccct	gtcatgtac	ctgcaacaag	caaggatgat	780
attgctgaag	gtgaagcagc	agaaatgat	aaaaaagtca	atcaactctt	ccctgaaaat	840
agcgtagata	ttgtctttgc	tggacacaaat	catcaatata	caaatgggtct	tgttgggttaa	900
actcgcattg	tacaagcgct	ctctcaagga	aaagcctatg	ctgacgtacg	tgggtgctcta	960
gatactgata	cacaagattt	cattgaaacc	ccttcagcta	aagtagttgc	agttgctcct	1020
ggtaaaaaaa	caggtagtg	cgatattcaa	gccattgttg	accaagctaa	tactatcggt	1080
aaacaagtaa	cagaagctaa	aattgggtact	gccgaggtaa	gtggcatgat	tacgcgttct	1140
gttgatcaag	ataatgttag	tccagtaggc	agcctcatca	cagaggctca	actagcaatt	1200
gctcgaaaaa	gtgggcaga	tatcgatttt	gccatgacaa	ataatgggtg	cattcggtgt	1260
gacttactca	tcaaacacaga	tggacaacatc	acctggggag	ctgcacaagc	agttcaacct	1320
tttggttaata	tcttacaagt	cgtcgaaatt	actggtagag	atctttataa	agcaactcaac	1380
gaacaatacg	acaaaaaaca	aaatttcttc	cttcaaatag	ctggtctgag	atacacttac	1440
acagataata	aagagggcgg	agaagaaaca	ccattttaaag	ttgtaaaagc	ttataaatca	1500
aatggtgaag	aaatcaatcc	tgatgcaaaa	tacaaattag	ttatcaatga	ctttttatcc	1560
gggtggtggtg	atggctttgc	aagcttcaga	aatgccaac	ttctaggagc	cattaatccc	1620
gatacagagg	tatttatggc	ctatatcact	gatttagaaa	aagctggtaa	aaaagtgagc	1680
gttccaaata	ataaacctaa	aatctatgtc	actatgaaga	tgggttaatga	aactattaca	1740
caaaatgatg	gtacacatag	cattattaag	aaactttatt	tagatcgaca	aggaaatatt	1800
gtagcacaag	agattgtatc	agacacttta	aaccaaaca	aatcaaaaatc	tacaaaaatc	1860
aacctgttaa	ctacaattca	caaaaaacaa	ttacaccaat	ttacagctat	taacctatg	1920
agaaattatg	gcaaacctac	aaactccact	actgtaaaat	caaaacaatt	acaaaaaaca	1980
aactctgaat	atggacaatc	attccttatg	tctgtctttg	gtgttggact	tataggaatt	2040
gcttttaata	caaaagaaaa	acatatgaaa	taa			2073

SeqID 101

atggcatata	tttggcttta	tttgaaaagg	taccccaatt	ggttatggct	tgatttacta	60
ggagctatgc	ttttgtgac	ggttatccta	ggaatgcca	cagccttagc	gggtatgatt	120
gataattggc	ttacaaaagg	tgatcggaat	ggagttatc	tgtggacgtt	catcatgttt	180
atatttgggt	tactaggtat	tattgggcgt	attacgatgg	cttacgcac	tagtcgctta	240
acgacaacaa	tgattagaga	tatgcgtaat	gatagtgatg	ctaagcttca	agaatactcc	300
catcatgaat	atgaacagat	aggtgtatct	tcactagtga	cacgtatgac	aagcgatact	360
tttggtttga	tgcaatttgc	tgaaatgtct	ttacgtttag	gcctagtaac	tcctatggta	420
atgattttta	gcgtggttat	gatactaatt	acgagtccat	ctttggcttg	gcttgtagcg	480

gttgcgatgc	ctcttttggg	aggagtcggt	ttatatgtag	ctataaaaaac	aaaaccttta	540
tctgaaagac	aacagactat	gcttgataaa	atcaatcaat	atgttcgtga	aaattttaaca	600
gggttacgcg	ttgttagagc	ctttgcaaga	gagaattttc	aatcacaaaa	atttcaagtc	660
gctaaccaac	gttacacaga	tacttcaact	ggctctttta	aattaacagg	gctaacagaa	720
ccacttttcg	ttcaaattat	tattgcaatg	attgtggcta	tcgtttgggt	tgctttggat	780
cccttacaaa	gaggtgctat	taaaataggg	gatttagttg	cttttatcga	atatagcttc	840
catgctctct	tttcattttt	gctatttgcc	aatcttttta	ctatgtatcc	tcgtatgggtg	900
gtatcaagcc	atcgatttag	agaggtgatg	gatatgccaa	tctctatcaa	tcctaatgcc	960
gaaggtgtta	cggatacgaa	acttaagggg	catttagaat	ttgataatgt	aacattcgct	1020
tatccaggag	aaacagagag	tcccgttttg	catgatattt	cttttaaaagc	taagcctgga	1080
gaaacaattg	cttttattgg	ttcaacaggt	tcaggaaaat	cttctcttgt	taatttgatt	1140
ccacgttttt	atgatgtgac	acttggaata	atcttagtag	atggagtga	tgtaagagat	1200
tataacctta	aatcacttcg	ccaaaagatt	ggatttatcc	cccaaaaagc	tcttttattt	1260
acagggacaa	taggagagaa	tttaaaatat	ggaaaagctg	atgctactat	tgatgatctt	1320
agacaagcgg	ttgatatttc	tcaagctaaa	gagtttattg	agagtcacca	agaagccttt	1380
gaaacgcatt	tagctgaagg	tgggagcaat	ctttctgggg	gtcaaaaaca	acggttatct	1440
attgctaggg	ctgttggtta	agatccagat	ttatatattt	ttgatgatcc	attttctgct	1500
ctcgattata	agacagacgc	tactttaaga	gcgcgtctaa	aagaagtaac	cggtgattct	1560
acagttttga	tagttgctca	aaggggtggg	acgattatgg	atgctgatca	gattattgtc	1620
cttgatgaag	gcgaaattgt	cggctcgtgg	acccacgctc	aattaataga	aaataatgct	1680
atztatcgtg	aaatcgctga	gtcacaactg	aagaacccaa	acttatcaga	aggagagtga	1740

SeqID 102

atgaaaaaag	gacaagtaaa	tgataactaag	caatcttact	ctctacgtaa	atataaaattt	60
ggtttagcat	cagtaatttt	agggccattc	ataatgggtca	caagtcctgt	ttttgcggat	120
caaactacat	cggttcaagt	taataatcag	acaggcacta	gtgtggatgc	taataattct	180
tccaatgaga	caagtgcgtc	aagtgtgatt	acttccaata	atgatagtgt	tcaagcgtct	240
gataaagtbt	taaatagtca	aaatacggca	acaaaggaca	ttactactcc	tttagtagag	300
acaaagccaa	tggtggaaaa	aacattacct	gaacaaggga	attatgttta	tagcaaagaa	360
accgaggtga	aaaatacacc	ttcaaaatca	gccccagtag	ctttctatgc	aaagaaaagg	420
gataaagttt	tctatgacca	agtattttaat	aaagataatg	tgaaatggat	ttcatataag	480
tctttttgtg	gcgtacgtcg	atacgcagct	attgagtcac	tagatccatc	aggaggttca	540
gagactaaag	cacctactcc	tgtaacaaat	tcagggaagca	ataatcaaga	gaaaatagca	600
acgcaaggaa	attatacatt	ttcacataaa	gtagaagtaa	aaaatgaagc	taaggtagcg	660
agtccaaatc	aatttacatt	ggacaaagga	gacagaattt	tttacgacca	aatactaact	720
attgaaggaa	atcagtgggt	atcttataaa	tcattcaatg	gtgttcgtcg	ttttgttttg	780
ctaggtaaa	catcttcagt	agaaaaaact	gaagataaa	aaaaagtgtc	tcctcaacca	840
caagcccgtg	ttactaaaac	tggttagactg	actattttct	acgaaacaac	tacaggtttt	900
gatattttta	ttacgaatat	taaagatgat	aacggtagct	ctgctgttaa	ggtagcgggt	960
tggaactga	aaggagggca	agatgatatt	aaatgggata	cagctgtaac	tactggggat	1020
ggcaactaca	aagttagctgt	atcattttgct	gaccataaga	atgagaaggg	tctttataat	1080
attcattttat	actaccaaga	agctagtggg	acaactgttag	gtgtaacagg	aactaaagtg	1140
acagtagctg	gaactaattc	ttctcaagaa	cctattgaaa	atgggttagc	aaagactggg	1200
gtttataata	ttatcggaag	tactgaagta	aaaaatgaag	ctaaaatata	aagtcagacc	1260
caattttact	tagaaaaagg	tgacaaaata	aattatgatc	aagtattgac	agcagatggg	1320
taccagtggg	ttctttacaa	atcttatagt	gggtgttcgtc	gctatattcc	tgtgaaaaag	1380
ctaactacaa	gtagtgaaaa	agcgaaagat	gaaggcagta	aaccgactag	ttatcccaac	1440
ttacctaaaa	caggtaccta	tacattttact	aaaactgtag	atgtgaagag	tcaacctaaa	1500
gtatcaagtc	cagtgggaatt	taatttttcaa	aaggggtgaaa	aaatacatta	tgatcaagtg	1560
ttagtagtag	atgggtcatca	gtggattttca	tacaagaggt	attccgggtat	tcgtcgctat	1620
attgaaattt	aa					1632

SeqID 103

atggaaaatt	ggaagtttgc	cctatcatcg	attctagggc	acaagatgcg	tgcttttctg	60
accatgttag	ggatcatcat	tgggggttgc	tcagttgtgt	taattatggc	cttaggttaag	120
ggcatgaaag	attcggttac	aaatgagatt	acaaagtctc	agaagaacct	tcagattttat	180
tataaaaaca	aagaagacca	aaaaaatgag	gataactttg	gagctcaagg	ggctttcatg	240
caaggtagtg	ataccaaccg	taaggaaacca	attattcaag	aatcatgggt	aaaaaagatt	300
gctaagggaag	tagatgggtg	tagtggctac	tatgtaacca	atcaaacaaa	tgctccagta	360
gcttaccttg	aaaaaaaggc	aaagacgggt	aatataacag	gagttaaacc	cacttaacct	420
ggtatcaaaa	agttcaaaat	taaaagtggg	cgtcaattcc	aagaggaggga	ttataaccaa	480
ttctcgagag	ttatttttact	agaagaaaaa	ttagctcaga	gattattcca	gacaaatgaa	540
gcagcggtta	ataaggtggg	gactgtaaaa	aataaatctt	acttagtagt	gggggtttat	600
tcggatccag	aagctgggtc	aggcttatat	ggaagtaatt	ctgatgggaa	tgctatttta	660
accaatacac	agtttagcttc	ggagtttggt	gctaaagaag	cagaaaacat	atattttcat	720

cttaaatgatg	tatcgcaatc	caatcgcatt	ggtaaagaaa	taggcaaacg	tttaacagac	780
attagtcatg	ctaaggatgg	gtactatgat	aattttgaca	tgacatctat	agttaaatct	840
atcaataccc	aagttggtat	tatgacaggt	gttattggag	cgattgcagc	aattttctctc	900
ctagttgggtg	gtatcggagt	gatgaatatt	atgttagtct	ctgtaactga	gcgcacgaga	960
gaaattggcc	ttcgtaaagc	ccttggggca	actcgacgta	aaatttttagc	tcaatttttta	1020
attgaatcaa	tgggtcttaac	gatttttgggt	ggattaattg	ggttattact	agcctatgga	1080
ggtagcatgt	taattgctaa	tgcgcaagat	aagattactc	cttctgtgtc	acttaacgtg	1140
gctataggca	gtttaatttt	ctcagcattt	attggaatta	tatttggttt	attacctgct	1200
aataaagcca	gcaaattaaa	cccaattgat	gctttacgat	atgaataa		1248

SeqID 104

atgcagattt	cagaaattat	gattcgttat	ggagaactct	ctactaagaa	gaaaaaccgt	60
atgcgcttca	tcaataagtt	aaaaaataat	atggagcatg	tactctccat	ttatccagat	120
gtttcagtaa	aaacagatcg	tgatagagga	catgtatatac	tcaatgggtac	agattatcat	180
gaagttgcag	agtccttaaa	agagattttt	ggtagccaag	ctttttctcc	atcttttaaa	240
gtagaaaaaa	atgttgatac	attggtaaaa	gctgtccagg	aaattatgac	ttccgtttat	300
aaagatggga	tgacttttaa	aattaccgca	aaacgtagtg	accactcatt	tgaattggat	360
agccgtgctc	taaatcatac	tttaggagat	gccgtttttt	cagtcttgcc	aaatattaag	420
gctcagatga	agcaaccaga	tatcaatctt	aaagtcgaga	tacgagatga	ggctgcttat	480
atttcatatg	agaatattag	gggtgcagga	ggattaccgg	taggaacatc	tggaaaagg	540
atgtctgatg	tgtctgggtg	gattgattct	coggtggcag	gttacctagc	gttaaaacgt	600
ggtgtagata	tagaagcagt	tcattttgca	agtcctcctt	atactagccc	aggtgcattg	660
aaaaaagcac	atgatttaac	acgtaaattg	acaaaatttg	gtggtaatat	tcaatttatt	720
gaagttccat	tcacagaaat	tcaagaggaa	attaaggaaa	aagctcctga	agcctacttg	780
atgacgttaa	cacgtagggt	tatgatgcgt	attacagatc	gtattcgtga	gaaccgaaat	840
ggtcttggtt	ttattaacgg	tgaagtttta	gggcaggttg	caagccaaac	gctagaaagt	900
atgcaagcca	ttaatgctgt	cactgcaaca	cogattattc	gtcctgtggt	cacgatggat	960
aagctagaaa	ttattgatat	tgtcaaaaaa	atagataact	ttgatatttc	aattcaacca	1020
tttgaggatt	gctgtacgat	ttttgcacca	gatcgcccaa	aaactaacc	taaaattaag	1080
aatacagaac	agtatgagaa	acgtatggat	gtagaaggtc	tggtagagag	ggcagttgca	1140
gggattatgg	taactactat	tcaacctcaa	gcagatagtg	atgatgttga	tgacttgatt	1200
gacgatttat	tataa					1215

SeqID 105

atggctcgtg	ttaaagggtg	agttgtttca	cgtaaacgtc	gtaaacgcgt	acttaaatta	60
gctaaagggt	actatgggtg	aaaacatatac	ttgttcogta	ctgcaaaaga	acaagtaatg	120
aattcttact	actatgcata	ccgtgaccgt	cgtcagaaaa	aacgtgactt	ccgtaaatta	180
tggatcactc	gtatcaatgc	ggctgctcgt	atgaatgggt	tatcatattc	gcaattgatg	240
cacggtttga	aattagctga	aatcgaaagt	aaccgtaaaa	tgcttgctga	tttagcagtt	300
aacgatgcag	cagctttcac	agctcttgca	gatgcagcta	aagctaaact	tggtaataaa	360

SeqID 106

atgttttaaag	cttcaaaaaa	actcgttcaa	aaaaataagt	caaatacattt	ttggcttggt	60
tttttcataa	cacttatact	atctcttatt	ggttgttaacg	ccagcttaacg	atttgggtgct	120
atcaatttca	agactagtga	tttaataact	gttttaaaaa	atcccttaaa	aaactctaata	180
gctcaggatg	ttatttttga	cattagacta	ccacgcataa	ttgcagctat	cttagtaggt	240
gcagctatgt	cacaagcagg	tgctattatg	cagggagctca	ctcgaaacgc	cattgtctgat	300
cctggactac	taggtattaa	cgccggagct	gggttagccc	ttgttggttg	atatgctttt	360
ttagggagca	tgactatag	tacgattctc	attgtctgct	tactagggtc	tgtcatttct	420
tatcttttag	tcttcacact	ctcttataca	aagcaaaagg	gttaccacca	actacgactc	480
attttagctg	gagcgatgat	ctccacactt	tttacgtctg	ttggacaagt	ggttacatta	540
tactttaaac	tcaatcgaac	tgttatcggt	tggcaagcag	gtggttttatc	ccaaattaac	600
tggaaaatgc	taatcataat	agcacctatc	attatttttag	gtttacttat	ttcacaactc	660
ctagcacatc	aatttaactat	cttgagcctt	aatgaatctg	tggccaaagc	attgggacaa	720
aaaactcaat	taatgactgc	gtttctatta	cttattgttt	tggtttttatc	ggcttcattca	780
gtcgcgttga	taggaaccgt	ttcttttcatt	ggattgatta	ttccacattt	tattaagctt	840
tttattccca	aagattatcg	tctgttatta	cctttaatag	gatttttcagg	ggctactttc	900
atgatctggg	tagacttatc	atctcgtatt	ataaatcccc	cttcagagac	accaatttagt	960
tctataatca	gtatcgtagg	gcttccatgt	ttcctatggt	taattagaaa	agggaaaaat	1020
ctatga						1026

SeqID 107

atgattaaaa	gaccaattca	tctttctcat	gatttttttag	cagaagttat	tgataaagaa	60
gcaataacgc	ttgatgcaac	tatgggaaat	gggaatgata	ctgttttttt	agcgaaaagt	120
tctaaaaaag	tttatgcatt	tgatattcaa	gaagaagcaa	tagcaaaaac	gaaagcaag	180

ctcacggagc	aagggtatttc	taacgctgaa	cttatcttgg	atgggcatga	aaatttggaa	240
cagtatgttc	atacaccttt	aagagcggct	atattttaatc	tgggatactt	accctcagcg	300
gataaaacag	ttattacaaa	acctcacaca	actatcaagg	caatcaaaaa	cgttttagac	360
attttagaag	taggtggacg	tctatcaactt	atgggttatt	atgggtcatga	tggtggaaaa	420
agtgagaaag	atgcggtgat	agcattcgtg	gaacaattac	cacagaataa	tttcgctaca	480
atgctttatc	aaccactcaa	tcaagttaat	acgccccct	ttttaattat	ggtagaaaag	540
ttacaatcat	atgaaaatga	ggtgtaa				567

SeqID 108

atgcgagtac	atattacaag	tatatatggg	cagtcaccgc	gtagcattgc	ccttatatca	60
caaaaactag	ttaaggatgt	cggacgtcaa	cttggttatg	atgaaatggg	aatctacttt	120
tataatgatc	atgctgaaac	gcattggtgaa	agaagtacta	ggatggatgg	tatcattgcg	180
ggattaggca	gaggggat	tgttgtttt	caagtaccta	catggaattc	aacagaattt	240
gatgaacttt	ttctagataa	attacaggca	tacggtgcta	gaattataac	ttttgtacat	300
gataattgtt	ccttaattgtt	tgagtcta	ttttatttat	tagatagagt	aattgacatg	360
tataatcggt	cggatgttgt	tattctacct	acaaaagcga	tgcatgatta	tctaattgaa	420
aaagggatga	ctacctctaa	agttctttat	caagaagtat	gggatcatcc	agttaatata	480
gacctccctc	gtccagaatg	tcaaaaagtc	cttagttttg	caggcgatat	tcaacgcttt	540
ccctttgtca	atgactggaa	ggaaaatatc	ccgctcatct	attatggaga	cgggaagcaga	600
ctcaattctg	aggcaaatgt	tcattgctcag	ggatggaaag	atgatgtaga	attgatgcta	660
agtcttttcta	agcgggtagg	atttggcctg	tgttggagtg	aagatagaga	ggagttagtc	720
gagcgtcggt	attcgaggat	gaatgcctcg	tataaattat	ctactttctt	ggctgctgga	780
cttccaatta	ttgctaacca	tgatatttca	agtagagact	ttatcaaaca	acacggatta	840
ggattttacag	ttgaaacgct	agaagaagct	gttgaaaaaa	ttaataatat	ggaaaaagag	900
acttatgaca	gctatgtgga	aatgtttgag	aagatagcaa	ctctcttgcg	aatgggttat	960
atcactaaaa	aattgttgat	agatgctgtg	catatgcttt	atagatag		1008

SeqID 109

atgtcccaaa	agacttttgg	caagcagtta	acagttgtag	atactaagag	tagagtcaag	60
atgcataaat	caggaaaaaa	ctgggtaaga	acagtaatgt	cgcattttta	tctattttaa	120
gcgattaaag	ggagagcaac	tgttgaagca	gatgtgtgta	ttcaagatgt	tgaaaaagaa	180
gaccgactat	cttcaggaaa	tttgacctat	ctcaaaggaa	tactagctgc	cggagctctg	240
gtaggtggag	cgagtttaac	cagtcgtgtt	tatgcagatg	agactccagt	tgttcaagaa	300
caatcaagtt	ctgtaccaac	actggcagaa	caaacggaag	tgactgttaa	aacaactact	360
gttcaaaaatc	atcaagatgg	gacagtatcg	aaaaacatta	ttgatttctaa	tagtgtatct	420
atgtcagagt	cagcctcaac	aagtactagt	gaatctgtaa	gtatgtctat	gtcaggggtca	480
actttaacaa	gtgtaagtga	atctgttaag	acatctgctt	taacaagtgc	ttcagaatcg	540
ataagcacgt	cagcctcaga	aagtgtttca	aaatctacaa	gtattagtga	ggtttcaaat	600
attcttgaaa	ctcaagcttc	tttaactgat	aaaggaagag	agtcgttttc	ggcaaaccag	660
atagtaacag	aaagtactgt	agttactgat	gctggtaaaa	atgcttcagt	atctagccta	720
attgaaatta	caaaacccaa	atcggagtta	cagacttcca	aaatgtcaaa	tgagtcgctt	780
ataactccag	agaaatccca	agtaatgatt	gcaagcgata	aaactgggaa	tgagagtcta	840
actccgacaa	ttagattaaa	atcagttatt	cagccaagga	gtatgaactt	gatgactttg	900
agttcggaga	tggaacttgat	accactagaa	gaagtgtctg	atactgaaat	gttaggtaaa	960
gatgtatcaa	gcgagttgca	gaaagttaat	attgcgttaa	aagataaacac	tcttagtgag	1020
cctggaaacg	ttaaattaga	tagttcagaa	aacctgtttt	tgaactttgc	cttttcaatc	1080
gcttctgtta	acgagggaga	tgtctttact	gtaaagcttt	ctgataacct	tgacacacaa	1140
gggattggta	ctattctaaa	agttcaagat	ataatggatg	aaacggggca	gttattagcg	1200
actgggtcat	atagtccttt	aacacataat	attacataca	cctggacaag	gtatgcttct	1260
acgttgaata	atattaaagc	tagagtcaat	atgccagttt	ggcctgacca	gagaataatt	1320
tctaaaacaa	cttcagataa	gcagtgcctt	actgcaacat	tgaacaatca	agttgcttca	1380
attgagggaac	gtgttcagta	taatagtcct	tcagtgcacg	aacatactaa	tgtaagaca	1440
aatgtaagat	ctcggatcat	gaagcttgat	gatgaaagac	agacagaaac	ttatatatt	1500
caaattaatc	ctgaaggtaa	ggaaatgtat	ttcgcatacg	gacttgggaa	tctatatact	1560
attatcgggt	cagatgggaa	atcaggttca	ccagtttaatt	tattaaatgc	ggaagttaaag	1620
attctaaaaa	ctaattcaaa	aaatcttaca	gatagtatgg	atcaaaatta	tgattcgcct	1680
gagtttgaag	atgtgacttc	ccagtatagt	tatactaacg	atggttctaa	aattaccata	1740
gattggaaaa	caaattctat	ttcttccact	acatcttatg	ttgttttggg	caaaataacct	1800
aaacaaagtg	gtgtattgta	ttcaactggt	tctgatataa	atcaaacata	tggttctaaa	1860
tattcttatg	ggcatacgaa	tataagtggg	gactcagatg	cgaatgccga	aattaaactt	1920
ttatcagaaa	ctgcttctac	gagtgcgtcg	acgtcagcaa	gtaccagcgc	ttccatgagt	1980
gcctcgacat	cagcaagtac	cagcgttcc	atgagtgcct	cgacatcagc	aagtaccagc	2040
gcttccatga	gtgcgtcgac	gtcagccagc	accagcgtt	caaccagcac	ctcaacgagt	2100
gcctcgacat	cagccagcac	aagtgcctca	acaagtgcaa	gtatgagtgc	ttcaacaagt	2160
gcaagtagca	gtgcatccac	gtcagcaagt	actagcgctt	ccacaagtgc	cagcaccagc	2220

gcctcaacga	gtgcctcaac	gtcagccagc	actagcgctt	caacgtcagc	cagcaccagc	2280
gcctcaacca	gtgcttcaac	cagtgccttc	acatcagcca	gcactagcgc	ctcaatgagt	2340
gcgtcgatgt	cagccagcac	aagtgccttc	atgagtgcct	cgacgtcagc	cagcactagc	2400
gcctcaacca	gtgcttcaac	cagtgccttc	accagtgcct	ccacctcagc	aagtatgagc	2460
gcctcaacaa	gtgcaagtac	tagcgcttca	acaagtgcac	gtatgagcgc	ctcaaccagt	2520
gcaagtacta	gtgcttcaac	aagtgccttc	accagtgcct	cgacgtcaac	aagtactagc	2580
gcttccacgt	cagcaagtac	cagtgccttc	acatcagcaa	gtatgagcgc	atccacgtca	2640
gccagcacca	gcccctcaac	cagtgccttc	accagtgcct	caaccagtgc	ttcaaccagt	2700
gcttccacat	cagccagcac	tagcgcttca	atgagtgcct	ccacgtcagc	aagtactagc	2760
gcctcaatgt	cagccagtac	tagcgcttca	accagtgcct	gtaccagtgc	ttccacctca	2820
gcaagtatga	gcgcctcaac	aagtgcacgt	actagcgctt	ccacaagtgc	aagtatgagc	2880
gcctcaacca	gtgcaagtac	tagtgccttc	accagtgcct	gtaccagtgc	ctcgacgtca	2940
acaagtacta	gcgcctccac	gtcagcaagt	accagtgcct	ccacatcagc	aagtatgagc	3000
gcctccacgt	cagcaagtac	cagtgccttc	acgtcagcaa	gtatgagcgc	ctccacaagt	3060
gcaagtatca	gtgcatccac	gtcagcaagt	atgagcgctt	ccacaagtgc	aagtaccagt	3120
gcctccacgt	cagccagtac	tagcgcttca	atgagtgcct	cgacgtcagc	cagcaccagt	3180
gcttccacaa	gtgcaagtac	tagcgcttca	atgagtgcct	cgacatcagc	aagtaccagt	3240
gcttccacaa	gtgcaagtac	gagtgccttc	acatcagcaa	gtactagcgc	ctcaacatcg	3300
gcaagtataa	gttcttccac	aagtgcacgt	accagtgcct	cgacatcagc	cagcactagc	3360
gcctcaatga	gtgcctccac	gtcagccagc	acaagtgcct	ccatgagtgc	gtcgacgtca	3420
gccagcacta	gcgcctcaac	gagtgccttc	atgtcagcca	gcacaagttc	ttcaacaagt	3480
gcctcgatgt	cagccagcac	tagcgcttca	atgagtgcct	cgacgtcagc	tagcactagc	3540
gcctcaacga	gtgcgtcaat	gtcagccagc	acaagttctt	caacaagtgc	ctcgatgtca	3600
gccagcacta	gcgcctcaat	gagtgccttc	acgtcagcca	gcaccagcgc	ttcaacgagt	3660
gcgtcaatgt	cagccagcac	tagcgcttca	atgagtgcct	cgacgtcagc	cagcaccagt	3720
gtctcaacga	gtgcctccac	atcagcaagt	accagcgctt	ccacaagttc	ttcaagctca	3780
gtgacttcta	attcatcaaa	agagaaggtg	tattctgcct	taccttctac	gggtgaccaa	3840
gattattctg	taactgctac	tgcttaggt	ttaggtttta	tgactggtgc	aacctttttg	3900
ggagcaaaaa	aatctaaaaa	agataaagac	ttaa			3933

SeqID 110

atgatagata	gaaaagatac	taaccgattt	aaattagttt	ccaaatatag	cccttcggga	60
gatcaacctc	aagctattga	aacgttgggt	gacaatattg	aaggaggaga	aaaagctcag	120
attttaaaag	gtgctactgg	tactggtaaa	acctacacaa	tgagccaagt	tatcgcccaa	180
gttaacaagc	caaccttggg	gattgcacat	aataaaacct	tagcaggtca	actttatgga	240
gagtttaaa	aattttttcc	tgacaatgcc	gtagagtact	ttgtttcata	ttatgattat	300
tatcaaccag	aagcttatgt	gccttcttcg	gatacttata	ttgaaaaaga	tagttcagtc	360
aatgacgaaa	ttgacaaaat	acgtcactca	gcgacttctt	cgttattaga	aagaaatgac	420
gttattgttg	tagcatctgt	ttcttgtatt	tacggtttag	gttctcctaa	agagtatgca	480
gacagtgttg	ttagccttag	gccaggctaa	gaaatttcac	gtgatcagtt	attgaacaat	540
ctcgttgata	ttcaatttga	gcgtaacgat	attgattttc	aacgtggaaa	atttcgcggt	600
cgtggcgatg	ttgtagaagt	ttttcctgog	agtcgtgatg	agcatgcctt	tcgaattgaa	660
ttttttgggtg	atgaaattga	tcgtataaga	gaaatagaat	cgttaacagg	gcgtgtgcta	720
ggagaagtg	aacattttagc	tattttccca	gcaacacact	ttatgacaaa	tgatgaacat	780
atggaagaag	ctattttcaaa	aatacaagct	gaaatggaaa	atcaagtaga	actttttgaa	840
aaagaaggga	aatttgattga	agcgcaacgt	attcgacaaa	ggacagaata	tgatattgaa	900
atgcttcgtg	aaatgggata	tacaaaatgg	gttgagaact	actcacgtca	catggatggg	960
agaagtgaag	gtgagccacc	ttttactttg	ttagattttc	tcccagaaga	ttttttgatt	1020
atgattgatg	agagtcacat	gacaatgggg	caaatcaaag	ggatgtataa	tggagaccgt	1080
tcgcgtaaag	aaatgttggg	taattacggg	ttccgtttac	catctgcctt	agataaaccgt	1140
ccacttcgtc	gtgaagaatt	cgaagccat	gtccatcaaa	ttgtctatgt	atctgcaacg	1200
ccaggagact	atgaaatgga	gcaaacagat	acagttgttg	agcaaattat	cggccaaca	1260
ggacttcttg	atccagaagt	tgaagttaga	ccaagtatgg	ggcagatgga	tgacttgcct	1320
gggtgaaatca	atttgaggac	tgaaaaaggt	gagcgtacct	ttattacaac	attgacaaag	1380
cgtatggcag	aagacttaac	agattatctc	aaagaaatgg	gagttaaagt	taagtatatg	1440
cacagcgata	ttaaaacctt	agaacgtaca	gagattatlc	gtgatttaac	acttgggtgtg	1500
tttgatgttt	taatttggtat	taatctctta	cgtgaaggaa	tagatgttcc	tgagggtttcc	1560
cttggttgcaa	tcttagatgc	tgataaggaa	ggtttctctc	gtaatgagcg	tgggtcttatc	1620
caacaatcgc	gacgtgcagc	acgtaacagt	aatggtcatg	ttattatgta	tgctgataaa	1680
ataacagatt	ctatgcaaa	agctatggat	gaaacgcgtc	gccgtcgtcg	ttacacaaatg	1740
gattataatg	aaaagcatgg	aattgtgcca	caaacatta	aaaaagaaat	cogtgattta	1800
attgctatta	ctaaaagtaa	tgacagcgat	aagcctgaaa	aagttgtoga	ttacagtagt	1860
ttatctaaaa	aagaaaggca	agctgaaatt	aaagctcttc	aacagcaaat	gcaagaagca	1920
gctgaattat	tggactttga	gctagctgca	caaatccgag	atgttatctt	agaactaaaa	1980
gcaatcgatt	aa					1992

SeqID 111

atgaagcaca	agttaaaagc	ttttacgctt	gctttactct	caatattctt	tgtgttttgg	60
ggaaagggtca	gtgcagaaac	tgtgaatatt	gtttctgata	cagcatatcg	tccattcgaa	120
tttaaagatt	ctgatcaaac	ttataaagga	atcgatgttg	acatcggtta	cgaagtcgct	180
aagcgtgctg	gctggaatgt	taacatgacg	tacccagggt	ttgatgcgcg	agttaacgct	240
gttcaatctg	gacaggcaga	cgcgctaatt	gccggaacta	ctgttactga	agcacgtaaa	300
aaagtcttcta	atttctcaga	tacttattac	gatacttccg	ttattcttta	tactaaaaat	360
aataataaaag	tcacaaaacta	caaacaacta	aaaggaaaaag	tagtcgggtg	aaaaaatgga	420
acagctgctc	aaagcttctt	agaggaaaaat	aaatctaaat	acggctataa	agttaaaaca	480
tttgatacaa	gtgacctaat	gaataacagc	cttgattctg	gttctattta	cgcgcctatg	540
gacgatcaac	cagttgtgca	atttgcgata	aatcaaggaa	aagcttacgc	cattaacatg	600
gaaggcgagg	cagttggtag	ctttgcattt	gctgtcaaaa	aaggtagtgg	acacgataac	660
ctaattaaag	aatttaacac	agcttttgca	caaataaat	cagatggcac	ttataatgac	720
atcatggata	aatggcttgg	gaaagacgct	acaaaaacaa	gcggcaaaag	aacaggtaat	780
gccaatgaaa	aagcaactcc	tgtaaagcca	agttataaaa	ttgtttctga	ttcttcattc	840
gcaccattcg	aatatcaaaa	cggtaaaggg	aaatatactg	gttttgatat	ggaattaatc	900
aagaaaattg	ctaaacagca	aggttttaaa	cttgatatct	caaataccagg	ttttgatgcc	960
gctttaaatg	ctgtccaatc	tggacaagct	gacgggtgta	ttgcaggagc	tacaatcaca	1020
gaagcacgcc	aaaaaatctt	tgatttttct	gatccttatt	acacatctag	cgttatctta	1080
gcggttaaaa	aaggaagcaa	tgtcaaatca	taccaagatt	taaaaggaaa	aacagttggg	1140
gctaaaaatg	gtactgcctc	atatacttgg	ttatcagacc	acgcagataa	gtacaactat	1200
catgttaaag	catttgatga	agcatctaca	atgtatgata	gtatgaactc	aggttcaatt	1260
gatgctctaa	tggatgacga	agcagttctt	gcttacgcta	ttaatcaagg	tcgtaaattt	1320
gaaacaccta	tcaaagggtga	aaaatcaggc	gatatcggat	ttgcagtga	aaaaggggca	1380
aatccagaat	taattaaaaat	gtttaacaac	ggtcttgctt	cactcaaaaa	atcgggtgag	1440
tacgataaac	ttgttaaaaa	atacctttcc	acagccagca	cctcttcaaa	cgataaagct	1500
gctaaccctg	tagatgaatc	aactatttta	gggttaattt	ctaataacta	caaacaattg	1560
ctatctggta	ttggaactac	tttaagttta	actcttatct	catttgcgat	tgctatgggt	1620
attgggtatta	tctttgggtat	gatgagcgta	tcaccaagta	atactctccg	cacaatttca	1680
atgatttttg	ttgatattgt	ccgtgggtatt	ccactcatga	ttgtggccgc	ttttattttc	1740
tgggggtattc	ctaattttaat	cgaagcgatc	acaggtcacc	aaagtccaat	taatgacttc	1800
gttgcgtgta	ctatcgctct	ttcttttaaa	ggtgggtgct	acattgctga	aattgtacgt	1860
gggtggatttg	aagctgttcc	ttctgggtcaa	atggaagcaa	gtcgtagttt	aggattttct	1920
tacggcaaaa	ctatgcaaaa	gggtatcttg	cctcaagcag	tacgccttat	gttaccaaac	1980
tttatcaacc	aatttgtcat	ctcattaaag	gatacaacaa	ttgtatcagc	aatcggactt	2040
gtggaactct	tccaaactgg	taaaatcata	attgcacgta	actatcaatc	attccgtatg	2100
tatgctatcc	ttgcaattat	gtatcttgta	atcattaccc	ttctcaccgc	tctagcaaaa	2160
cgttttagaaa	agaggcttaa	ataa				2184

SeqID 112

atgggagata	aaccgatatc	atttcgtgat	aaagatggga	attttgtttc	agcggccgat	60
gtctggaatg	ctgaaaaatt	agaagaactc	tttaacacat	taaatcctaa	tcgtaaaactt	120
cgttttagaac	gcgaaaaatt	agcaaaaagaa	aaaggatag			159

SeqID 113

atggaaacat	atactctatc	gaatactctt	aacatttccta	aaatttggtt	tgggacatgg	60
caactaaactg	aagggtgaaga	agcttataag	gcagtgactc	atgctttaaa	agttgggttat	120
actcatattg	atactgctca	gatttatggc	aacgaacaca	gtgttgagcg	tgctataaga	180
gacagtgggt	tggcgcgaga	aagtatcttt	ttgacaacta	agatttgga	tgacaaacat	240
gactatcatt	tagccaaaagc	ttctattgat	gaatctctgc	agaaattagg	tggtgattat	300
attgatcttc	ttttgattca	ttggccaaa	ccaaaagctc	ttcgtgaaa	tgatgcgtgg	360
aaagctggga	atgcaggcac	ttggaaagcg	atggaagaa	cttataaaga	aggaaaggta	420
aaagctattg	gtgtttcgaa	tttcatgaaa	catcacttag	aggctttatt	tgaaactgcc	480
gaaataaaac	ctatgggttaa	tcaaattatc	ctagcaccag	gttgtgctca	agaggatttg	540
gttcgcttct	gtaaaggaaa	tgatatctta	ttagaagctt	acagtcatt	tggaacagg	600
gctatttttg	aaaatgaatc	tataaaagct	attgctgaaa	aatatggtaa	atcagttgca	660
caagtagctc	ttcgtgggtc	acttgataat	ggctttttac	cattaccta	gtcagcgact	720
cccaaaaata	ttgaagcaaa	ccttgatatt	tttgattttc	aattaaacga	agatgatatt	780
actaccttaa	tacaactaga	ttcagggtatt	aaacccaaag	atccagataa	tgtctcattt	840
taa						843

SeqID 114

atgggttaaa	gtcaaggaaa	cgttgtagca	caaaaataaaa	aagcgcacat	cgactatact	60
atcgttgaaa	caatagaagc	aggaattgtt	ttgacaggaa	cagaaatcaa	aagtgtccgc	120

gcagcgcgta	ttacattgaa	agatggatat	gcacaaataa	aaaatggtga	agcgtggttg	180
attaatgttc	atattacacc	atacgatcaa	ggtaatatat	ggaatcaaga	tcctgatcgt	240
acacgaaagt	tattactaaa	aaaacgtgag	attgaaaaaa	tatcaaatga	actgaaaggg	300
actggtatga	ctctggtacc	tctaaaagtt	tacttaaaag	atgggttttg	taaagttcta	360
ttgggttttg	caaaaggaaa	acatgattat	gataagcgag	agtctatcaa	acgtcgtgag	420
caaaaccgtg	atattgcccc	tcagttaaaa	aactataatt	cacgatga		468

SeqID 115

atggaccatt	tcacaaaact	ctggcaagat	ttctctaaac	ttccaaatgt	tgttgctata	60
gcactcggag	gctcacgctc	tggtgacagt	tttgaccaat	cttccgatta	tgatttgtat	120
gtttattgtg	cagcaactcc	tgatatcact	agtcgtaaac	gtatccctaa	caagcactgt	180
cattacattg	aacttaacaa	tcattactgg	gagcttgaag	ataatggtac	tttaaacgac	240
ggaactgata	ttgatattct	ctatcgtaac	atagataact	ttttatcaga	cttagaagat	300
gtcgttgaac	accacaattc	tcgaattgga	tacactactt	gtttttggca	taacctcatc	360
aattgccaaa	tactctatga	tcctgaaaaa	caattacaat	cactcaaaga	gagattcgaa	420
gtttcttctc	ccagtcagtt	acaaaaacaa	attatcattc	aaaatcgtaa	cttattaact	480
ggcaagcttc	cctcttacga	taaacaaatt	ataaaagccc	ttaaacgcca	agactttggt	540
agtactcacc	atagaactac	tgctttctta	gattccctact	ttgatattat	ttttgcactt	600
aataagttga	cacatcctgg	cgaaaaaaga	atgatttcct	atgctaagaa	gaatgctaca	660
ttgcttctca	aacatttcga	agaaaatatc	attaaactat	gtcatcacia	ctccaacgaa	720
cacactgtta	aagaaacatt	aaacgatata	ataatgcatc	tcgacgtcat	gcttaaagaa	780
aattttcaac	acttttatagg	ttaa				804

SeqID 116

atgaaaaaaa	ttatttatct	tggttttagcc	tgtgtcagta	tattaaacttt	aagtgggttg	60
gagtcaattg	agcgtttctc	aaaaggagac	cgttatgttg	accaaaaaact	agctgaaaaac	120
tcttcaaagg	aagctactga	acaactaaac	aaaaaaacta	agcaagcctt	aaaagctgat	180
aaaaaagctt	ttcctcaatt	ggacaaggct	gttgccaaaa	acgaggcaca	agtgcctata	240
aaaacctcta	aagggtgatat	aaatatcaag	ttatttccaa	aatatgctcc	tttagctggt	300
gaaaattttc	taacacatgc	aaaagaagga	tactataatg	ggttaagttt	ccacagagtt	360
atcaaagatt	ttatgatata	atctggtgac	cctaattggag	acgggaccgg	tggaaaatct	420
atatggaata	gcaaagataa	aaagaaagat	tctggaaatg	gttttggttaa	tgaaatatcc	480
ccttacctct	acaatatcag	gggaagttta	gcaatggcaa	atgctggagc	tgataactaat	540
ggcagccaat	tctttatcaa	tcaaagccag	caagatcatt	ccaaacaact	gtcagataaa	600
aaagtctcta	aggtgattat	taaagcctat	tcagagggag	gaaatccaag	tttagatggt	660
ggttataacc	tctttggaca	agtaatctct	ggcatggaaa	ctgtggataa	aattgcttcg	720
gtagaagtta	caaaatcaga	tcaacccaaa	gaaaaaatta	ctattacaag	tatcaaagtt	780
attaagact	acaaatttaa	ataa				804

SeqID 117

atgaaaattg	gaattattgc	agccatggag	gaagagttaa	aactccttgt	ggaaaatctt	60
gaggataaat	ctcaagagac	agtattatca	aatgtatat	acagtggacg	ttatgggtgaa	120
catgagcttg	tttttagtaca	gtctggtgtt	gggaaagtca	tgtcagcgat	gagtgttgct	180
attttagtag	aaagctttta	agttgatgct	attabtaata	caggatcagc	tggtgcagta	240
gcaacaggat	tgaatgtagg	agacgtcggt	gtcgcagata	cattagttta	tcacgatgta	300
gatttaaccg	ccttttggtta	tgactatgga	caaatgtcaa	tgacgccact	ttattttcat	360
tcggataaga	ctttttgttc	cacttttgaa	gcagttttat	ctaaagaaga	aatgactagt	420
aaagtgtggt	taattgcaac	tggggatagt	tttattgctg	gccaggaaaa	gattgatggt	480
attaaggggc	atttttccaca	ggtttttagct	gtcgagatgg	aagggtgcagc	aattgccccaa	540
gctgctcaag	ctacaggaaa	gccctttgtg	gtggtacgtg	ctatgagtga	tactgcagct	600
catgatgcca	atatcacatt	tgatgaattt	atcattgaag	ctggtaaacy	ctctgcccaa	660
gtattaatgg	catttttgaa	agcattataa				690

SeqID 118

atggaaaaga	gacttagttt	aggagctctt	gttttagcta	gtacagttct	tttagcagca	60
tgtggaaatg	tcggaggagg	agcatcttcg	acaggaaaca	aaatagggaa	agatattaag	120
gtagggtata	actgggaatt	atcaggaaac	gtttcttcgt	atggaaattc	aatgaagaat	180
ggagctgact	tagcagtaaa	agaaattaat	gctgctggag	gggttgccgg	caagaagtta	240
aaagtccat	cacaggataa	taaatcagaa	aatgcagagg	cagcaacggg	tgccacaaac	300
ttggttacca	aaggagctaa	tgctattatc	ggaccagcaa	catcgggtgc	agctgcactc	360
tcaactccaa	aagtaaattgc	agcagcagtt	ccaatgattg	cacctgctgc	gacacaagac	420
aatttagtct	atggttctga	tggaaaaacc	ttaaatcagt	atctcttcgg	agctactttt	480
gtcgataaatt	atcaaggaaa	gctattgtct	cagtatgcta	cagacaacct	taaagctaaa	540
aaagtgttct	tattttatga	taattcatca	gattactcaa	agggggtagc	aaaatcattt	600
aaggaaagtt	atagtggaaa	aattgttgat	agcatgacat	tctccgctgg	tgatactgat	660

ttccaagcgt	cattgactaa	gttgaaaggg	aaagaatatg	atgctattgt	gatgccaggt	720
tactataccg	agacaggatt	aatagttaag	caagcgctg	athtaggtat	ctctaaaccg	780
gttcttgggc	ctgatggttt	tgatagtccg	aaatttgtgc	aatcggaac	acctgtggga	840
gcttcaaagc	tttattat	gacaggtttc	actacacaag	gatcaaccaa	agctaaagct	900
ttccatgatc	attacgttaa	ggcatatggt	gaagaaccat	ccatgttctc	ggctttatca	960
tacgatgccg	tgtatatggc	agctaaatct	gctaaaggag	ctaaaacttc	aattgatctt	1020
aaaaaagctt	tagctaagct	gaaagatttt	aaaggtgtga	cagggaaaat	gtctattgat	1080
aaaaatcata	atgttggttaa	atcagcttac	gttgtcaaat	tagacgatgg	aaaaacaagt	1140
agcggttaaca	ttatttcagc	aaaataa				1167

SeqID 119

atggagaatc	ataattctat	taaacagacc	tatggattaa	tgactacaat	tgotatgatt	60
gtaggtgtag	tgattgggtc	aggcatttat	tttaaagttg	atgacatcct	taaatttact	120
gggtggagat	tcttttttagg	catggtaatt	ttagtactag	gttcttttttc	gattgttttt	180
gggaagttgt	caatttctga	gctagctatt	agaacgagtg	aaagtgggtg	tattttttct	240
tactacgaaa	aatatgttag	cccagcttta	gcagcaactt	taggcttggt	tgcgtctttt	300
ttgtatcttc	caactttaac	agcaatcgtt	tcatgggtag	ctgcatttta	tacttttaggt	360
gaatcatcaa	gtttggaatc	acagattatt	ttagctgctg	tttatatttt	agcacttagt	420
ctcatgaata	tctttgctaa	gcgtattgca	gggggattcc	aatctttaac	gacctttgta	480
aaaatgattc	cttttagtctt	aattgcttta	attgggtgctt	tttgggtctga	taaagctcca	540
caacttccac	aacattttaac	agctattcag	ccgtcaaatg	ttggatggag	ttgggtgtca	600
gggtctggtac	cattgtat	tgcatatgat	ggttggacaa	tttttggttag	tattgcacca	660
gaagtcaaga	atcccaagaa	gaatttacca	cttgcttttg	tcattgggtcc	agcgcttata	720
ttattatcat	atgtggcatt	tttctatgg	ttgacacaaa	tttttaggtgc	tagctttatt	780
atgacaaccg	gtaatgatgc	tatttaattat	gcagctaaca	ttattttcgg	tcctagtgtt	840
gggctgttat	tatctttcat	tgttat	tctgtattag	gtgttgccaa	tggactttta	900
cttgggacga	tgcgtctacc	tcaagctttt	gcggaacg	gatggatcaa	aagtgaagg	960
atggctaaca	taaatttgaa	gtatcaaatg	tcatgtccag	ctagtttgac	gggtgacggt	1020
gtagctat	tttggctttt	tgttcacttt	atgggtacaa	aatttaattt	attgccgggt	1080
agtgatatta	gtgaaattgc	tgtgggtgtt	aataatacta	gtttaatcat	tctttatgtt	1140
ttagtactca	gccttttatct	caaaaaagat	attaaaaata	aatttaccgg	cttagtttca	1200
ccgattctag	caatttttagg	cggtttgatc	ctctttatcg	ggagtttggt	aagtaatttc	1260
tttacggttt	taattttcca	atgtttttgc	ttattattct	gtttgatttg	tcattatata	1320
tatcaaaaaa	ataaccctaaa	aactcatgaa	tag			1353

SeqID 120

ttgaccgaat	ttaatgacga	tcagcattct	aaccatgatc	agaaaagttt	taaagaacaa	60
attctggcag	agttagaaga	agctaaccgt	ttgagaaagt	tgcgtgaaga	agaactctat	120
caaaaagagc	agaagccaa	agaagctgct	cgcagaacag	cacaattgat	ggcagattat	180
gaagcgcaac	gtttgaaaga	cgaacaagaa	gctagagcaa	aggcgctaga	gactaagcaa	240
cgcttagaag	agcaagagaa	ggctcggtat	gaggcgaaac	ttctggcaga	agctgctoga	300
gaagaagaaa	gacgtcaggc	ggaacaagca	ttagcttccc	aagaagaaca	agttatcaat	360
caagggatgg	aaccttcaag	agagcttgat	agcggctcca	aatctagtga	atttaggaca	420
actgaaaatg	tacctgacat	agatttataa	gcagataaga	ctgatgttgc	aactgctgtg	480
cctaatacaag	aaacggaaga	aatctttctt	gtgagagcaa	cagatattcc	tacagaagg	540
gaaaatgtaa	aacttggtga	gacatcagag	ttagagcccg	tagcaaagga	acctatccga	600
gtagaggatt	tgtcaaaaga	agaagaggat	atagctttgt	cagccaagaa	caaacataac	660
aagcgtgaaa	agcgtcagaa	agcagataat	gtggcaaaac	gaattgcacg	tattctgata	720
tcaattatca	tacttgtatt	gctcttgaca	gcattttag	gttatcgttt	tgtagatagt	780
gctattaaac	ctgttgattc	caattcaaat	aaatttgtac	aagttgaaat	tccgatagga	840
tctgggaata	aattaattgg	tcaaat	gaaaaagcag	gagtcattaa	gagcgccaca	900
gtctttaaat	actattccaa	gttcaaaaac	tatagtaatt	ttcaaagtgg	atactacaat	960
cttaaaaaaa	gtatgacttt	agatcagatt	gctgctgaat	tggaaaaagg	cggaaactgca	1020
gaaccgacaa	aaccagcttt	aggtaagata	ttaattaccg	agggttacac	tattaaacag	1080
attgctaaag	ctattgagtc	taataaaatt	gatacaaaaga	ctacaagtac	accttataaa	1140
gctgatgatt	tcttgaaact	tgttcaagat	gaaacgttta	ttaaaaaat	ggtagctaaa	1200
tatocaaatt	tactaggaag	tctacctgat	aaatcaaaag	ctatttatca	attggaagga	1260
tattttattcc	cagctactta	caactattat	aaagatacaa	ccttagaagg	acttggtgaa	1320
gatatgattt	caacaatgaa	tactaagatg	gcaccttact	ataaacactat	taaagcgaag	1380
aatatgtctg	taaatgatgt	tttgacatta	tcatctcttg	ttgaaaaaga	gggatcaaca	1440
gacgaagatc	gccgtaaaat	agcaagtgtc	ttttataacc	gattatcagc	cggtaagctt	1500
cttcaaaagta	acattgcaat	tttgtatgct	atggggaaat	taggtgataa	aacaagttta	1560
gctgaagatg	ctcaaattaa	tacttcaatt	aaatcaccat	acaacatcta	tactaataact	1620
ggtttgatgc	ctggaccagt	tgatagtcca	agtatctcag	caattgaagc	gactataaaa	1680
cctgcttcaa	cagattatct	ttattttgtc	gctgatgtga	agaccggaaa	tgtatactac	1740

gctaaagact	ttgaaacaca	caaggctaac	gttgaaaaat	atatcaatag	tcaaattaac	1800
taa						1803

SeqID 121

atgagtagaa	tgattccagg	acgtattcga	aatcaaggta	tagaactcta	cgaacaagggt	60
ttgggtgtcct	tgattttctca	agaaggtaat	ctattaaaaag	ctaaagttgg	ggattgtcag	120
attgaatatt	cattagtaac	agaagaaaca	aaatgttctt	gtgatttttt	tgcaagaaaa	180
ggctattgtc	aacatttagc	tgctctggag	catttcttga	aaaacgaccc	agaggggtaaa	240
gcaatcttat	ctaaagttca	agttcaacaa	gaaagtcaac	aagaaactaa	gaagaaaacc	300
tcttttggta	gtgttttttt	agatagtcta	attattaatg	aagatgatac	tataaaatat	360
caactatcgg	ctcaaggaga	acaaaatcct	tatgctaattg	atatctgggtg	gacttttaaaa	420
attagacgac	tgcttgatga	tagaagttat	gttattcgtg	acatcaaagc	ttttttaaat	480
actgttcgaa	aagaagctta	ttatcagatt	ggaaaaaat	actttgaaac	tttgtctttg	540
atacagtttg	atgagaccag	tcaagaattg	atagaatttt	tatggaggct	cattccaagt	600
cattcaagca	aaattgatct	agagtttatt	ttaccaaatc	aaggctcgta	ccttagtctc	660
actcgtgggt	tttttgaaga	gggcgttact	ttgatgaatg	ctttagaaaa	tttttcattt	720
gaaagtgatt	ttcatcaatt	taatcacctc	tactttaagg	aattagaagg	tgaggatcat	780
ctttatcaat	ttaaggttat	tgtccatagg	caatcaattg	aattagaaat	caaagagaaa	840
gacttaaaac	cactattttgc	gaattcttat	ttgtttttatc	gcgatacttt	ctaccatctt	900
aatttgaagc	aagaaaagat	ggtaacggct	attcgtagtc	ttcccattga	gggagattta	960
gcaaaacata	tccatttttga	tttagatgat	caagataatg	tagcagctca	tttactggat	1020
tttaaggaga	ttggactagt	agatgctcca	cggagcttct	ctattcatga	ttttaaggta	1080
aatttttgagt	tcgatattaa	tagtcaaaat	gaaattttat	tgcaaattgg	atttgattat	1140
ggtaattgatt	taactgttca	taatcgtcaa	gaactagaac	agttaacatt	tgctagtccac	1200
ttcaaacatg	aagaaaaaat	atttaaaactc	ttagaaagat	atggctttgc	accccacttt	1260
tcaaccagcc	atccagcata	cagtgcacaa	gaattatacg	atttttatatac	ctatatgctt	1320
ccacaatttca	aaaaaatggg	aacagtgagc	ttatccgcaa	aattggaaaag	ttatcgtctc	1380
atagaacgac	cgcaaattga	tattgaagct	aagggaaagc	tgctagatat	ttcttttgat	1440
ttctctgatt	tactggaaaa	cgatgttgat	caagctctgg	tagctttgtt	tgacaataat	1500
ccttatttttg	tgaataaatc	agggcaatta	gttatttttg	atgaagagac	taagaaagta	1560
agtgcactt	tgcaaggggt	gagagctaga	cgagcaaaga	atgggcatat	tgaattagat	1620
aatattgcag	catttcaatt	atcagaactg	tttgcaaactc	aagataatgt	tagcttttca	1680
caacattttt	accaattgat	tgaagatttg	agacaccag	aaaagtttaa	aatacctgggt	1740
ctatctgttt	cagcttcctt	gcgcgattat	cagctttacag	gtgtccgttg	gttaagtatg	1800
ttagatcatt	atggctttgc	agggatttta	gctgatgata	tggggcttgg	aaaaaacactt	1860
caaacgattt	cattttttaag	tacaaaacta	actagagatt	ctcgtgtgct	tatttttatca	1920
ccatcaagtt	taattttataa	ttggcaagat	gaattccaca	aatttgcgcc	agacgtagat	1980
gtagcagttg	cctatgggtc	taagattcgt	agagatgaaa	ttattgctga	acgtcatcaa	2040
gtaatcatta	caagttattc	atcatttagg	caggattttg	agacttattc	tgaaggaaat	2100
tatgattatt	taatttttga	tgaagcacag	gttatgaaaa	atgctcaaac	taaaatagcc	2160
catagcttga	gatcttttga	ggtcaaaaac	tgttttgcat	tatcgggaac	acctattgag	2220
aataaactgt	tagaaatttg	gtccattttc	cagatcattt	tacctgggtt	attacctgggt	2280
aagaaagagt	ttttgaagtt	gaaccctaaa	caagttgctc	gttatatcaa	accattttgtg	2340
atgagacgtc	gaaaagaaga	agttctccca	gaattaccgg	atttgattga	aatgaactat	2400
ccaaatgaaa	tgacagacag	tcaaaaagtt	atctattttg	cgcaattacg	ccaaattcaa	2460
gaaagtatacc	aacattctag	tgacgctgac	ttaaatcgtc	gtaaaattga	aatttttatct	2520
ggcatcacac	gatttgcgac	actccacgtc	tttttatgga	ttatgatggg	ttatgatggg	2580
gaaagcggta	agttagaag	cctacatcaa	cttttaacac	aaattaagga	aaatggacat	2640
cgtgctctga	ttttttctca	gttcaggggt	atgttagata	tcgcagaacg	tgagatggta	2700
gctatggggc	ttacaactta	taaaattact	ggttctacac	cagcaaatga	acgtcatgaa	2760
atgaccagag	catttaattgc	aggatcaaaa	gatgctttct	tgatttcttt	aaaagctgggt	2820
ggcgttgggt	tcaaccttac	aggagctgat	accgttggtc	tgattgactt	gtgggtggaat	2880
ccagctgttg	aaatgcaggc	gattagtcgc	gcacataagg	tggggcaaaa	agagaatgtc	2940
gaggtttatc	gcttgattac	tagaggcaca	atcgaagaaa	aaattctaga	aatgcaagaa	3000
actaaaaaac	atttggttac	aacagttctg	gatggaaatg	aaaccatgc	tagcatgagt	3060
gtagatgata	ttcgagagat	acttggagtt	tctaaataa			3099

SeqID 122

gtgttactta	cagaaatcaa	aaaatcacca	gaggggcttt	attttgataa	aaaaatagat	60
atcaaagagt	cgcttatgga	gcgtcattca	gagataatgg	atattttctga	tattcaagtt	120
tcaggctcatg	tggtgtatga	agatgggtctc	tatctacttg	actataatat	ggcttacgat	180
attacattac	cgtctagtgc	ttctatgaaa	ccagttgttt	tatctgaaaa	gcaaactatt	240
aatgaagttt	ttattgaagc	tgaaaatgtt	agcactaaaa	aagagctcgt	tgatcaggat	300
ttgggtcttaa	tattagagga	agatgatatt	aatttagaag	aaagcgttat	cgataatatc	360
ttgttaataa	tacctcttcg	tgttctggca	gctgatgagg	ttggggtaga	agcggattta	420

tcaggtaaaa	attgggtcgtt	aatgactgaa	aagcagtatg	aagaaaaaca	agctaagaa	480
aaagaaaaat	ctaatacctt	cgcagcctta	gaagggtatg	ttgatagtga	ttag	534

SeqID 123

atggaagtaa	aaactgcaat	agaatggatg	cacactttta	acaaaaaaat	tcaatccaac	60
aaggactatt	tatccgaact	agatactcca	ataggtgatg	gcgaccatgg	tggcaatatg	120
gcgcgtggta	tgactgctgt	tattgaaaac	cttgataaca	atgaatttag	tagtgctgcc	180
gatgttttca	aaaccgtatc	catgcaactt	ttaagcaaaag	taggcggagc	atctggacca	240
ctctatgggt	ctgcatttat	gggaattaca	aaagctgaac	agagtgaag	taccatttca	300
gaggcacttg	gcgcaggact	tgaaatgatt	caaaaacgtg	gtaaagctga	acttaatgaa	360
aaaacaatgg	ttgatgtttg	gcacgggtgt	attgaagcga	ttgaaaaaaa	tgaattgact	420
gaagaccgta	ttgattcctt	agtagatgct	acaaaaggga	tgaagcaac	aaaaggacgc	480
gcttcttatg	ttggagaacg	ctcatttagga	cacattgatc	cagggtcatt	ttcttcagga	540
ttattattta	aagcattact	agaagttgga	ggtgtctaa			579

SeqID 124

atgcaagata	aattaatgat	aagaggagca	agagctcaca	atttaaaaaa	tataagtgtc	60
gacatcccac	gagacaagtt	agttgtcgtt	acgggactat	caggatcagg	taagtctagt	120
ttggcctttg	acactatcta	tgcagaagga	caacgtcgtt	acgttgaaaag	tctttctgct	180
tacgcgcgcc	aatttttggg	aaatatggaa	aagcctgatg	tagattctat	tgatggcctt	240
agtcacgcta	tttctattga	tcagaaaaa	acaagtaaga	atcctcgctc	tactgttggg	300
actgtaacag	aaattaacga	ttatttacgt	ttgctttatg	ctcgtgttgg	aaccccatat	360
tgtatcaatg	gtcacggagc	catcacagca	tcttctgtag	agcaaattgt	ggataaggta	420
ctagcgcttc	cagagcgaac	aaagatgcaa	attttagccc	caattatacg	tcgaaaaaaa	480
ggacaacaca	aatcaacatt	tgagaaaata	caaaaagatg	gttacgttcg	tgttcgtatt	540
gatggtgata	ttcacgatgt	tactgaggtg	cctgaattat	caaaaagtaa	gatgcacaat	600
attgatattg	tagtagatcg	attaattaat	aaagagggca	ttcgttcccg	cttatttgat	660
tcogttgaag	cggtctacg	tttgtcggat	ggttatgtcg	ttattgatac	aatggatggc	720
aatgagttat	tgttttcaga	gcattattct	tgctcctgaat	gtggttttac	tgttcctgaa	780
ttagagccac	gccttttttc	ttttaatgct	ccctttgggt	cttgtagcac	ctgtgatggc	840
ttaggaatta	agttagaagt	ggatatagat	ttggttattc	cagataaaag	caagaccctt	900
agagaagggg	ccttagttcc	ttggaatcca	atttcatcaa	attattatcc	aacgatgcta	960
gagcaagcta	tgactcaatt	tgatgttgat	atggatacgc	catttgaaaa	attaagcaag	1020
gcggagcagg	acctagccct	atatggttca	ggcgaacgag	agttccattt	ccattatatt	1080
aacgattttg	gaggcgagag	aaatattgat	ttgccttttg	aaggggttgt	caataatatt	1140
aatcgtcgtt	accatgaaac	taatagcgat	tacacacgca	atgttatgcg	agaatatatg	1200
aacgagctaa	aatgtaacac	ttgtcatggc	tatcgtctca	atgatcaagc	actttgcgta	1260
agagttgggg	gagaagaagg	tcttaatat	gggcaagtct	cagatttatc	gatagcagac	1320
catttagaac	ttttagaac	gttgcgttta	tcttcaaagt	aacaattaat	tgctcgacca	1380
attatcaaac	aaattcaga	ccgcctaagt	ttcttaaaat	atgttgggct	taattattta	1440
aatctgtcac	gttctgcagg	aacgctttcc	ggggcgagag	gtcaacgtat	tcgtttggct	1500
actcaaattg	ggtctaattt	atcaggtgtc	ctttatgtac	ttgatgaacc	gtccattgga	1560
cttcatcagc	gagacaatga	ccgtttgatt	gatagtctta	agaaaatgcg	tgatttgggt	1620
aatacgctta	ttgttgttga	acatgatgaa	gatacaatga	tggcagctga	ttgggttaac	1680
gatgtgggac	ctggcgctgg	tgcgtttggt	ggtgagattg	tggcctctgg	cacaccgaag	1740
caagtagcta	aaaatactaa	atctattaca	ggacaatatt	tgtcaggtaa	gaaagtgatt	1800
cctgtgccat	ctgaacgaag	agtaggcaat	ggtcgctttt	tagaaatcaa	aggtgcggca	1860
gaaaacaacc	tacaaaattt	agatgtcaag	ttccctctcg	gtaaatttat	tgccgtaact	1920
ggtgtctcag	gttctggaaa	atcaacctta	attaatagta	ttttgaaaaa	agctgttgcg	1980
cagaagctta	accgtaactc	agataaacca	ggtaaatatg	tttctttaga	aggcattgaa	2040
tatgttgatc	gattgattga	tattgaccaa	agtcgaattg	gtcggacccc	acgttctaata	2100
cccgcaacct	atacagggtg	ttttgatgat	attcgtgatc	tttttgctca	aactaatgag	2160
gcaaaaattc	gaggttataa	aaaaggacgc	ttctcattta	acgtcaaagg	tggacgttgt	2220
gagtcctgtt	ctgggtgatg	tatcatcaaa	attgagatgc	attttttacc	agatgtctac	2280
gttccttctg	aagtatgcca	cggcacgcgc	tataatagtg	agactctgga	agtagcattac	2340
aaagaaaaaa	atattgcaca	aattcttgat	atgacagtga	atgatgcagt	tacatttttt	2400
gcagctattc	ctaaaattgc	tcgtaagtta	cagactatta	aggatgttgg	tttgggatat	2460
gtcacttttg	ggcaaccagc	tacaacctta	tcaggaggag	aagctcagcg	aatgaagttg	2520
gcaagtgaat	tacataagcg	ttcgacagg	aagagtcttt	acataattaga	cgaaccaaca	2580
acggggcttc	atgcagatga	tattgctcgc	ttacttaagg	ttttggatcg	tttttgtagat	2640
gatggtaata	cagtgcttgt	tattgagcat	aaccttgatg	ttattaaaaa	tgctgaccac	2700
attattgatc	tcggccctga	aggaggtatt	ggtggcggac	aaattgtagc	tatcggaaca	2760
ccagaagaag	ttgctgaaaa	tcctaaatcc	tatacaggat	attattttaa	agagaagtta	2820
gcaagatag						2829

SeqID 125

atgtggcctg	aagatagaat	cgcttctttt	cgtcgcacac	ttttaggggtg	gtatgaccaa	60
gaaaaacgtg	atctcccttg	gcgaagaact	actaatccat	actataatttg	ggtttctgaa	120
atcatgttgc	aacaaacaca	agttaataca	gtaatccctt	attataaacg	ttttctagag	180
tggtttcctc	aaataaaaaga	tttggcagac	gctcctgaag	aacaattact	aaaggcatgg	240
gagggactag	gttattatct	tcgggtgcgt	aatatgcaaa	aggctgcaca	gcaagtgatg	300
gttgattttg	gtggcatatt	tcctcacact	tatgatgata	ttgcttcatt	aaaagggatt	360
ggtccttata	ctgcagggtgc	tatcgccagc	atctcattca	acttaccaga	gcctgccgtt	420
gatggcaatg	tgatgcgtgt	catggctcgt	ttgtttgaag	ttaattatga	catcggtgac	480
cctaaaaatc	gtaaaatttt	tcaagctatt	atggaaatac	taattgaccc	tgacagaccc	540
ggtgatttta	accaagcact	tatggatctg	ggtacagaca	togaatccgc	taagacacct	600
agacctgatg	aaagccctat	tcgtttcttt	aatgctgctt	atttgaatgg	tacttatagt	660
aaatatccca	taaaaaatcc	taagaaaaag	cctaaaccaa	tgccaattca	ggcttttgct	720
attcgtaac	aaaatggcca	atatctactg	gagaaaaata	ctaaagggag	acttctaggg	780
ggttttttgt	catttccctat	tatcgaaacg	tcacctcttt	ctcaacaatt	agattttatt	840
gatgacaatc	aatccaaccc	cataatctgg	caaacccaaa	atgaaacttt	ccaaagagaa	900
tatcaattaa	agccccaatg	gactgataat	cactttccca	atattaagca	cacttttagt	960
caccagaagt	ggacaataga	actcatagag	gggtgggtca	aagcaacaga	tttaccta	1020
gctcctcacc	taaagtgggc	agcaattgag	gacttttctc	tgtatccctt	tgcaacgcca	1080
caaaagaaaa	tgctggagac	ctacttaaaa	cagaaaaatg	cttaa		1125

SeqID 126

ttgatcgaaa	tcacttggac	tgtgaagtat	atcacagaat	ttatcgcaac	cgcttttctt	60
atcatcttag	gaaatggggc	tgtagctaac	gttgacttaa	aaggcaca	aggaaataat	120
tcaggttggg	ttattatttg	aattgggtat	ggtttaggtg	ttatgatgcc	agcgcttatg	180
tttggtaatg	tctctggaaa	ccatattaac	ccagctttca	cacttggatt	ggcattttca	240
ggctctttcc	cttgggcaca	cgttggcaca	tacattcttg	cacaaatttt	gggagcaatg	300
tttggacagt	tagttgtcgt	tatggtttat	caaccttact	ttgttaagac	agaaaaatcca	360
aatcatgttc	ttggatcatt	ttcaactatt	tctgcattag	atgatggaca	gaaatcaagt	420
cgtaaagcgg	cttacattaa	tggtttctta	aatgaattcg	ttggttcttt	tgttcttttc	480
tttggagctt	tggctttaac	gaagaactat	ttcgggtgtag	aacttgttgg	taaaacttgtt	540
caagctgggt	atgaccaa	gacagcagcg	acaaggattt	caccatacgt	aactgggttca	600
cttgcgtgtag	ctcacttagg	tattggtttc	ttggtaatga	ctctagtgtg	ttcttttaggt	660
ggaccgagct	gacctgcatt	gaacctgcg	cgtgaccttg	gtccacgtat	tgttcacgcg	720
ttattaccaa	aacaaattct	tggaacaagt	aaagaagatt	caaaatgggtg	gtatgcatgg	780
gtgccagttt	tagcaccaat	cgtagcaagt	atactcgctg	tagccttggt	caaactatta	840
tatcttta						849

SeqID 127

atgtcatctt	attggaataa	ctatcctgaa	cttaaaaaaa	atattgatga	aaccaatcaa	60
ctaattcaag	aaagaataca	ggtcagaaat	aaagatatgg	aagcggcgct	aagccaactc	120
acagctgcgg	gaggaaaaca	gctcagacca	gcattctttt	accttttttc	tcaacttgggt	180
aataaggaga	atcaagatac	tcagcaacta	aagaaaatcg	ctgcttcttt	agaaatcctt	240
cacgttgcta	cattaatcca	tgatgatgtc	attgatgact	caccactaag	acgtggaaat	300
atgaccattc	aaagcaagtt	tggcaaagac	atcgcagttt	atactgggga	tttacttttc	360
acagtctttt	tcgatcttat	tttagaatct	atggctgata	caccatttat	gaggattaat	420
gcaaaatcta	tgcgtaaaat	tctcatggga	gaattggacc	agatgcacct	tcgttacaat	480
caacaacaag	gtatccatca	ctattttcgt	gcgattttcag	gtaagacagc	cgaactcttt	540
aaattagcta	gcaaaagaagg	agcttaactt	ggtgggtgcag	agaaggaggt	tgttcgtcta	600
gcaggccata	tcggctttta	cattgggtatg	acattccaaa	ttttggatga	tatcctggat	660
tatactgcag	ataaaaaaac	atttaataag	cctgtcttag	aggattttaac	acaaggcgtt	720
tacagccttc	ctctacttct	tgccattgaa	gaaaatcctg	atattttcaa	acctatttta	780
gataaaaaaa	cagatattggc	tactgaagac	atggaaaaaa	ttgcttatct	cgtcgtttcc	840
catagagggtg	ttgacaaagc	tcgccatcta	gctcgtaaat	ttactgagaa	agctattagt	900
gacataaata	agctacccca	gaactctgca	aaaaaacagt	tgctacaatt	aactaattac	960
cttttaaaac	gcaaaattta	a				981

SeqID 128

atgtttaaaa	tccctttgtt	taaagaatta	aagacagatc	aatgggtaaa	accatttttc	60
aaacaatata	aagtttcctt	agtaattgct	cttttccctg	gttttatgac	tttcttttct	120
gccagtgcct	ttatgtttta	ttcgggctat	ctgattagta	agtcagcttc	actaccgagt	180
aatattcttc	tagtatatgt	tccaattgta	ctaacaagtg	cttttggtat	tggaagctct	240
gtttttcgtt	atatagaacg	cctaacaggt	cacaattggg	tattacgaat	gacttcacaa	300
ctgcgcttga	agctttacca	ttccttagaa	agcaatgcta	tctttatgaa	gcgtgatttt	360
cgtttaggag	atgttatggg	gcttttagcg	gaggatatta	attatttgca	aaatttgtat	420

cttaggacaa	tatttccaac	gattatagcg	tgggtattat	atagctttat	tattattgca	480
acaggcttct	tttctctatg	gtttgcttta	atgatgttgc	tttatttagc	tattatgatt	540
tttctttttc	cacttttggtc	gatttttagct	aatggtgctc	gtcagactcg	tgaaaaagaa	600
ttaaaaaatc	atctttatac	tgatttgacg	gataatgtct	taggtatttc	agactggatt	660
tttagtcaac	gtgggtcaaga	gtacgtcgcc	ttgcatgaac	gttcggaaag	tgaactaatg	720
gctattcaga	aaaaaattcg	ttcctttaat	aatcgtagag	ctcttattgt	ggaattagtt	780
tttggctttc	tagctatttt	gggtattatt	tgggctagta	atcagtttat	tgggtcacaga	840
gggtggcgaag	ctaactggat	tgacgcattt	gttctaacag	tatttccctt	gtcagaggca	900
tttgctgggt	tgtctgctgc	tgctcaagaa	acaaataaat	attctgattc	aattcatcgt	960
cttaatgaat	tatcagaaac	gtattttgaa	acaaactcaa	atcaattgcc	taataagcca	1020
tatgattttt	ccgtcaagaa	tttaagtttc	cagtataagc	cacaagagaa	atgggttttg	1080
catcattttg	atttggatat	taaagaagga	gaaaaaattg	ctatttttagg	gcggagtggg	1140
tctggcaaga	tagctattagc	tagtctactt	cgtgctgact	tgaaagcaag	tcaagggaag	1200
attaccctag	gcgggtgctga	tgtttcaata	gttggtgatt	gcatttctaa	ctatatggga	1260
gtgatacaac	aagcgcctta	cctttttaat	acaaccctgc	taaataacat	tgcattgga	1320
aaccaagatg	ctagtgaaga	agatgtatgg	aaagtctctg	aacgagttgg	attgaaagag	1380
atggctactg	atztatcaga	tggctctctat	acaatgggtg	atgaagctgg	acttaggttt	1440
tcagggtggcg	aaaggcatag	aattgctttg	gctagaatct	tactaaaaga	tgtcccaatt	1500
gttatctttg	atgagccaac	tgttggactt	gatcctatta	ctgaacaagc	cttactaagg	1560
gtattttatga	aagaatttga	aggtaagacc	ttagtttggg	ttacacatca	cttaaaagggt	1620
attgaacatg	ctgatcgtat	cctattttata	gaaaatgggc	aatttagagtt	ggaagggtct	1680
cctcaagaat	tgtctcaaag	tagtcaacgt	taccgtcagc	tgaaagccgc	tgatgatggg	1740
gatctatga						1749

SeqID 129

atgaaaaaac	ttattacaga	aaaaaaagtc	aacaacgtct	caactgttaa	ctatttgaaa	60
ctcggctctg	tctcagcaat	gtttgctgga	ggagcattcg	tagctcttgg	ttctacacaa	120
gggtgtttcag	cttcaacttt	cacagcaccg	caagcaacac	atccaaaagc	agaacgtcag	180
ttaacagatt	cagaaatcta	tgaacgtgcc	caaaaacaag	tgttaccaaa	atatatocaa	240
ggttctctct	caggtatcct	taaccaacat	tcaacacttt	acaaacaaca	aaacgcagca	300
gtgacaccgc	aagtatcaag	ccccaaagca	gaacgtcagt	taacagattc	agaaatctat	360
gaacgtgcc	aaaaacaagt	attgccaaaa	tatattcaag	gttctctctc	aggtatcctt	420
aaccaacatt	caactttgaa	tgcttaa				447

SeqID 130

atggaggaaa	acatgaacat	aaaacaatta	aagtctaaaa	caatgcttgg	aacagtggct	60
ttgggtgtccg	ctttttcatt	tgcttcaaca	aatgcagatg	cgaatacata	taactatgca	120
gtagatgtag	actacctagc	aagtgcggag	gaaattgtct	aagcacatcc	agctagtaat	180
acgtttccac	taggtcaatg	cacatggggg	gtaaaaggaga	tggcaacatg	ggcaggtaac	240
tggtgggggaa	acgggtggtga	ttgggtctgc	agcgcgcgat	cagctgggta	tacagtagga	300
acacaacctc	gcgtgggttc	tatcgtatgt	tggactgatg	gtagttatgg	acatgtggct	360
tatgttacag	ctgtagatcc	tgtcactaat	aaaattcagg	ttttagaatc	taattatgca	420
ggatcatcaat	ggattgataa	ttatcgtggg	tggtttgatc	cacaaaatac	agcgacacca	480
ggggtagtta	gctacattta	tccgaattaa				510

SeqID 131

atgaaaatta	accaaagtaa	aaaagacgag	cttttttgagg	ggttttacct	tataaagaaa	60
gcagaagttc	gtaaaacgcg	tgacggtaaa	gacttttattg	cotttacott	togagatgat	120
actggcgaaa	tttcaggaaa	tatgtgggat	gcacaaacct	ataatgtaga	agagtttgta	180
gccggtaaaa	ttgttcatat	gaaagggcgt	cgtgaagttt	ataatggaac	tccccagtc	240
aaccaaatta	cattaagaaa	catcaaagat	ggtgaacctt	atgatcctag	agatttttaa	300
gaaaaacctc	caatcaatgt	tgacaacgtg	agagagtaca	tggaacaaat	gctcttttaa	360
attgaaaatg	caacctggca	gcgtgtggta	agagcacttt	atcgtaaata	caataaggaa	420
ttttttacct	atccagccgc	caaaaacaaac	caccacgcct	ttgaatcagg	attggcatat	480
cacacggcaa	cgatggttcg	tttggcagat	agtattggag	atatctatcc	agaacttaat	540
aaaagtttga	tgtttgctgg	tattatgcta	catgatttag	ccaagggtcat	tgagttatcg	600
ggtcctgata	atacagaata	tactatttga	ggtaacctta	tccggtcatat	ttcacttatt	660
gatgaggaat	taacaaaaat	actagcagag	cttaatatgt	atgatacaaa	agaagaggtt	720
acagtgttac	gccatgttat	tctgagtcac	catggacaat	tagaatatgg	aagcccggtt	780
cgtcctagaa	tcatggaggc	agaaattatc	catatgatcg	ataacattga	tgcaaatatg	840
atgatgatga	caacagcttt	aaatcgtgtc	aacgaagggtg	aaatgacaaa	tccgattttt	900
gccatggata	accgttcttt	ttataaaccg	aacattaaat	aa		942

SeqID 132

atggttggttg	acaagaagtg	gcgtttttgaa	gatagtgcac	gttatttctgc	ttgtcctaaa	60
-------------	------------	-------------	------------	-------------	------------	----

tggtcaaaatc	ccttgataaa	agaaagtaac	agcctcaaat	gctctgataa	tcattgtttt	120
gattttatcca	aattttggata	tggttaatcct	cctggaggaa	agaagataga	tgaacattat	180
gataaaaaat	cattttgaaaa	tcggcagcct	gtccttagaaa	acgggtatta	taatcatatt	240
ttagaagcta	tttcaaagggt	tttggaataat	aattctcagt	ttcattcggt	tttagatatt	300
ggttgtggag	agggctttta	ttctcgtcaa	ttagttaaca	agtatgagaa	gactttcttg	360
gcttttgata	tttctaaaga	ttcgattcaa	ttagctgcta	aaagtgatca	atctaggcct	420
gtgaaatggg	ttgtttctga	tttagctaac	cttcctattc	aagactcatc	aattgatatc	480
atttttagaca	ttttttctcc	tgcaaatat	aaagaattta	ggcgggtact	gagtgatgat	540
ggatcccttg	taaagggttg	tcctgtagct	gaacatgtcc	aagaattgct	agaaaaagct	600
agtcaatact	tgaacacagaa	agattactct	aatcaaaaaa	ttctagatca	cttttagagaa	660
aattttgaaa	ttattttctga	gcagaaaggt	gttcaaaggt	ataactgttc	tcaacaagaa	720
cgtcaagcct	ttattgatat	gacaccgttg	ttattcagcg	tagataaaac	gactattgat	780
tgggcgagta	tatcagaaat	tacagtaggt	gccttaatat	taattggaaa	aaagcgcagt	840
gtatctaaat	aa					852

SeqID 133

atgtgtctta	tttgtcaacg	tattgaaatg	attgaacgaa	atgagaatcc	ttattttgtg	60
aaagaatatg	aaacgggtta	tcttgttctg	ggagaccatc	aatattttca	aggttattgc	120
ctttttctct	ctaaaaaaca	cgtaacagag	ttacatgaat	tgcttagaga	ttggcgaaat	180
cagtatcttt	ccgaaatggc	agatgcttct	gaaatagtgt	ctaaggcttt	tagagcagat	240
aagatgaata	ttgagagttt	gggaaatgga	gacgctcatc	tacattttca	tctttttcca	300
agaaaaacag	gtgatttaag	gaactatggg	cataatggaa	aagggtccagt	ttggtggtat	360
ccttttgaga	agatgtatgc	agatagtgtc	agagcaactg	gtgcagaaat	agaaaaatta	420
aaagagaaat	tgtttagatg	cttaggatag				450

SeqID 134

atgttttagtg	atttacgcaa	aaaatttgtc	tttttgacca	tgtcaatcct	tattgtcgtt	60
gttctctttc	tctttgcagt	gagtaatcgc	tacaatcaat	attgggatga	atatgatgca	120
tataggattg	ttaaattagt	tgccaaaaat	gattatttag	gaataccagg	cgatgaaccg	180
attgcttttg	tgactataga	taaccaaaag	atgggttaaga	ttcaaagcaa	taatactgat	240
ttgacaaatg	atgttatcga	aaaatctagt	ttgaagctcc	ttgagcaagg	aaagaagtca	300
cgaaaatgga	agtcttttat	atattccata	aaagaatata	aagataaaac	ctacaccata	360
gctattatgg	atttggctag	ttatgaagtc	ccttatgcaa	ggcgttttct	aattcttggt	420
tttactattt	ttggattttg	tttattagca	gctgtaagtc	tttatctttc	tcgattttatc	480
gtagggcctg	tagagacaga	aatgactcgc	gaaaaaacagt	tcgtttcaga	tgcgagtcac	540
gagctgaaga	cccctattgc	agctatacga	gccaacgttc	aggttctgga	acagcaaatt	600
ccaggaaatc	gttatctgga	tcagtgtgtt	tcggagacta	agcgaatgga	gttttttaatt	660
gaagatttgc	ttaatttgtc	tagacttgat	gaaaaacgct	ccaaggtaaa	tttcaaaaag	720
ttaaacttat	ctgtcttatg	tcaagaagta	cttctgacat	atgaaagtgt	ggcatatgaa	780
gaagaaaagt	gtttaaatga	tacgattgaa	gatgatgtct	ggattgttgg	agaagagagt	840
cagattaagc	aaattttta	aattcttttg	gataatgcta	ttaggcatc	tttgtcaaaa	900
tcagaaatcc	agtttagtct	taaacaggct	cgaagaaaag	ctattctgac	aatatcaaat	960
ccaagtgtca	tctattccaa	agaggttatg	gataatctct	ttgagcgttt	ttatcaagct	1020
aaagatgatc	atgcagattc	tctcagtttt	ggtctaggct	tatctattgc	taaggcaatc	1080
gtggaacgcc	ataaggggag	aattagagca	tatcaagaaa	aagaccaatt	acgtcttgaa	1140
gtccagttac	caattgatgg	attttggacc	aataccatga	ttaattaa		1188

SeqID 135

ttgattatcc	tcgataaaaa	aagttatgac	ctcctctttt	acctattgaa	attagaggaa	60
cctgaaacag	ttatggcaat	tgccaaacga	cttaatcagt	ctaggcgtaa	agtgtattat	120
cacttagaga	agataaacga	tgactgcct	agcgatgtgc	ctcagattgt	tagttatcca	180
cgtgtaggaa	tcttgctaac	cgaaaaacaa	aaagcagcct	gtcgtctttt	attagatgaa	240
gtaactgatt	atagttacgt	catgaaaagt	agtgaagggt	tgcaactaaa	cttagtatct	300
atcgtggtag	ctaaggaccg	cataacgatt	gatagggtga	tgcaactaaa	cgatgtttct	360
cgaaatacta	tcttaaacga	tttaaacgaa	ttagaagtg	agttagcaga	gaaagaatat	420
aatttacagt	tacaatcaac	aaaatgtcgc	ggttattttt	tagatgggtca	cccatgtgcc	480
attatccagt	acttatataa	gctcttagat	gatatctacc	ataatggaag	tagtagtttt	540
atagaccttt	ttaatcataa	actgtctcaa	gcttttgggtg	ccagcacata	tttttctaaa	600
gaggttcttg	attattttca	ccattatctc	ttcattttctc	aacgaagtct	aggtaagaaa	660
atcaacagtc	aagatgggtc	gtttatgatt	cagattttgc	cttttatact	aatggcttat	720
cgtaagatgc	gattaagtcc	tgaagtacag	acctctctta	atagtgattt	tagcttgggt	780
tggcaacgta	aggaatatga	gattgctaaa	gagttggctg	atgagctgga	agaaaaattt	840
cagttatcac	tggatgagat	tgaagtggga	ctagtggcca	tgcttatgct	tagtttccgc	900
aaggaccgtg	acaatcattt	agagagccag	gattatgatg	atatgcgagc	tactctaacc	960
agttttttga	aagaattgga	agaacgatat	caccttcaact	ttgttcataa	aaaggactta	1020

ctaagacaac	ttctaactca	ctgcaaggca	ctcttatatc	gtaaacgtta	tggtattttt	1080
tctgttaatc	ctttaacaga	gcataattaa	gacaaatatg	aagaactttt	tgccataacc	1140
tctgtcttctg	taaagctttt	agagaaagct	tggcaaataca	aattgaccga	tgatgatgta	1200
gcataatctaa	cgattcattt	aggaggggaa	cttcgtaata	gtcaacaatc	tcctaataaaa	1260
cttaagttag	ttattgtatc	tgatgaagga	atagcgattc	agaaacttct	tttaaagcaa	1320
tgtcaacgct	acttaacaaa	cagtgatata	gaagctgttt	ttacaaccga	acagtaccaa	1380
agtgtgagtg	atcttatgca	tgtagatatg	gttgtctcta	ctagtgcgc	tttagaatct	1440
cgttttccga	tgttagtagt	tcaccctgtt	ttgacagatg	atgatattat	tcgcttgatt	1500
cgcttttcaa	aaaaaggtaa	ctgtgcaaat	agtaatcaat	ttaccaatga	acttgaaaaa	1560
acgattgctc	aatatgtcaa	ggaagatagt	gaacgctacg	tgctgaaatc	taagattgag	1620
aaacttattc	atcaagaatt	gctccaagac	gtccttcccc	ttcaaagtac	agtttgtaa	1680

SeqID 136

atgaaatact	ttttagatac	tgccgatgtt	tctgaaattc	gtcgtcttaa	tcgttttagga	60
atcgttgatg	gtgttactac	caatccgact	attatttcac	gtgagggcg	tgactttaaa	120
gaagttatta	acgaaatttg	ccaaatcggt	gatggcccag	ttagtgcaga	agtgcacggg	180
ttaaactgtg	atgaaatggg	taccgaagct	agagaaatcg	ctaagtgggc	accaaagtgt	240
gttggttaaaa	ttccaatgac	tgaagaagg	ttagcagcag	tttcacaatt	atcaaaagaa	300
ggataaaaga	caaatgtgac	attaatatatt	actgtggctc	aaggtctttc	ggcaatgaaa	360
gctggtgcaa	catttattag	tccttttgtg	ggctgctctg	aagatatttg	aacagatgct	420
tatgctttga	ttcgtgacct	tcgtcacatt	attgattttt	atgggtttcca	atctgagatt	480
attgctgcta	gcattcgtgg	attggcgcat	gtggaggggc	tcgctaaatg	cggtgcgcac	540
attgccacta	ttccagataa	aacatttgca	tcactattta	ctcaccgcgt	tactgataaa	600
gggattgaaa	ctttcttaaa	agattgggat	agtttcaaga	agaagtag		648

SeqID 137

atgagtcatt	attccataaa	attacaagaa	gtattcagat	tggcgcaatt	tcaagcagca	60
cgctatgaaa	gtcactatatt	agaaaagctgg	catcttcttt	tagcaatggg	tttagttcat	120
gattcagtag	ctggtttgac	atttgcgtgaa	tatgagtcctg	aagttgcaat	tgaagagtag	180
gaagcagcaa	caatttttagc	tttaggtaga	gcaccgaaag	aagagattac	caattatcaa	240
tttttagagc	aatcaccagc	tttgaaaaag	atcttaaaag	tagcagaaaa	tattagtagtc	300
gtagtaggag	ctgaagatgt	gggtactgaa	catgtcttgc	ttgctatggt	ggttaataaaa	360
gatttattag	ccacacgtat	cttagagtta	gttggtctta	gaggtcaaga	cgatgggtgaa	420
tcagttcgta	tggttgattt	acgtaaaggct	ctagaacgtc	atgccgggtt	tacaaaagat	480
gatatcaaag	caatttatga	attacgtaat	cctaaaaaag	caaagtcggg	tgcttctttt	540
tctgatatga	tgaaccacc	gagtactgct	gggtatttag	ctgatttcac	acgtgattta	600
tcacagatgg	cggttgatgg	ggaaattgaa	cctgttattg	ggcgtgataa	agaaatttca	660
cgtatgggtc	aagtcttaag	tcgtaaaaaca	aagaataatc	ctgtcttagt	tggagatgcg	720
gggtgcggta	aaacagcttt	ggcgtagcgt	ctagcacaac	gtattgctaa	tggaaatatt	780
ccttatgagc	ttagagatat	gcgtgttcta	gagttagata	tgatgagcgt	tgttgctgga	840
actcgttttc	gtggtgattt	tgaggaaagct	atgaatcaaa	tcattgcaga	tattgaagaa	900
gacggtcata	ttattctttt	cattgatgaa	ctgcatacta	ttatgggttc	tggctctggt	960
attgatagca	catttgatgc	tgctaataatt	ttaaaaccag	ctttggcccg	aggcacttta	1020
cgcactgttg	gagcaacaac	tcaagaggaa	tatcaaaagc	atattgaaaa	agatgctgct	1080
ttatctcgtc	gctttgcaaa	agttttagta	gaagaaccaa	atcttgaaaga	cgcataatgaa	1140
attctacttg	gattgaagcc	agcgtatgaa	gcctttcata	atgttactat	ttcagatgaa	1200
gcagttatga	ctgctgttaa	agtggtctcat	cgtttattga	caagtaagaa	tttaccagac	1260
tcagctatag	acttacttga	tgaagcttct	gccactgtgc	aaatgatgat	taagaaaaat	1320
gctccttcgc	ttttaacaga	agttgaccaa	gctatttttag	atgatgatat	gaaatctgct	1380
tctaaagctc	taaaagcaag	ttataagggt	aaaaagcgta	agcctattgc	cgtaacagaa	1440
gatcatatta	tggcaactct	cagtcgtcta	tctgggtattc	ctgttgaaaa	attgacacaa	1500
gctgatagta	aaaaatacct	caatttagaa	aaagaattgc	ataaacgtgt	tatcgggtcaa	1560
gatgatgcag	ttactgccat	tagtcgtgct	atccgtcgca	atcaatctgg	cattcgtact	1620
ggtaagcgct	ctatttgctt	ctttatgctt	ttggggaccac	ctgggtgttg	taagacagag	1680
ttagcaaaaag	ccttggcaga	agtgttggtt	gatgatgaat	cagccctaata	tcgttttgat	1740
atgtcggaa	atatggaaaa	attcgcagct	tctcacctga	atggggcacc	tccagggttat	1800
gttggttatg	atgaaggagg	agagttgact	gaaaaagtag	gcaataaacc	atattcagtt	1860
ttactttttg	atgaagttga	aaaagctcat	ccagatattt	ttaatgtatt	attacaagtg	1920
cttgatgatg	gcgttttaac	agatagtcga	ggacgaaaaag	ttgatttttc	aaatactata	1980
atcattatga	cttctaattt	aggagcaact	gctatgcgtg	acgataaaaac	agttgggtttt	2040
ggagctaagg	atatcagcca	tgattatact	gctattgcaaa	aacgtattat	ggaggagctt	2100
aaaaaagctt	atcgaccaga	gtttatcaat	cgtattgatg	agaaagttgt	attccatagt	2160
ctcagtcaag	ataatatgctg	tgaagttgtg	aaaattatgg	ttaaaccttt	aatttttagcg	2220
cttaagata	aagggtatgga	tctgaaattc	cagccttcag	ccttgaaaca	cttggcagag	2280
gatggctatg	atatagaagt	gggtgctcgt	ccactgcgta	gaactattca	aacgcaagta	2340

gaggatcatt	tatcagaact	actattggca	aatcaagtga	aagaggggca	agtaattaag	2400
attggcgtat	ccaaaggcaa	attgaaattt	gatattgcaa	aatcataa		2448

SeqID 138

atggtcttag	ataaagaaat	caaggctcaa	ttagcgcaat	atntagattt	gctagaatct	60
gatattgtat	tacaagctga	tttaggagat	aacgataatt	ctcaaaaagt	aaaggatttt	120
ctagatgaaa	ttgtcgctat	gtctgatcgc	atcagccttg	aatcaacaca	tttaaaacgt	180
caacctagtt	ttggaattgc	aaaaaaagg	catgaaagtc	gcgttatttt	ttcaggcttg	240
ccaatggggc	atgaattcac	atctttcatt	ttagctttgt	tgcaagtcct	tggtcgcgca	300
ccaaaagttg	atgaagatat	tatcaaacga	attaagggga	ttgagaaaac	tatcaatcta	360
gaaactttat	tttcattaac	ttgccataat	tgtccagatg	tcgttcaagc	ctttaatatata	420
atggctgttt	tgaatccgaa	tatcactcat	actatgattg	aaggaggcat	gtatcaagac	480
gaagtcaaat	caaaaaggtat	catgtctgtt	cctactgttt	ataaggacca	agaagaattt	540
acttctggcc	gtgtcacaat	tgaacagctt	ttagaacaac	tagatggacc	tcttgatgct	600
gaagcatttg	ctgacaaagg	tgtctatgat	gttctagtta	ttggtgggtg	tcctgcaggt	660
aacagtgcctg	caatttatgc	cgcccgtaaa	gggttaaaaa	caggtatttt	agcagaaact	720
tttgggtggac	aagttatcga	aacagttggt	attgagaaca	tgattgggtac	actgtacaca	780
gaaggcccta	aattaatggc	tcaaattgaa	gagcatacca	aatcttacga	tattgatatt	840
atcaagagtc	aattagcaac	tggcattgag	aaaaaagaat	tagttgaggt	aacactggct	900
aacggagcta	ttttacaagc	taaaactgct	atcctagctc	tgggtgctaa	gtggcgaaat	960
atcaacgttc	ctggcgagga	agaattccgc	aataaagggtg	ttacttactg	tccacattgt	1020
gatggccctc	ttttcgaaagg	aaaagatggt	gctgtttatg	gtgggtggtaa	ttcagggtatg	1080
gaagctgctt	tagatctagc	cggtgtcact	aaacatgtta	cagtcctaga	attcttacct	1140
gagctcaaag	cagaccaagt	actgcaagaa	cgagcagcta	aaactgacaa	tttaactatt	1200
cttaagaatg	ttgctactaa	agatatcggt	ggtgaagatc	atgtcactgg	tttaactat	1260
accgatcgtg	atacaaacga	agaaaaacac	attgatttag	aagggtgtttt	tgtacaaatt	1320
ggtcttgatc	caagtacatc	ttggctcaag	gatagcggca	ttgaactcaa	tgaacgtcaa	1380
gaaattgtcg	ttgataaaatt	ttgctcaaca	aatatccctg	gtatttttgc	tgcaggtgac	1440
tgtacagatg	ctgcctacaa	gcaaatcatt	atttccatgg	ggtctggtgc	cacagctgcc	1500
attggcgcac	ttgattattt	aatcagacaa	taa			1533

SeqID 139

atgataaaat	atcaagatga	tttttaccaa	gcggttaaatg	gggagtgggc	taagacagct	60
gttatttcctg	atgacaaacc	aaggacaggt	ggtttttctg	atcttgctga	tgacattgaa	120
gcattaatgc	tgtcaacgac	agataagttg	ctggctgatg	aaaataaaac	aagtgatagc	180
atttttaaatc	attttattgc	ttttcataaa	atgacagctg	attatcaaaa	acgtgaagag	240
gtaggagtat	caccagtatt	accattaatt	gaagaatata	aaggcctaca	atctttctct	300
gagtttgcat	caaaagttgc	agaatatgaa	ctagagggta	aoccaaata	atttccattt	360
ggtgtggctc	ctgactttat	gaatgctcaa	ttgaatgtac	tttgggctga	agcgcctggg	420
attattttac	cagatacaac	ttattatagt	gaagataatg	aaaaaggaaa	ggaactcctt	480
gctttttggc	gtaaaaatca	agaagacctt	ctgcctttgt	ttggcctttc	agaacaggaa	540
attaaagata	tcttggtata	ggttttagca	ttggatgcaa	aattggcaca	atatgtctta	600
tctcgcgaag	agagttcgga	atatgttaaa	ctttaccatc	cttataactg	ggaagatttc	660
acaaaattag	cacctgaact	tccattagat	gctattttcc	aaaagatatt	aggacaaaaa	720
ccagataaag	ttattgttcc	tgaagaacgt	ttctggacag	aatttgcac	tgactattac	780
tcagaatcta	attgggaatt	attaaaggca	gatcttattt	tatcagctgc	gaatgcctat	840
aatgcttact	taactgatga	tattcgtatc	aaatcgggag	tttacagtcg	agctttatca	900
ggcacaccac	aagcaatgga	taagaaaaaa	gcagcttact	accttgcttc	aggaccttac	960
aatcaagctc	taggtttgtg	gtatgcagga	gaaaaattct	ctccagaagc	taaagctgat	1020
gttgagcata	agattgcaac	gatgattgat	gtctataagt	cacgcttaga	aaaggcggat	1080
tggcttgcac	agtcaacgcg	agaaaaagct	attatgaaac	ttaatgttat	cacaccacat	1140
attggatacc	ctgagaaact	accagagact	tatactaaaa	aaatcattga	tcctaaacta	1200
tcgcttgctg	aaaatgctac	taatttagac	aaaatttcaa	tagcctatgg	ttggagtaaa	1260
tggaataaac	cagttgatag	aagtgaatgg	catatgcctg	ccacatgggt	caatgcgtat	1320
tatgatccac	aacaaaacca	aattgtcttc	ccagcagcca	ttttacaaga	accattttat	1380
gcttttagagc	aaagttcatc	agcaaattat	gggggaattg	gtgcagtgat	tgcacatgaa	1440
atatcacacg	cttttgacac	taatggagct	tcatttgatg	aacatggaag	tttgaataat	1500
tgggtggactg	atgaagattt	tgaagctttc	aaaaaactta	cagataaagt	agttgagcag	1560
tttgatggac	tggaatctta	tggcgcaaaa	gtcaatggta	aactaacagt	atcagaaaaa	1620
gttgcgagatt	taggtggagt	tgcttgctgc	ttagaagctg	cgcagcgtga	gtcagatttt	1680
tcagcagagg	atttctttat	taactttgcg	acaattttggc	gtatgaaggc	acgtgatgag	1740
tatatgcaaa	tgtttagctag	tgtagatgtt	cacgcccag	cacaatggcg	aactaatatt	1800
acagtaacga	attttgaaga	attccataaa	gagtttgatg	ttaaagatgg	tgataacatg	1860
tggcgtccag	ttgaaaaacg	tgttattatt	tggttaa			1896

SeqID 140

atgtctaaga	ttcttttttt	cgggtgaacct	ctcattcgca	tcactccaaa	agaaaatgac	60
tattttgcag	atagtatctc	aactaaacta	ttctatgggtg	gctctgaagt	taataaccgca	120
agagctctac	aaggcttttg	gcaagatact	aaactcctct	cagccttacc	caataatccc	180
ataggttaata	gttttcttca	atttttaaaa	gcacagggta	ttgatactca	ttctattcag	240
tgggttgag	aacgtgttg	gttatatttt	ttagaagatt	cctttgcttg	cagaaaagg	300
gaggtggtct	acgaccgca	tcatagtagt	ttacatgact	ttaggataaa	tcaaattgat	360
ttcgatcaat	tatttgaagg	agtttctctc	tttcatttta	gtggtattac	actatcattg	420
gatgagtcta	tccaagagat	aacactgctt	cttttaaaag	aagctaaaaa	aagagagata	480
acaatctcct	tagatctcaa	ttttcgagct	aaactaattt	ctcctaaaaa	tgccaaaatc	540
cttttttctc	agttcgctac	ctttgctggat	atgtgttttg	gtattgaacc	tcttatgggt	600
gactcacagg	acactacctt	cttcaatcgc	gatgaagcta	caatagagga	cgtcaaagaa	660
cgaatgattt	cgcttataaa	tcactttgac	tttcaagtca	ttttccatac	taaacgtcta	720
caggatgatt	gggaccgaa	ccactaccga	gcttcatatg	caaatacgtaa	acaagagttt	780
gtcacttcaa	agaaaatcac	cacagctgta	aaccagagaa	ttggaagcgg	agatgctttt	840
gtggcgagg	cgctatatca	actacttcag	cactcagaca	gcaagacagt	cattgatctt	900
gctgtcgcta	gtgcatcttt	aaaatgtgct	ttggaagggg	acaatatgtt	tgagaccggt	960
accgcagtta	acaaagtact	aatcaatcgc	aaagacatta	ttcggttag		1008

SeqID 141

atgaaaagtc	gaaaaaaaga	taaattggta	ttgaggttaa	caacaacact	attgggtttt	60
ggtttggtg	gggttggtt	ttataattat	aaaaatgata	atgtcgaacc	gacagtcact	120
agtgcacgg	atcaaacgac	gacttttatt	caaacgattt	ctccaacagc	tattgaaatt	180
tctaagacct	atgatttgta	tgcgtcagtc	ttattagcac	aagctatttt	ggaatcatcc	240
agtggacaat	cagatttgct	taaggctcct	aattataacc	tctttggcat	caaaggagaa	300
tataaaggta	aatctgtcca	aatgcctact	ttagaagatg	atgggaaagg	caatatgact	360
caaataccaag	ctccttttcg	cgcctatcca	aattattctg	cttactata	tgattatgct	420
gagttagtat	ctagtcaaaa	gtatgcactc	gtttggaaat	caaatacctc	ttcttataag	480
gatgctactg	cagctctaac	aggtctttat	gcgacagata	ctgcttatgc	tagtaaatta	540
aaccaaatta	ttgaaaccta	cagtctagat	gcttatgata	aatag		585

SeqID 142

atggcagacg	tgaaggtagt	gaataatgag	gattctagag	gtcaaaagca	agacttaaaag	60
gctaaactat	ttcatattaa	gatagggtca	gttcccctac	cagtatatgt	ttgttttagca	120
ttattgattc	ttctagcagg	ctttttacaa	aaattgccag	tcaatatgct	aggaggattt	180
gcagttatct	taacaatggg	gtgggttctta	gggactatcg	gagctagcat	tcctgggttt	240
aaaaacttcg	gtggcccagc	tattttatct	ttattagtac	catctatttt	ggtgtttttc	300
aacctcatta	ataaaaaatgt	tttagaatca	acaaatatgt	tgatgaagca	agctaaactt	360
ctttattttt	atattgcttg	tttagtgtcc	ggtagtattt	tagggatgaa	tcggaaaatg	420
ttgattccagg	gattgctaag	aatgattttc	cccatgttat	taggaatggt	ttgtgcatg	480
atggtaggga	catttgctcg	tgttatttta	ggcttagagt	ggcgacacac	tttgttttat	540
atcgtaacac	ccgttttagc	tggtgggtatt	ggtgaaggta	ttttaccatt	atcgttaggc	600
tatagttcaa	ttaccgggtg	agctagttaa	caactagtgt	ctcaactcat	cccagccact	660
attattggta	atctctttgc	cattttatgt	actgcactat	tgaatcggtt	gggagaaaag	720
aaaccacact	tgtctggtca	agggcaatta	gtaagggtta	ataaaggaga	ggacatgtca	780
gatattattg	ctgctcattc	tggcccaatt	gacgttaaga	aaatgggtgg	aggtgtttta	840
acagcatgta	gtgatcttat	ttttggacat	ttgttcgagc	aattaactgg	atttcctggg	900
cccgatttaa	tgattgttgc	agcagctatt	ttgaaatata	ttaatgttat	tcctagagaa	960
acacaaaatg	gagctaagca	actttataaa	tttattttctg	gtaattttac	atttcctcta	1020
atggcagggc	taggattgct	ttatatcccg	ttaaaagatg	ttgtggcaac	gcttagcata	1080
caatatttca	tagttgttat	tagtgttgta	ttacagttta	tttctgttgg	attcttttga	1140
tcgcgattcc	ttaatatgaa	tcctgttgaa	gcaggtatta	tttcagcttg	tcaaagtggg	1200
atgggaggaa	caggagatgt	tgccatttta	agtacagcag	accgaatgaa	cttgatgcca	1260
tttgctcaag	ttgctacgcg	tttaggagga	gctattactg	ttatcacaat	gacagccatt	1320
ttacgcagtg	tattctaa					1338

SeqID 143

agaggcaaaa	aagctggtaa	atacacaaca	tctgatgggt	acatttttga	tgccaaagat	60
attaaaaaag	atacaggtac	aggttatgtc	attccacata	tgacacatga	gcattgggta	120
ccaaagaaaag	atttatcaga	gtcggaatta	aaagcagctc	aagaatttct	ttcaggaaaa	180
tctgaagcaa	atcaagacaa	acaaaaaaca	ggtaaaaacag	ctcaagaaat	ctatgaggca	240
attgaaccaa	aagcaattgt	taaacctgaa	gattttattat	ttggaattgc	acaagcgaca	300
gactataaga	atggtacatt	tgtaattcct	cataaagatc	attaccatta	tgtggaatta	360
aatgggtttg	atgaagaaaa	agatctttta	gctgattcag	ataagacata	ttcttttagaa	420
gactatttag	ctacggctaa	atattacatg	atgcacccag	aaaaacgtcc	taaagttgaa	480

ggatggggta	aagatgctga	aatttataag	gaaaaggact	ctaataaagc	agataaacca	540
agtcctgcac	caactgataa	taaatcaaca	tcaaattcta	gtgacaaaaa	cttaagtgc	600
gcagaagtat	tcaaacagc	aaaaccagaa	aaaattgtac	cgcttgataa	aattgctgct	660
cacatggcat	atgcagttgg	atttgaagat	gatcaattga	ttgttcctca	tcatgatcat	720
tatcataatg	ttcctatggc	atggtttgac	aagggtgggt	tatggaaagc	accagaaggc	780
tatacattac	aacaactcct	ctcaacaatt	aaatactaca	tggaacatcc	taatgaatta	840
ccaaaagaaa	aaggttgggg	acacgacagt	gatcataaca	aaggctcaaa	taaagacaat	900
aaagccaaaa	attatgctcc	agatgaagaa	cctgaagatt	cagggaaggt	aactcacaac	960
tatggttttt	atgatgttaa	taaaggttca	gacgaagaag	aaccagaaaa	acaagaagat	1020
gaatcagagc	tagatgaata	tgaactagga	atggcacaaa	atgctaagaa	atatggtatg	1080
gatagacaat	cttttgaaaa	gcaactcatc	caattatcaa	ataaatatag	tgtaatgttt	1140
gaaagcttta	attatattaa	tggtagtcaa	gttcaagtta	ctaaaaaaga	tggctctaaa	1200
gtgcttggtg	atattaaaa	actaacagaa	gtgaaataa			1239

SeqID 144

atgaatcgta	aaaaaacagt	tattattagt	gctttatcag	tagctctatt	tggtactggt	60
gtagggtgctt	accaattagg	tagctataat	gccccaaaat	cagacaatag	tgtttcttat	120
gtgaaaacag	ataaatctga	tagcaaagca	caagcaacag	ctgtaaataa	aacgcccagc	180
caaatacagta	aagaagaagg	catatctgca	gaacaaatcg	ttgttaaaat	tactgacgac	240
ggttatgtga	cttctcatgg	agaccattac	cattattaca	atgggaaagt	gccatatgat	300
gccatcatta	gtgaagaatt	gattatgaaa	gaccctagct	atgtctttta	taaagctgat	360
gtcattaatg	aagtcaaaga	tggttatatt	atcaaagtta	acggtaagta	ttacctctat	420
cttaaagaag	gtagcaaacg	aacaaatggt	cgtacaaagg	aacaaatcca	aaagcaacgc	480
gaagaatggg	ctaagggtgg	ttctaaggga	gaatcaggaa	agcatagtag	tgcaaaaact	540
caagctttat	cagccagcgt	acgtgaagcg	aaagctagcg	gtcgcctatac	tacagatgat	600
ggttatgttt	ttagtccaac	agatgtcatt	gatgacatgg	gagatgcctt	tttagtacca	660
catggcgatc	atttccatta	tatcccga	gctgatttt	ctccatcaga	gttatcagcc	720
gcacaggcat	attggaaccg	caagactggc	cgatcaggta	atagctcaaa	accatcaaat	780
tcaagttcat	acattcatgc	aagtgcacca	agcggtaatg	tatcaacagg	aagacatgct	840
aatgccccta	tttctattcc	aagagtcact	cacgcaaact	actggtcaaa	accagctggg	900
aatcatgcta	cggcacccaa	acaccatgca	cctacaacca	aaccaatcaa	caaagattct	960
gcttttagaca	aaatgttgaa	acgtttatat	gctcaaccgt	tatatgctcg	tcacgtagaa	1020
agtgatgggt	tggtttatga	cccagcaca	gttaatgctt	tcacagcaat	cgggtgtttct	1080
attccgcacg	gtaatcattt	ccactttatt	cactataagg	atatgtctcc	attagagtta	1140
gaagcaacaa	ggatggtggc	agagcataga	ggacatcata	ttgatgcatt	agggaaaaaa	1200
gattctacag	agaaacccaa	gcatatttct	catgaaccta	ataaggaacc	tcacacagag	1260
gaagaacacc	atgcagtaac	accgaaagac	caacgtaaag	gcaaaccaaa	tagccagatt	1320
gtctacagtg	ctcaagaaat	tgaagaggca	aaaaagctgg	taaatacaca	acatctgatg	1380
gttacatttt	tgatgccaaa	gatattaaaa	aagatacagg	tacaggttat	gtcattccac	1440
atatga						1446

SeqID 145

atggctaaat	ttggattttt	atcgggtacta	gaagaagaat	tggataagca	tttacagtat	60
gactttgcc	tggattggga	taagaaaaat	catactgtag	aagtcacttt	tatattagaa	120
gcacaaaaca	gctctgctat	tgaaccctg	gacgaccagg	gggagacgag	tagcgaggac	180
atcgttttt	aggactatgt	actcttttac	aaccctgtca	agtctcgctt	tgatgctgag	240
gactatctgg	tgactatccc	ctatgagcct	aagaagggtt	tgctgcgtga	gtttctggct	300
tattttgctg	agactctcaa	cgaggttgcc	actgaagggt	tgagcgacct	catggacttc	360
ctcaccgatg	acagtatcga	agagttcggt	ctttcttggg	atacgggatgc	ttttgaaaat	420
ggcagagcag	aactgaaaga	gacagagttt	tacccttacc	cgagatatta	g	471

SeqID 146

atgaacacaa	aacagcgttt	ttcaatccgg	aaatataagt	taggtgcccgt	atctgtactt	60
ttgggaaccc	tatttttttt	aggtggtatc	acaaatgtag	ctgctgattc	tgtcataaat	120
aagccatctg	atattgcagt	tgaacagcaa	gtaaaagaca	gtccaacgag	catagcaaat	180
gagacaccta	ctaacaacac	gtcatcagcc	cttgctgcga	cagctcaaga	caatcttggt	240
acaaaggcta	ataatagtcc	aacagaaaaca	caaccagtag	ctgagtctca	ctctcaagcc	300
accgagacat	tttcccagct	cgcaaatcaa	ccggttgaaa	gcaactcaaga	agtttctaaa	360
actcctttta	ccaaacaaaa	tttagcagtc	aaatctacac	cagctatttc	taaagaaacc	420
cctcaaaata	ttgatagtaa	taaaattatc	actgtcccca	aagtatggaa	cacaggctac	480
aaaggagagg	gaactgttgt	agcaattatt	gactcaggac	tagatatcaa	tcacgatgct	540
ctccaattaa	atgattcgac	aaaagcaaaa	taccaaaaacg	aacagcaaat	gaatgctgct	600
aaagcaaaag	ctggtataaa	ctatggaaaa	tggtataaca	acaaagtaat	ctttggtcac	660
aactatgttg	atgtcaatac	agagctaaaa	gagggtgaaa	gcacttctca	tggtatgcac	720
gtaaccagta	tcgcaacagc	taatcctago	aagaaagata	caaatgaatt	aatctatggt	780

gttgctcctg	aagcacaagt	aatgtttatg	agagtcttct	ctgatgaaaa	aagaggaact	840
ggaccagccc	tttatgttaa	agctattgaa	gatgccgtta	aactcgggtg	tgacagcatt	900
aatttaagtt	taggtggagc	taatgggtct	ttagttaatg	ccgatgaccg	acttataaaa	960
gcttttagaga	tggctagact	cgctggcggt	tctgttggtta	tagcagcagg	taacgacggt	1020
acatttgggg	gtggagcatc	aaagccttct	gctctttatc	ctgattatgg	tttagttggt	1080
agtccatcaa	cagctcgtga	ggccatttct	gtagcatcat	ataataatac	aacactgggt	1140
aataaaagtct	tcaacattat	cggattagaa	aacaacagaa	atctcaacaa	cggattagct	1200
gcttatgcag	atcctaaaag	tagtgataag	acctttgaag	tagggaaaca	atatgattat	1260
gttttcgtag	gaaaaggaaa	cgacaatgat	tataaggaca	aaactttaaa	tggtaaaatc	1320
gccttaattg	aacgtggaga	tattactttt	acaaaaaaag	tcgtcaatgc	tattaatcac	1380
ggtgctgtgg	gagctattat	ctttaataac	aaagctgggg	aagctaactc	aacaatgagt	1440
ttagatcctg	aagcaagtgc	tattcctgct	atttttaccc	aaaaagagtt	tggagatggt	1500
ttagctaaaa	acaactataa	aattgtatit	aacaatatca	aaaataaaca	agccaaccct	1560
aatgcagggt	tcctatctga	cttttcaagc	tgggggttaa	cagcagacgg	acaattaaaa	1620
cctgacttat	ctgctcctgg	aggctctatt	tacgcgctta	tcaatgataa	tgaatatgat	1680
atgatgagtg	ggacaagtat	ggcttctccc	catgtcgtcg	gtgctactgc	tctagttaaa	1740
caatacttat	tgaaagaaca	tccagaactt	aaaaaagggt	acattgaaag	aactgtcaaa	1800
taccttctta	tgagtactgc	taaagcacac	ctaaacaaag	atacaggcgc	ttacacctca	1860
ccacgccaac	aaggagcagg	tattatcgat	gtcgcagcag	cagttcagac	aggattatac	1920
ctaactgggt	gggaaaacaa	ctatggcagc	gttacattag	gaaatattaa	agataaaatt	1980
tcctttgatg	ttactgttca	taatatcaat	aaagttgcaa	aagatttaca	ctatacaacc	2040
tatttaataa	ctgatcaagt	taaagatggc	tttgtcacat	tggtcctcca	acaacttggt	2100
acattttacag	ggaaaaacgat	acggattgaa	ccaggggcaa	cccaaacgat	tacaattgat	2160
atagatgttt	cgaaatacca	tgacatgtta	aaaaaagtaa	tgccaaacgg	ctatttccta	2220
gaaggctacg	tacgtttttac	agaccctggt	gatggtgggg	aagttcttag	tattccttat	2280
gttggattta	agggagaatt	ccaaaactta	gaagttttag	aaaaatccat	ttataagctt	2340
gttgctaaca	aagaaaagggt	attttatttc	caaccaaaac	aaacaaacga	agttcctggg	2400
tcagaagatt	atactgcctt	aatgactaca	agttcagagc	ctatctactc	aacagacggg	2460
actagtccta	tccaattgaa	agccttggga	agctataagt	ctatagatgg	aaaatggatc	2520
ttacaactag	atcaaaaagg	ccagcctcat	ctagccattt	cacctaataa	tgaccaaaat	2580
caagatgccg	ttgcagtga	aggtgttttc	ttacgtaatt	tcaataattt	aagagccaaa	2640
gtctatcgtg	cagatgatgt	taattttacaa	aaaccactat	gggtaagtgc	tccccaagca	2700
ggagataaaa	attactacag	cggaaatact	gaaaatccaa	aatctacatt	tttatatgac	2760
acagaattga	aaggaaccac	tactgatggt	atctccttag	aagatggaaa	atacaaatat	2820
gttttaactt	attactctga	tgtccctggc	tctaagccac	aacaaatggg	gtttgatatc	2880
actttggata	gacaagctcc	tacactaaca	acagcaactt	atgacaaaga	tagacgtatc	2940
ttcaaagctc	gtcctgcagt	agaacacggg	gaatctggta	tcttttagaga	acaagtttgt	3000
tacttaaaaa	aagataaaga	tggtcattat	aatagcgtct	tacgtcaaca	aggagaagac	3060
ggtatccttg	ttgaagataa	caaagtattt	atcaacaag	aaaagaatgg	tagctttatt	3120
ctacctaaag	agggttaacga	tttctctcat	gtctactata	ctgttgaaaga	ttatgcaggc	3180
aatctagat	cagcaaaact	cgaagatttg	atcctaattg	gcaataaaaa	tggttttagta	3240
aacgtcaaa	tggttagccc	tgagcttaac	agtaatgtcg	atattgattt	ctcttactct	3300
gtcaaagatg	acaaaggtaa	tatcatcaaa	aagcaacatc	acgggaaaga	cctcaattta	3360
ttgaaattgc	cttttggtac	ctatacgttt	gatctattct	tatacgatga	ggaacgagca	3420
aatctaata	gtcccaaaag	tgtcactgta	actatttctg	aaaaagatag	ccttaaagac	3480
gtcttattta	aagttaactt	actcaagaaa	gcagccttac	tcgttgaaat	tgacaagctt	3540
ttaccaaaa	gagcaacagt	ccagttgggt	actaagacaa	atactgttgt	tgatctacca	3600
aaagcaactt	attctcctac	tgactatggg	aaaaacatac	ctgtaggaga	ctatcgttta	3660
aacgtaacgc	tgcttagtgg	gtatagcaat	ttagagaact	tagatgattt	acttgtatcc	3720
gtaaaagaag	atcaggtaaa	cctaacaaaa	ttgacgctga	ttaataaagc	tcctctgatt	3780
aatgccctag	cagaacaaac	tgatattatt	accagcctg	tgttttataa	tgctggaact	3840
cacttaaaaa	ataattacct	agctaactct	gaaaaggcac	aaactttaat	taaaaaataga	3900
gtggaacaaa	caagtattga	taatgctatt	gctgctttga	gagaaagtcg	ccaagctctt	3960
aacggtaaa	aaacagatag	ttctttactg	gcaaaagcta	tttttagctga	aacagaaatc	4020
aagggaaaact	atcaatttgt	taatgctagt	ccattaagcc	aatcaactta	tatcaatcaa	4080
gtccaattgg	cgaaaaacct	tctacaaaaa	cctaacgtca	ctcaatcaga	agtagacaaa	4140
gccttagaaa	atcttgatat	tgctaaaaat	caattaaatg	gtcatgaaac	tgattactct	4200
ggtttacacc	atatgataat	taaagcaaac	gttctgaaac	aaacatcatc	taaatatcag	4260
aacgccagtc	aatttgctaa	agaaaattat	aataacctta	tcaagaaagc	agaattgctg	4320
ctttccaata	gacaagctac	acaagctcaa	gttgaagagt	tattaaacca	aataaaagca	4380
accgaacaag	agcttgatgg	ccgtgataga	gtttcttccg	cagagaatta	tagtcaatca	4440
ctcaatgata	atgactctct	caataaccaca	cctatcaatc	cgccaaatca	gccccaggcg	4500
ttgatattca	aaaaaggcat	gactaaagaa	agtgagggtg	ctcagaagcg	tgtcttaggg	4560
gtgactagcc	aaaccgataa	tcaaaaggta	aagacaaaca	agcttcctaa	aacaggcgaa	4620
agcactccta	aaataaccta	tacaatattg	ctattttagtc	tctctatgct	aggtctggca	4680

acaatcaaac taaagtctat caaaagagaa taa

4713

SeqID 147

atgaataata	acgaaaaaaaa	agtaaaatatac	tttttaagaa	aaacagctta	tggtttggcc	60
tcaatgtcag	cagcgtttgc	tgtatgtagt	ggtattgtac	acgcggatac	tagttcagga	120
atatacggctt	caattcctca	taagaaacaa	gttaatttag	gggcggttac	tctgaagaat	180
ttgattttcta	aatatcgtgg	taatgacaaa	gctattgcta	tacttttaag	tagagtaa	240
gatttttaata	gagcatcaca	ggatacactt	ccacaattaa	ttaatagtag	tgaagcagaa	300
attagaaaata	ttttatatca	aggacaaaatt	ggtaagcaaa	ataaaccaag	tgtaactaca	360
catgctaaag	ttagtgtatca	agaactaggt	aagcagtc	gacgttctca	agatatcatt	420
aagtcattag	gtttcctttc	atcagaccaa	aaagatattt	tagttaaatc	tattagctct	480
tcaaaagatt	cgcaacttat	tcttaaat	gtaactcaag	ccacgcaact	gaataatgct	540
gaatcaacaa	aagctaagca	aatggctcaa	aatgacgtgg	ccttaataaaa	aaatataagc	600
cccgaagtct	tagaagaata	taaaagaaaa	aatcaagag	ctagcactaa	gagtcaagtt	660
gatgagtttg	tagcaagaagc	taaaaaagtt	gttaattcca	ataaagaaac	ggttggtaaat	720
caggccaatg	gtaaaaagca	agaaattgct	aagttagaaa	atttatctaa	cgatgaaatg	780
ttgagatata	atactgcaat	tgataatgta	gtgaaacagt	ataatgaagg	taagctcaat	840
attactgctg	caatgaatgc	tttaaatagt	attaagcaag	cagcacagga	agttgccag	900
aaaaacttac	aaaagcagta	tgctaaaaaa	attgaaagaa	taagttcaaa	aggattagcg	960
ttatctaaaa	aggctaaaga	aatttatgaa	aagcataaaa	gtattttgcc	tacacctgga	1020
tattatgcag	actctgtggg	aactttattg	aataggttta	gagataaaca	aactttcgga	1080
aataggagtg	tttggactgg	tcaaagtggg	cttgatgaag	caaaaaaat	gcttgatgaa	1140
gtcaaaaagc	ttttaaaaga	acttcaagac	cttaccagag	gtactaaaga	agataaaaaa	1200
ccagacgtta	agccagaagc	caaaccagag	gccaaacca	atattcaagt	acctaaacaa	1260
gcacctacag	aagctgcaaa	accagctttg	tcaccagaag	ccttgacaag	attgactaca	1320
tggtataatc	aagctaaga	tctgcttaaa	gatgatcaag	taaaggacaa	atacgtagat	1380
atacttgtag	ttcaaaaagc	tggtgaccaa	gcttatgata	atgtggaaga	gggaaat	1440
attaccactg	atcaagcaaa	tcaattagct	aacaagctac	gtgatgcttt	acaaagt	1500
gaattaaaag	ataaaaagt	agccaaacca	gaagccaaac	cagaggccaa	accagaagct	1560
aagccagaag	ctaagccaga	agctaagcca	gaagctaagc	cagaggccaa	accagaagct	1620
aagccagacg	ttaagccaga	agctaaacca	gacgttaaac	cagaggctaa	gccagaagct	1680
aaaccagagg	ctaagtcaga	agctaaacca	gaggctaagc	tagaagctaa	accagaggcc	1740
aaaccagcaa	ccaaaaaatc	ggttaatact	agcggaaact	tgccggctaa	aaaagctatt	1800
gaaaacaaaa	agtataagtaa	aaaattacca	tcaacgggtg	aagccgcaag	tccactctta	1860
gcaattgtat	cactaattgt	tatgttaagt	gcaggtctta	ttacgatagt	tttaagcat	1920
aaaaaaaaatt	aa					1932

SeqID 148

atggcaaaag	atattaaatt	ttcagcagat	gcccgcctcag	caatgggtgcg	tggtgttgat	60
attttagctg	atacagtc	agtaacatta	ggctcctaaag	gccgtaatgt	tgctcttgaa	120
aaagcatttg	gttctccttt	aattacaaat	gatgggtgtga	caattgctaa	agaaattgag	180
ctagaagatc	actttgaaaa	tatgggagct	aaacttgtgt	cagaagtggc	ttcaaaaact	240
aatgatattg	caggggatgg	cactacaact	gctactgttt	tgaccacaagc	tattgtacgg	300
gaaggtctta	aaaatgtaac	tgcaaggggca	aatccgattg	gcattcgtcg	tggtattgaa	360
acagctgttt	cagcagcagt	tgaagagcta	aaagagattg	cacaaccagt	ttcaggcaaa	420
gaagctattg	ctcaagttgc	ggctgtgtct	tcacgttctg	aaaaagtgg	ggaatacatt	480
tctgaagcta	tgggggcgcg	gggtaatatg	gggtgttatca	ctattgaaga	atcgcgaggt	540
atggaaaacag	agcttgaagt	tgtggaagga	atgcagtttg	accgtgggta	cttgtcacag	600
tatatggtaa	ctgataacga	gaaaatggtc	tctgaacttg	agaatccgta	tatccttatt	660
acagataaga	aaattttcaa	tatccaagaa	attttaccat	tattagaaga	ggttcttaaa	720
acaaatcgtc	cgttgcta	catcgtgat	gatgttgatg	gagaagctct	cccaacgctt	780
gttcttaaca	aaattcgtgg	aactttcaat	gtcgtagctg	ttaaagcgcc	tggtttgggt	840
gatcgtcgta	aagccatgct	ggaagatat	gctatcctaa	caggaggaa	tgctgttact	900
gaagaccttg	gttttagact	aaaagatgct	actatgcaag	ttttaggaca	gtctgctaaa	960
gtaacagtag	ataaagattc	tactgttatt	gtcgaagggtg	ccgggtgactc	atcagcaatt	1020
gctaatecgcg	tagctatcat	taagtcacag	atggaggcta	caacttctga	ttttgatcgt	1080
gaaaaattac	aagaacgact	tgctaagtta	gocgggtggg	tagcagtaat	taaagttgggt	1140
gcagcgactg	aaacagaatt	aaaagagatg	aaacttcgca	tcgaagatgc	gttaaatgca	1200
acgcgtgctg	cagttgaaga	aggtattggt	tcaggtggag	gtacggctct	tgtgaacggt	1260
attgaaaaag	tagcggcact	gaaactta	gggtgatgagg	agactggacg	taatatgtt	1320
cttcgtgctc	tcgaagagcc	tggtcgtcaa	attgcttaca	atgctggata	tgaaggttca	1380
gttattattg	aacgtttaaa	acagtctgaa	attggtacag	gatttaatgc	ggccaatgga	1440
gaatgggtag	atatggttac	cacaggtatc	attgacctg	tcaaagtaac	acgttctgca	1500
cttcaaaatg	cggcatctgt	agcaagctct	atcttgacta	cagaagcagt	agtagcaaat	1560
aaacctgaac	cagaagctcc	tacagctcct	gcaatggatc	catctatgat	gggtggcttc	1620

taa

1623

SeqID 149

gtggttagaaa	acctagaaaa	accaattgga	gtgagctata	aaaatagccc	atcaatgagt	60
aaacgaacgg	ctatcagaat	gaagaaatct	agtcgatttt	caatttttact	atatagtgtt	120
ttgtcaactc	tcttagcaat	tgcaaatcct	ttattgactt	attttgcaaa	tggtttgacg	180
actcagaatc	tctatacagg	tttgatgatg	accaaaggac	agatccctta	tagtgatgtt	240
tttgctacag	gaggattttt	atactatgta	acgatttgctc	taagttacct	tttaggggtct	300
agtatctggg	tacttattgt	acagttttatt	gcttactatg	tatctggaat	ttattttttat	360
aaatttagttt	attatgtggc	acaaagtga	attgtctcga	taggcatgac	gttgatttttc	420
tatataatga	atattgtctt	aggattcggg	ggtagtgacc	caatacagtg	ggcattacct	480
tttatgctca	tttcgctatg	gttttttaatt	aaattttgtg	tcgataatat	cgttgatgaa	540
gcattttatat	tttatggcat	tttagcagca	ttctcactat	ttatagatcc	ccaaacactg	600
attttttggc	tttgctcttt	tgttctctta	acagcaacca	atattaaagca	aaagcagtc	660
ctacgaggat	tttatcgatt	tttatgcgtt	gtttttggta	tgattttta	tgcttatact	720
gttgggttact	ttatgtttta	tctacagatt	atctcttctt	atattgacaa	agctattttt	780
tacctcttta	cgtatttcgc	taggacaaac	cactcattcc	ttcttagttt	agcaattcaa	840
attgtttgtcc	ttctaggggc	aggttgtctc	tttggaactat	gggattttat	tcaaaatcgt	900
aaaaaagcat	cttatcaaat	cggcttgaac	tttattgcct	gtatttttat	tattttacgt	960
ataatggcca	ttttttcaag	agattttaac	ctttaccact	ttttacctgc	tttaccattt	1020
ggctcttttgc	taacgagtaa	taaaattact	attctttacc	aaaaagtgat	tgacagacgt	1080
tcacatagac	gtcaggtatt	ctctggtaaa	tctcttatcg	tagacctttt	tgtaaagaaa	1140
acatattatt	tgccccctct	actagtttcc	ttatcgatag	ggttactagt	ttataatact	1200
tatcaaaatg	ttactcttag	taaagaaagg	cgtgacattt	cacattat	gactacaaaa	1260
attgatagag	atggtaagat	ttatgtttgg	gacaaaagtg	ctagcattta	tagccagact	1320
cgggttaaaat	ctgcttctca	atttgttttg	ccacatatta	atacagcgca	aaaaaataat	1380
gagaaaaattt	tgaaggacga	gctgcttcag	catggggcta	aatactttat	cttaaatata	1440
aatgagaagt	taccaaatga	actgaaatct	gatattaaga	agcactacca	agaagttcct	1500
ctatcaata	tcactcattt	tgttctatat	cgtttcaaat	ag		1542

SeqID 150

atggccaagc	caacgatatc	accgggaatg	caacagtatc	tggatataaa	agagaattat	60
ccagatgctt	ttttgctttt	tagaatgggt	gattttttat	aattatttta	tgatgatcg	120
gtaaaagcag	cacaaatcct	ggaaattagc	ttgactagtc	gaaataagaa	cgcagaaaaag	180
ccaatcccaa	tggcaggagt	tccctatcac	tcagctcaac	agtataattga	cgttttagtt	240
gaattagggt	acaaagtagc	cattgctgag	cagatggaag	atcctaaaaa	agctgtggga	300
gtggtcaagc	gtgaggtagt	gcaagttgtt	accccaggaa	cggttgtgga	gtcaacgaa	360
coggatagtg	ctaataat	cttagtagcg	attgatccgc	aagatcaaca	aacattttgt	420
ctagcatata	tggatgtctc	aactggagag	tttcaggcaa	cccttttaac	agatttttag	480
tccgtccgta	gtgaaatact	aaattttaaa	gctcgtgaga	ttgtagtagg	atatcaattg	540
acggacgaaa	aaaatcacct	actgacgaag	cagatgaact	tgctttttatc	atacgaagac	600
gaacgactta	atgatattca	tttgattgat	gagcagttaa	ctgatttgga	aatatctgct	660
gcggaaaaaac	ttttacaata	tgtgcataga	acacaaaagc	gtgaacttag	tcattttacag	720
aaagtagttc	attatgaaat	aaaggactat	ttacaaatgt	catatgcaac	gaaaaatagt	780
ctagattttac	tggagaatgc	tagaacaagc	aagaagcatg	gaagtcttta	ctggttggtta	840
gatgagacta	aaacagcgat	gggaactcga	atgctgagaa	cttggtattga	caggcctttg	900
gtaagtatga	atcgaatcaa	ggaaagtcga	gatattttc	aagtgtttct	tgattatttt	960
tttgagagaa	acgatctcac	agaaagttta	aagggtgtat	atgatattga	acgcctagca	1020
agtcgagtat	ctttcggaaa	agccaaccct	aaagatctat	tgcaactcgg	acagacctta	1080
tcacaaatc	ctcggattaa	aatgatttta	cagtccttca	atcaacctga	gcttgacatc	1140
attgtcaaca	aaattgacac	tatgcctgaa	ttagaaggtt	taattaatac	ggcgaatagc	1200
ccagaagcac	aggctactat	cactgaggga	aacattatca	agtctggatt	tgataagcaa	1260
ttggataatt	atcgaacagt	gatgcgtgaa	ggtagcaggt	ggattgtctga	tattgaagct	1320
aaggaaaag	cagcaagtgg	tatcgggtact	cttaaaaattg	attataataa	aaaagacggg	1380
tattacttcc	atgttaccac	ttccaattta	tcactagtag	cggagcattt	tttccgtaaa	1440
gcgacattaa	aaaattctga	acgctatgga	acagcagaac	tagccaaaat	tgaaggtgaa	1500
atgctcgaag	ctcgcgagca	atcttcaaat	ttagaatatg	atattttttat	gcgtgttcgt	1560
gcccaagtag	aatcttatat	taaacgtctt	caagagttag	caaagacgat	tgcaaccgtt	1620
gatgttctac	agagtttggc	agtagttgca	gaaaattatc	actatgttcg	tcccaaattt	1680
aatgatcaac	atcagattaa	gattaagaat	gggcgtcatg	caactgttga	aaaagtgatg	1740
ggagtgcgaag	aatatattcc	caatagcatc	tattttgata	gtcagacaga	tatccagttg	1800
attacaggac	caaatatgag	tggttaagtcg	acctatatgc	gccagtttagc	tttgacagtt	1860
attatggcac	aaatggggagg	ttttgtatcg	gcagacgaag	ttgattttgcc	tgtattttgat	1920
gcaatattta	ctaggattgg	tgctgctgac	gacttaattt	ctgggcaatc	aaccttttatg	1980
gtagaaatga	tgggaagcgaa	tcaagctgta	aaacgagcca	gtgataaatc	tttgattctt	2040

tttgatgaat	taggtcgagg	gacagccact	tatgatggta	tggcattagc	tcaatcgatt	2100
atagaatata	ttcatgacgg	tgtaggggca	aaaacaatgt	ttgcgactca	ttaccatgag	2160
ttgacagatt	tatctgaaca	gttgacaagg	cttgtcaatg	tacacgtggc	tacttttagag	2220
agagatggag	aagttacctt	cttacataaa	attgaatctg	gacctgcgga	taagtcttat	2280
gggatacacg	tcgcaaaaat	agctgggttta	ccaattgact	tattggatag	ggcaactgat	2340
atthttatcac	agttggaagc	tgatgcagta	cagttgatcg	tatcgccctc	ccaagaagct	2400
gttactgctg	acttaaatga	ggaactagat	tctgagaagc	aacaaggaca	attatcgctt	2460
tttgaagaac	cttcaaatgc	aggtagggtt	attgaggagt	tagaagcgat	agatataatg	2520
aatctaactc	caatgcaagc	tatgaatgct	atatttgact	taaagaaatt	attataa	2577

SeqID 151

atgttgaaac	tggattttaa	aacaaagata	aaagaagcta	ttttaattgc	ctttgggtgtg	60
gctctctata	ctttcggctt	tgtcaaat	aatatggcta	atcatttggc	tgaaggagggt	120
atttcgggtg	tcactttgat	tatccatgca	cttttcggag	ttaatccagc	actttcatca	180
cttctcctta	atatcccgtt	atthtatatta	ggggctagga	ttttaggga	aaaatcctta	240
ttattaacta	tatatgggtac	agtgttaatg	tcttttttca	tgtgggtttg	gcaacaaatc	300
cctgtaacag	tccttttgaa	aaacgatatg	atgttagttg	cagtagctgc	tgggaatttta	360
gcaggaaactg	gtagtgggtt	agtatttaga	tatgggtgcaa	ctacaggtgg	tgcagatatt	420
attgggtcgta	ttgtagagga	aaaatctgga	ataaaattag	ggcaaacctt	attgthttatt	480
gatgctatag	ttctaacgctc	ttcacttggt	tatatthaatt	tacaacagat	gctatatacg	540
ttagttagcta	gcttttgatt	tagtcaagt	ttacaaatg	ttgaaaatgg	gggctacact	600
gttcgtggaa	tgatcattat	taccaaagaa	tcagaatctg	cagcagcaac	cattttgcat	660
gaaattaata	ggggtgtaac	ttttttacgg	ggccaagggtg	cctactcagg	tagagagcat	720
gatgtcttgt	acgtagctct	taacccaagt	gaagtgcgtg	atgtgaaaga	aatcatggct	780
gatttagacc	cagatgcttt	tatttctgtt	ataaatgtag	atgaagttat	tagctcagat	840
tttaaaattc	gacgaagaaa	ttacgataaa	taa			873

SeqID 152

atgaaacgta	gtatgtatgc	tgggcgtgtt	cgtagtgagc	acataggaac	atcgattact	60
ttaaaaggat	gggttgggtcg	tcgtcgtgac	cttggaggcc	ttatttttat	tgatcttcgc	120
gatcgcgagg	gaatcatgca	atttagttatt	aatcctgaag	aagtagcagc	ctcagttatg	180
gcaaccgcag	aaagtctccg	tagtgaattt	gttatagagg	ttagcgggtg	agtgcagca	240
cgagaacaag	ctaattgataa	tttaccacaa	ggagaagttg	aattaaaagt	gcaagaatta	300
tcggttctta	atacctcgaa	aacaacacca	tttgaaatta	aagatgggtat	tgaggcaaat	360
gatgatacac	gcatgogtta	ccgttacttg	gatcttcgtc	gtccggaaat	gcttgaaaat	420
ttcaaattac	gtgogaaagt	aacacactca	atccgtaatt	accttgacaa	cttagagttt	480
attgatgtcg	aaactccgat	gctaacaaaa	tcaactccag	agggggcacg	agactatttg	540
gttccatcac	gtgtcaacca	aggacatttt	tatgcccttc	cacaaagccc	tcaaattaca	600
aaacagctat	tgatgaatgc	aggatttgat	cgttattatc	aaattgtcaa	atgttttcgt	660
gatcaggatt	tacgtggaga	tcgtcaacct	gagtttacac	aagttgactt	agagacatca	720
ttccttagtg	atcaagaaat	tcaagacatt	gttgagggtta	tgattgctaa	agtaatgaaa	780
gacactaaag	gttttagagg	ttctttacca	ttcccaagga	tggcatatga	tgatgcaatg	840
aataactacg	ggctctgataa	gcctgatata	aggtttgata	tgctttttaca	agacttgaca	900
gaaattgtta	aagaagttga	cttcaagggtg	ttctcagaag	cttcagtagt	taaagcgatt	960
gttgtcaaaag	acaaggcgga	caagtactct	cgaaaaaata	ttgataaatt	aacagaaatt	1020
gcaaaaacat	acgggtgcca	aggtttagca	tggctaaaa	atgtagataa	tactatttca	1080
ggtcoggttg	ctaagttctt	gacagctatt	gaaggtaggt	tgacagaagc	tttgagctta	1140
gagaataatg	acttaattct	atthgtagca	gatagctctg	aagtagctaa	cgagacttta	1200
ggagcgcttc	gtacacgcac	tgcaaaaagaa	cttgaactca	ttgattattc	taaatttaatt	1260
ttcctatggg	ttgttgattg	gccaatgttt	gagtggctag	aagaagaggg	acgatatatg	1320
tcggctcatc	atccattcac	cttgccaaca	gcggagacag	cgcagtagtt	ggaaggggat	1380
ttggctaaag	tacgtgcagt	tgccatgat	attgttttga	atggatatga	gttaggcgggt	1440
ggtagcctac	gtattaaacca	aaaagataca	caagagcgta	tgttcaaggc	tttaggattt	1500
agcgctgaat	cagctcagga	acagtttggt	ttcttacttg	aagctatgga	ttacggcttc	1560
ccaccacatg	gtggattggc	aataggccct	gaccgctttg	ttatgttggt	agcaggcaag	1620
gacaatatcc	gagaagttat	tgcattccct	aaaaacaata	aggctagtga	tccaatgact	1680
caagctccta	gtctcggttc	agaacaacaa	ttagaagaat	tatcacttac	tgtagaaagt	1740
tatgaaaact	ag					1752

SeqID 153

aaagaaaaag	gaaaactaat	aaagaaaaaa	attctagaaa	ataatactga	tattattcca	60
aaaattatag	aaaaaagtcc	tcaaaatctt	attcttacaa	gtaattacaa	cagagttaat	120
attgataaaa	taaaaaatat	aaaaaattht	gataaaggat	tcgaactagg	ctttccactt	180
tttgaaaaag	gagaaattct	gagaaaagaa	ggcgaaataa	ctagtgcatt	tgaattattt	240
gataaagcac	gtgaactagg	atatttttga	ccgccttat	acaattctta	tgcgatggct	300

tttaggaaaa	taaagaatta	tgatgatgaa	attctaatac	tacaagaagg	aattgaaaga	360
ttcaaaaaaa	gcaccctgtc	atcaaatatt	aacccaaaga	caatcgatag	atggagtact	420
cgtattttcta	gagctaaga	tttaaaatgt	aaataa			456

SeqID 154

ttgaatgtaa	aaaaacatca	tttagcttat	ggagctatca	ctttagtagc	cctttttttca	60
tgtatttttg	ctgtaatggt	catcttttaa	agttcacaag	ttactactga	atctttgtca	120
aaagcagata	aagttcgcgt	agccaaaaaa	tcaaaaatga	ctaaggcgac	atctaaatca	180
aaagtagaag	atgtaaaaaca	ggctccaaaa	cctttctcagg	catctaata	agcccaaaaa	240
tcaagttctc	aatctacaga	agctaattct	cagcaacaag	ttactgagag	tgaagaggca	300
gctgtagaac	aagcagttgt	aacagaaaaa	acccctgcta	ccagtcaggc	acaacaagct	360
tatgctgtta	ctgagacaac	ttatagacct	gctcaacacc	agacgagtgg	ccaagtattg	420
agtaatggaa	atactgcagg	ggctattggc	tcagcagctg	cagcacaat	ggctgctgca	480
acaggagtcc	ctcagttctac	ttgggaacat	attattgccc	gtgaatcaaa	tggtaatcct	540
aatggtgcta	atgcctcagg	agcttcagga	ctttttccaaa	cgatgccagg	ttgggggttca	600
acagctacag	ttcaggatca	agttaattca	gctattaaag	cttatcgtgc	tcaaggttta	660
tcagcttgagg	gttactag					678

SeqID 155

atgtcaaatt	gggatactaa	gtttttgaaa	aaagggtttta	cttttgatga	tgttctgctt	60
attcctgctg	aaagccatgt	tttaccaaat	gaagttgata	tgaagacaaa	gttggtgat	120
aatttgacat	taaaccattcc	aatcattaca	gctgcaatgg	atacagttac	agatagtaag	180
atggctattg	ctattgcacg	tgctgggtggg	cttggtatca	ttcataaaaa	tatgtcaata	240
gttgatcaag	cagaagaagt	tcgtaaagtt	aaacgctcag	aaaatgggtg	tattattgac	300
ccattcttct	tgacaccaga	taatactgtc	tctgaagctg	aggaattgat	gcaaaactat	360
cgcattagt	gagttcctat	tgtagagaca	ctcgagaatc	gtaaattagt	tgggaattatt	420
actaaccgtg	atatgcgttt	catttctgat	tataaacaac	taatctcaga	gcacatgaca	480
agtcaaaatc	ttgtaacagc	tcctattggg	acagatcttg	aaactgcaga	gctgattctt	540
catgagcatc	gtattgaaaa	gctaccttta	gtagatgatg	agggacgtct	ttcaggactt	600
attactatta	aggatatcga	aaaagttatt	gaatttccta	aggcagcaaa	agatgaattt	660
ggacgtctct	tagttgcagg	tgtagtaggt	gtaacctctg	atacttttga	acgtgcagaa	720
gctttgtttg	aagcaggtgc	agatgctatt	gtcattgata	cagcacatgg	acattcagct	780
gggtgtgctcc	gtaaaattgc	tgaaattcgt	gctcacttcc	ctaactcgac	attgattgag	840
ggaaatattg	ctacagcaga	aggagcgcgt	gcactttatg	atgcaggtgt	ggatgtcgtt	900
aaagttggta	ttgggtccagg	ttcaatttgt	acgactcgtg	tcgttgctgg	ggtaggtgtt	960
cctcagatta	cagctatttt	cgatgcagcg	gctgttgccg	gtgagtacgg	taagactatc	1020
attgctgatg	gtgggtattaa	atattcaggt	gatattgtaa	aagcacttgc	agcaggtgga	1080
aatgcagtta	tgctaggttc	aatgtttgca	ggaacagatg	aagcgccagg	agaaacagaa	1140
atttttccaag	ggcgtaagtt	caagacatac	cgtgggtatg	gctcaattgc	agcaatgaaa	1200
aaaggttcaa	gogatogtta	ttttccaagg	tctgtaaacg	aggctaacaa	attggttcca	1260
gaaggtattg	aagggtcgtg	agcatacaaa	ggttcagtag	ccgatattgt	tttccaaatg	1320
cttggtggca	ttcgtctctg	tatgggatat	gtaggtgcag	cgaacataaa	agaacttcat	1380
gataatgctc	aatttggtga	aatgtcagga	gctggcttga	aagaaagcca	tccccatgat	1440
gttcaaatta	caaagtgggc	accaaattat	tcagtacact	aa		1482

SeqID 156

atgacaatta	accactataa	gcttcgtata	ccttactata	caataagctt	tctacttccc	60
ttcataatca	tagtctgtat	cctctttact	aagaatattt	attggggaag	tccaacaacc	120
atattagcaa	gcgatggctt	tcataaatat	gttatcttta	atcaagcatt	aagaaatatt	180
cttcatgggt	caaacagctt	attctatacc	tttacaagcg	gttttaggtt	aaatttttat	240
gctctgagta	gttactattt	gggaagtttt	ttatcccca	tagtttattt	ctttaaccta	300
aaaaatatgc	ctgatgctat	ctacctttta	acaatatgta	aaatagggtt	gataggtttg	360
tcaatgtttg	tcactctttg	ttaaagctcat	tgtaaaagtt	atcgtgtctt	acttttagta	420
attttacttt	gctatagctt	tcaaatgttc	tcaattagcc	aaattgaaat	taatatgtgg	480
ctagatgtat	ttattctaat	tccccttggt	gttttaggag	ttgatcagct	actatgggaa	540
agaaaaacct	tactttattt	cctctctctg	acagccttat	tcatacaaaa	ctattatttt	600
ggttttatga	ctgccatctt	tactagcctt	tacttcatcg	tacaaataac	ccgtaatact	660
gatagtaagg	ttgcatttaa	acaattttct	cattttacct	ttttatctct	tttagctggg	720
atgactagta	gcattatgat	tttgccaact	tattttgatt	taactactca	tgggtgaaaag	780
ttgacaaagg	tatcgaagat	gtttacagaa	aattcttggt	acatggattt	gtttgctaaa	840
aatatgattg	gagcctatga	tacaacaaaa	tttggctcta	ttcctatgat	ttatgtagg	900
ttacttctct	tactcctttc	tttactttac	tttacaataa	aggaagttcc	tcgaaggact	960
agattagcat	atggattttt	aataatattt	gttattgcta	gtttttatat	aacacctcta	1020
gatttatttt	ggcaagggat	gcattgctca	aatatgtttc	tccatcgcta	ctcttgggta	1080
ctttcagtag	ttatctgtct	gtagctgctt	gaatgccttg	agtatttaga	caacatttct	1140

tggaaaaaga	ttttaggggt	caatttaatt	ttagtaagt	gtttcataat	cacgttttta	1200
tttaaaaagc	attatcatta	ccttaatcct	gaattacttc	ttttaacctt	aacttttctc	1260
tcagcttata	ttattctaac	tatttagtttt	gtcagtaagc	aaatccctaa	attagttttt	1320
tatccctttc	ttattggttt	tggtgtatta	gagatgacat	taaacacctt	ttaccaacta	1380
aatagtctta	acgatgaatg	gatattttcca	tctaggcaag	gatatgctaa	atataatcac	1440
agcattagca	aacttgtcag	aaagactgag	agaaataact	ctacattcct	cgtacagag	1500
cgctggttag	gacaaaccgg	caacgactct	atgaaatata	attataatgg	tatttcacaa	1560
ttttcatcta	ttagaaatcg	ttcttcaagt	caagtgcctg	atagacttgg	ctttaaatca	1620
gatgggtacaa	attttaaattt	acgttatcaa	aataatactt	tgatcgaga	tagtctattt	1680
ggtgtgaagt	ataaccttac	agaatatcct	tttgataaat	ttggttttat	caaaaaagct	1740
caagataaac	aaaccattct	ttacaaaaat	cagtttgcca	gtcaattagc	tatactaacg	1800
aatcaagtat	atcaagataa	accattttact	gtgaataactt	tggaataatca	gacaactcct	1860
ttaaatcaat	taagtggttt	gaaagagacg	tatttttgagc	atcttattcc	aaatagcgtt	1920
tctgggcaaa	ccactcttaa	taaacaagta	tttgttaaaa	agaataaaca	agggataact	1980
gaaattacct	ataacataac	tatccctaaa	aacagtcagt	tatatgttag	tatgccgttt	2040
ataaatttta	ataatgagga	aaataaaaatt	gttcaaactc	ccgttaataa	tggaaccattt	2100
gtacctaata	ctcttgataa	tgcttattca	ttttttaata	ttggtttcctt	tgctgaaaa	2160
agtcgtatca	aagtaaaaatt	tcaattttcca	cacaatgatc	aagtttcttt	cccaattcct	2220
cacttttatg	ggctcaagtt	agaagcttat	caaaaagcta	tgactgttat	taataaacga	2280
aaagtaaaag	taagaactga	tcacaataaa	gttattgcta	attatacaag	tcctaataga	2340
agttctcttt	tcttcaactt	tccctatgat	aggggttgga	aagcttatca	aaataataaa	2400
gaaataaaaa	ttttcaaagc	tcagaaaggt	tttatgaaaa	taaatattcc	taaaggaaaa	2460
ggcaaagtaa	cattaatttt	tatcccttac	ggctttaaat	ttggggtagg	cctatctatt	2520
actggaatag	tattattttac	tgtctattat	tttaaatgtg	gaaaaataaa	aataggatga	2580

SeqID 157
 tggtttatga agcactcggg tgggaagcgc cacaatttgg tcaca 45

SeqID 158
 atgaaagatc acctaagggtg cttcctccat taccgatcca aaaacggttg gaaaaatgga 60
 acgagattga agggaggaaa gcctaattgac 90

SeqID 159
 gacaaacagc ttttccaatg cgtgcagggc ttccaaataa ggaacctcaa tggcaagaag 60
 catgggatca agctgatatt tataaaaaac gtcaagcat 99

SeqID 160
 aacgaggaag ccatagatgg ggtgtccaag cttgggaaaa aaatcacctat tctaggaaat 60
 aattcatacc tttcttcc 78

SeqID 161
 atcaaacat ggctattggg gatgaagaaa atgaccgtgc tatgcttgaa gttgttgga 60
 atcctgttgt tatgcaaaac ggcaatcctg aac 93

SeqID 162
 aggcgcattt caaacaatct agggatttta aaggaagcga ccgttataca cgccgta 57

SeqID 163
 gagctctgcc taaagctgag caacgtcaag ccaatctata tgccttggca cttcgagcaa 60
 atcagtttga aaaaacaggt ttcaagggtt tatcacgctt tattcgaa 108

SeqID 164
 agaagctgct tcagtaggtg ctatccaaga tttaacagat tcagatatca ttttctcaaa 60
 ccaccgtgga caccgacaaa ctattgcaaa aggtat 96

SeqID 165
 agatggtttg gttttagata tgacgatggc agaaaattta gctttacaaa cttatta 57

SeqID 166
 cccttaaaaa gtttgtcgat gacatcaaga atgaagctat tgaggttatc acaaagaaaa 60
 gctatg 66

SeqID 167
 aggcacttgc gaaagagaca aaagcaaaat catttaatga atttatgctt tctatgtgcc 60
 gtgaaaaaat tgaaaaagga caatttaatt 90

SeqID 168						
aagttatttta	ttcagcctat	tcaggaaaat	atgaagcagc	caatcgagat	tatatcaaat	60
tactatgcaa	agcttgggtt	aatgaaaatc				90
SeqID 169						
tatcaaacgt	attcgaaaaa	ggcaagaaaa	tttggttccg	tttggcttaa	acctaag	57
SeqID 170						
acgctgttat	tccagatact	tctcctgctt	tctcatttga	aaaagaacat	ctttctggag	60
tggaatatgc	acgctactta	caat				84
SeqID 171						
aagaagtttt	acgaaataat	attagcaacc	aagtaccaca	catcagtgtt	caaatggagt	60
ttaaaactca	agaacaagtt	gacgaatacc	aaaaaaatct	cggaagcatc	atccgggaaa	120
ttggagatac	acttggaaca	gcaactgaat	tcaatgccaa	aagtaacatt	agcacttata	180
ctcttggtgg	acaaatccaa	cgcatatttg				210
SeqID 172						
ttaaagcaaa	tgttccgtcg	cgtattgcat	ttgtctgttc	aagtgggtact	gatagccgta	60
cgatccttga	tgaaaatggt	gctgaaaagc	tcttgggacg	gggtgacatg	ctctttaagc	120
ctattgatga	gaatcatcca	gtacgactac	aaggttcctt	tatttcagat	gatgatgttg	180
aaaggatcgt	tggttttatc	aaagaccaag	ccgaggctga	ctatgatgat	gcctttgatc	240
ctggagaagt	atctgaaaca	gataacggtc	ctggtggtgg	cggcggagta	cctgaaagtg	300
atcctctttt	tgaagaagcc	aagggtactcg	ttt			333
SeqID 173						
ggccggaaaa	ttaatttttag	tcgtccatca	cgattttgag			39
SeqID 174						
agagttaagt	ataaaaaatg	ggaaccttta	tcaatatccc	gttcctgcta	tgaaaaatct	60
tcgtcaacat	caagcagaat	t				81
SeqID 175						
acttgggtcaa	gatgtttgtat	tcccaggtgt	tactcgtggt	gcaaaattag	aagaagcaat	60
caatgctttg	gaagatggac	aagttctttt	ggt			93
SeqID 176						
aaggagaatt	tcgttcaaag	gttgaggagt	ctattgaaag	caatcagcaa	aaatataatc	60
atttatagt	tagtttctct	accattagct	agacacttg			99
SeqID 177						
agtataatca	atattaaact	agaaatatat	gacatatgtc	ctaaaactat	ctcaaatagg	60
gagtcaatac	atggatatag	aaaactactg	ccaagactac	tgtttggaga	ctatctttcc	120
aaaacattat	ttcaaggatt	tacaagtaat	caccctaact	gccggccaat	ccgtctg	177
SeqID 178						
ctttcttttca	gaagaagtgc	gcgaattggc	tcaagccatt	cgcaaata		48
SeqID 179						
ttcatttttca	aggatagggt	taaaatgaga	cacttcacgg	ac		42
SeqID 180						
gggttgattt	gtgcttgtaa	agcctttatc	tctgccatac	tggttaactt	atthttgttcc	60
tctgttatcc	ccattgccag	ttgtcctgaa	aatattttgog	ctaaaccaag	gactagggtt	120
tcctccacct	cagacattgt	cttatctcct	gcaaagtaca	tttttaaggc	acccacagtt	180
ttatcattta	tttttagagg	aactacaata	gcagaattta	ac		222
SeqID 181						
tcctcctctt	tggaacacca	ttacaaacat	agggagcttt	tcttagtagc	ggacagtcta	60
ggcagtcttt	ggttgattct	cttagttgct	tatttcggt			99
SeqID 182						
cacctgggtgc	ccactcaata	tcataaacag	aatctacctc	ttgaatataa	gaggctaaac	60
gctctagtc	ataag					75

SeqID 183							
gcacacctac	acgaagggtg	tcataagtat	ccactaaaaa	gacgcaatct	ttatgagttt	60	
ctgcgtaagc	tt					72	
SeqID 184							
ccattgaaag	agctccgcga	acattatata	attcctcgga	aaattcgtct	tcaaaacttt	60	
ccccataga						69	
SeqID 185							
aagtatacta	ttgcaggctc	tctgtgtcacc	cagcgtcgac	catcattttc	tgttactaaa	60	
gta						63	
SeqID 186							
gcagcttttt	catcaccagc	agctaaaaac	agagcattca	ttacaacacg	atcttca	57	
SeqID 187							
tccatgggta	aacaaatata	gttctctgac	catttgatat	cacgttttga	aggotttatgc	60	
ttgaggcgat	tttctgtgcg	attccgtttg	agacgctcac	ttagctctgt	ttctaattct	120	
acaaataata	cctcttggtt	g				141	
SeqID 188							
taccacgttc	tttctcgata	tcatttgaat	ccattgcacg	ttcttcaagc	tctttacgct	60	
catcaagagt	atgtgattgt	tttaataatt	catcaacgag	agttgtttta	ccgtgggtcaa	120	
cgtgggcaa						129	
SeqID 189							
gcacagcctt	cttcaactag	gatatcccct	aaaattgatc	gttttacacc	taag	54	
SeqID 190							
tggaaatagaa	ctatcaatta	ttttttgaat	aacctgcaat	tggtgactaa	tatcaagttg	60	
cccacgagaa	aaatttttcca	gtcccaaaac	aagtttctga	gcttcatcaa	aaac	114	
SeqID 191							
gtccaagaag	gccataaaat	tttcctctct	caaaga			36	
SeqID 192							
caacaaagca	ataacaccgc	caattatagt	cgcccctata	aaccttggca	taaaaagaaa	60	
aatggattga	gctgcagatg	ctttagc				87	
SeqID 193							
ttctttgatg	ataccaaagt	taacattcat	tggttggaaa	tgtttgctgt	ctgtatgtgt	60	
aatataatgt	ggcagtgac	caatagcagt	agtttgtggg	aaaactactt	cactctcccc	120	
attaaagcga	cgggcagcat	tgattcccgc	tacaagacca	cttgcgtccg	attctacata	180	
accttcaaca	ccggtcattt	gtccagcaaa	gaaaagattt	gggttcttac	gtgtagcaaa	240	
ggtttgggtc						249	
SeqID 194							
gtgtattcgt	tacgcatagc	gacattggaa	ctagaacgaa	acttgataga	caagcgacgt	60	
gggaaaccaa	ccgattctag	gtcaatagag	tttttagagg	ttagttagc	aatattatct	120	
tgcaagaata	agttaatacc	tgacatcatg	ctagagaaga	catttcctct	agtttcttct	180	
gaagcgaagt	cagaagacct	aaagttaaa	tcagccatat	ctctaaattt	ggaaaattgt	240	
tct						243	
SeqID 195							
ggccatagca	atggcattaa	agagggaaat	ggaggtatct	tcccagtatt	ttgcattgcc	60	
attaccgcta	ccagggtttcg	ttttacgata	aatggcttct	gcaacgcgat	taacccttgt	120	
ctgtgtcatt	tcatagtaac	ccttcttagc	tgctgcaatc	gcaagagc		168	
SeqID 196							
agaatagaga	aggctatcgt	ccctaaaccg	gccattagtg	ttctgatgat	aatctcaagg	60	
atggtattag	gaacaccaga	aaaagaacct	gtcatttgtt	ctgcaaacgg	aataatttca	120	
attgtaatag	ccacacctgc	tgatatagaa	atacaaatga	gtaaagcaga	cataatcaaa	180	
gctaaacctg	ttgaaaaatt	attctgtgaa	aattctctca	ccgaattaac	aaaggcagcc	240	
cctggcacca	taaccattag	tgccccta	ataataatgc	tacgatgtct	acctaatcct	300	

gaaaaatata	ataaattagc	acttaaagcc	actacagaac	tacctagaat	ggcctaaaaga	360
aatcctgtat	gtatacgact	ttccatcaaa	ttcagaaaat	atcctaaaaat	taagcctggt	420
acagcagcgg	aaaatgaatc	taataaggaa	ctacctagg	ctaaagaaaa	actaccgcgt	480
ccacaaaaa						489

SeqID 197

ccatattctg	taacatatgc	tgctccagta	atttgtaatg	gagcggattt	agcacgacga	60
acagcatatg	ctatgtcgtc	atcagttaca	aaaccttctg	atgtagaaga	attagttacc	120
ataggtgata	gaacaaaacg	atcttctagg	ctcaatccat	tgggaagtat	taatggacga	180
aataaattac	cttggacatt	attcatctct	gtcaccgctc	cccttattag	ccatagactt	240
agcctgaaat	ctatcaaact	ctgcaac				267

SeqID 198

gccaacccata	atgacaaaaa	taatacgata	agcgttaata	aatttagtgc	caaa	54
-------------	------------	------------	------------	------------	------	----

SeqID 199

tccttctgcg	tattttgttg	ccattccaaa	aaaggcagct	accacatcc	aaaacaaagc	60
tcctgggtcct	ccagatttaa	tagccgtagc	cacaccaacg	atattacctg	tccttaccgt	120
tgcagcaaga	gcagttgcaa	gggcagcata	act			153

SeqID 200

acattaggca	tttcttttaa	aataagaggg	tgccatttct	ccgcaaaaacc	ttttctaggg	60
ggtaaattctc	ctgattttcc	tttgctggg				90

SeqID 201

tttaatat	ctaatagt	cttaggtttt	ggtacttctg	ctaaatcagc	aagtacttcc	60
tcagctaatt	cttcctta	aatttctt	gataaggcca	cacattcatt	acaaatgaaa	120
acaccattac	ctgcaata	tttttttact	tcactcttgc	ttttgccaca	aatgaacaa	180

SeqID 202

ggtgtttata	aaaagcagag	cctaagcctg	atcttccatc	agattcacct	gattgtttat	60
cattttgatt	ttttgcatga	taggtttgtg	ccttattatc	gagaa		105

SeqID 203

atcttcttac	gatcagtatg	tggaaattca	cgacaagctt	taggtctgac	atcgtatata	60
ctacataagt	tatcatcgcc	taaaaacgga	caaggcatcg	ctttaaatac	tttatctcca	120
tcttcatcta	cttctaaaaa	taaatcttca	aaagccgata	acttcatccg	gaaatgttta	180
gaaatcctag	aaatatcagc	ttctgtaaat	agaggaccca	aagttttaca	acaattagca	240
catgctgtac	aatcaatttc	t				261

SeqID 204

agtagaataa	gtacaataac	aataccaata	aggataagcc	caactttttt	atatagagag	60
gacttttctt	caggacttaa	aggatcggtt	ggtctgagac	tctcttcagt	caaataattt	120
tttccatcta	aggtatattg	gaggagacca	agaacatac	caatagcagc	aagtgagaaa	180
ccaagatgga	aatttacttc	ttgtccgagg	tacccacta	caatgggtga	aataaaagca	240
ccaaggttaa	taccaaaaac	aaagatacta	aaaccagcat	cacgacgaga	atcattttct	300
ccatataaat	taccaaccat	ctctgataca	tttggtttta	atagtcacgt	accaaggata	360
attagagcaa	tcgaaatgaa	tagagctgtt				390

SeqID 205

tcttttcttc	gttcaaataa	tttatgtgct	tttaaagata	agttcaaagt	tcgcacaagt	60
tctcgattag	actgttta					78

SeqID 206

atccattcat	ttcatagaag	gaaattaaat	catcatggca	agttaaaact	ataccatctc	60
gttcttgaga	aacaaccagg	tctttcatcg	ctgctaataa	tgtgttacca	atccctgac	120
ctt						123

SeqID 207

ctgtcttttt	cgatagtatc	ccatttatta	actacaataa	taataccttt	accagcttca	60
tgtgcaaacc	ctgcaatagc	cttgtcatac	tcacgaatac	cttctctctg	attaatcacc	120
ataagaacaa	catctgagcg	gtcgatggcg	cgcatagaac	gcataacaga	atatttctct	180
gtgttttcat	ataccttacc	agatttacgc	ataccagcag	tatcaatcat	agtatactct	240
tgccctggc	tatcaacgaa	attagtatca	atagcatcgc	gcgtagtacc	agcaactggg	300
ctagcaataa	cacggtcttc	cccaaggatg	gcattaatta	aactagattt	cccaacattt	360

ggacgtccaa tcaaactaaa acgaataata tctggatttt catttttctc ttctaccgga	420
agattttcca caatagcatc caatatatca ccagtaccaa tacca	465

SeqID 208	
tgccatcct cagatatagc tggaattaat ttaccacaaa atagcggaaa aatagataaa	60
caaaccgtta ca	72

SeqID 209	
ccctttctca gaaatcattt ccataacaac gagaccagca ccaaattctt tagcgatagt	60
acgaaaaagca gaattggtaa tacctgccat cgggtgc	96

SeqID 210	
gcgtcgacag gatcagcagc gaatccacag actacgccag gaaaactatt acaagcaagc	60
atcgctccaa ttctgtccc acagcctgta ataacaaaat ctgcagcacc gctattaagt	120
aaaatagcag tcagtaaacc attttgtaca	150

SeqID 211	
gcaatgccta aacgttgctt cataccaccg gagtatgatg aaatcttctt ttacctaca	60
tcgcctaaac caacaagctc tagtaatcta ggaatttctt gtttagctt ctttttatca	120
acacctttta aggtagcgt a	141

SeqID 212	
cttttactga ttttaaaaaa tccagatact acacataaca ccaccataaa aagacaacct	60
aacaaacccc cttaaagtttt acgaaaaaga actgaaaaaa agagtattaa gcttatgaaa	120
agaataccga taaaccatgt tgcaccg	147

SeqID 213	
aatttcaaag cagcaccacc aggtgttggt tcagggttac caaacataac gcctactttt	60
tccttaact ggttgataaa aattgcgatt gtctttgtct tgtaaatgga tgctgacaat	120
ttacgcattg ct	132

SeqID 214	
aaaagagtag ggatttgcca catatatcat gtatcccaat ccagctgttt ccacaacaat	60
aaatttagcc gttattttac tcaattttcc tttaatataa tcgtacattc tattttccta	120
tctcaatatt tttcattttg g	141

SeqID 215	
aattcaacga caagtgcctc attgatttct gggttaattt catcgcgctc tggaaggcga	60
gtcaatgaac cttcaagttt ttcagcatca aatgatacga aagctggacg tcctaaagta	120
gcttcaacag cttcaaggat tgcaggctact ttcattgatt tttcacgaac tgaaataact	180
tgtcctggag taacgcggta tgatgggata tcaacacggt taccatcaac aaggata	237

SeqID 216	
acaagaccct tagtagaaat cttagttgat aaactagcgc catataagga agctaacttt	60
tctcgaaatt cttgtacctt aggatactta gcatttgcag taactaacat t	111

SeqID 217	
agaactcgaa atgcaattag atatcctaaa gcaagcagcg gtgattatgg cacaaaaagg	60
gaaataatca ctgctaataa ggataaatac agcatttcaa agatgtgtcg ctggctgaat	120
atgccacgct caagttatta ctatcaagcc gtggagtcag tatctaaaac ggagtttgaa	180
gaaactatta aaagaatttt tctcgatagc gagtctagat acggatccag aaaaatcaaa	240
atatgcttga ataacgaagg tatcacactt tcacgtcgtc ggattcgacg cattatgaag	300
cgactcaatt tggttttctgt ttatcagaaa gccaccttca aaccacattc tagaggcaag	360
aatgaagccc ctattcccaa ccacttagac aggcaattta agcaagaaa accactacaa	420
gccttagtca ctgacttaac ctatgttcgt gtaggcaatc gttgggctta tgtttgcctc	480
atcattgacc tatacaaccg tgaaatcacc ggctgtctc ttgggtggca caagaccgct	540
gaactcggtta agcaagccat acaaagcacc ccttacgccc tgaccaaagt caagatgttc	600
cattcagatc gtggcaaaaga gtttgataat cagttaattg atgaaatatt ggaagccttt	660
ggaatcacac gttcgcttag tcaggtcgtt tgccttatg acaatgccgt agctgaaagt	720
acgtatcgtg ctttcaaaat tgaatttggt tatcaagaaa cctttcaatc gctggaagaa	780
ctagctctta agactgaaaa ggcaacactt ttctgtacaa catttataaa gtgttgccct	840
ttcaggtttt taccaatgct a	861

SeqID 218

MKKVLTFLLCSLYFVSIPAISTEEPLTSLQNRRYALTQTVDKEMYFDAIPERPTTKIEISSFQDEALTITGETLVP
NTLLSIVSLTINSNGIPVFTLSNGQFIKASREAI FNDLVSKQSSVSLDYWLKPSFVTYEAPYTNVGVSEVKNLKPYS
RVHLVEQAETEHGIYYKTDSGFWISVEDLSVADNRMAKVQEVLLLEKYNKDKYGIYIKQLNTQTAVAGINIDRSMYSAS
IAKLATLYASQEQQVKGKLSLDSKFYKDNVNQFPNSYDPSGSGKLEKKADHKLYTVKELLEATAKESDNVATNMLG
YYVNNQYDSMFQTQVDTISGMHWMKKRQISPOAAGKMEAIYYQNGDIVNYLSKTDFTDNTRIPKNIPVKVAHKIGD
AYDYKHDAIVYAEQPFIMIIFTDKSSYDDITKIADDDVYQVLK

SeqID 219

MKKRILSAVLVSGVTLGTAAVTVNADDFDSKIAATDSVINTLSGQQAQAQNVTAIKGQVGALESQQSELEAQNACL
EAVSQQLGQEIQTLSNKNIVARNESLKKQVRSQAQKGNLTNYINTILNSKSVSDAVNRVVAIREVVSANEKMLAQQEAD
KAALQAKQIENQNAINTVAANKQAIENNKAALATQRAQLEAAQLELSAQLTTVQNEKASLIQAKAQAEAEARKAAEA
QAAAEAKAQAEAKAQAESVAKAQAAAQVESATAPTETVQTQPRTEIKPSNLATSSATTVATTTATATNEPKVTQPS
VVTKAVEAPKAVVSSTPRAVSKPVRSYDSSNTYPMGQCTWGAKSMASWVGNYWGNANQWGSARAAGYSVGTTPRV
GAVAVWPYDGGGYGHVAVVTSVANNSSIQVMESNYAGNMSIGNYRGSFNPSASGSVYYIYPN

SeqID 220

MNKRI FVEKKADFDIKSASLVKELTHNLQLTSLKDLRIVQVYDVFNLAE DLLLARA EKHFSEQVTDCLLTETEITAE
LDKVAFFAIEALPGQFDQRAASSQESLLLLGSDSQVKVNTAQLYL VNKDIAEAELEAVKNYLLNPVDSRFDITLPL
EEQAFSVSDKTIPSLDFFETYKADDFAAKYAEQGLAMEVDDLFIQDYFKSIGRVPTETELKVLDTYWSHDCHRTTF
ETELKNIDFSASKFQKLQATYDKYIAMRDELGRSEKPTLMDMATIFGRYERANGRLDDMEVSDENACSVIEVD
VDGKPEWLLMFKNETHNHPTEIEPFGGAATCIGGAIRDPLSGRSYVYQAMRISGAGDITTPIAETRAGKLPQQVIS
KTAAGHYSSYGNQIGLATTYVREYFHPGFVAKRMELGAVVGAAPKENVVREKPEAGDVVILLGKKTGRDGVGGATGS
SKVQTVESVETAGAEVQKGNAIEERKIQRFLRNGNVTRLIKKSNDFGAGGVCAIGELADGLEIDLKVPLKYQGLN
GTEIAISESQERMSVVVRPSDVTFFIAACNKENIDAVVVATTAKPNLVMTWDGETTVDLERRFLDTNGVRVVVDAK
VVDKDLTVPEVRTTSAETLEADTLKVLSDLNHASQKGLQTFDSSVGRSTVNHPIGGRYQITPTESSVQKLPVQHGV
TTTASVMAQGYNPYIAEWSPHYGAAYAVIEATARLVATGADWSRARFSYQYFERMDKQAEFRGQPVSAALLGSIEAQ
IQLGLPSIGGKDSMSGTFEELTVPPTLVAFGVTTADSRKVLSPFEKAAAGENIYYIPQAI SEDIDFDLIKANFSQFE
TIOAQHKITAASAVKYGGVLESALMTFGNRIGASVEIAELDSSLTAQLGGFVFTSAEEIADSVKIGQTQAAFTLT
NGNDLAGASLLSVFEGKLEEVYPTFEQADALEEVPVAVSDTVIKAKETIEKPVVYIPVFPGTNSEYDSAKAFEQVG
ASVNLVAFVTLNEAAIADSDTMVANIAKANI IFFAGGFSAADEPDGSAKFIVNILLNKKVRAAIDSFIEKGGLIIG
ICNGFQALVKSGLLPYGNFEEAGETSPTLFYNDANQHVAKMVETRIANTNSPWLVGVEVGDIIHAIPVSHGEGKFVVS
ASEFAELRDNGQIWSQYVDFDQPSMDSKYNPNGSVNAIEGITSKNGQIIGKMGHSERWEDGLFQNI PGNKDQALFA
SAVKYFTGK

SeqID 221

MKMNNKVVLLTSTMAASLLSVASVQAQETDTTWTARTVSEVKADLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVIAK
INNIADINLIYPETTLTVTYDQKSHATSMKIEPATNAAGQTATVDLKTNQVSVADQKVSINTISEGMTPEAATT
IVSPMKTYSSAPALKSKEVLAQEQA VVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVSPASVAAETP
APVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTS PATDSKLQATEVKSVPVAQKAPTATPVAQP
ASTTNAAAH PENAGLQPHVAAYKEKVASTYGVNEFSTYRAGDPGDHGKGLAVDFIVGTN QALGNKVAQYSTQNMMA
NNISYVIWQOKFYSENTNSIYGPANTWNAMPDRGGVTANHYDHVHVSFNK

SeqID 222

MLKHFGSKVRNLRVTRNITREDFCGDETELSVRQLARIESGQSIPNLTKAHYIAKQLNVKLDIILTGGESELELPKRYK
ELKYKLLRTPTYGDANRLAVREAYFDEIYEVFYEELPEDERLIIDCMQSKLDVHFSVNDNFGITILHDYFDQIKKKK
EYTTNDFVMIDL YLLCF SINYGMKSLYSL ENYHFIMSKLLEQDNLLPEDNFQLNNVLLNHVELAFQFKQKKYVQQII
HRSNAIMTEIHDFQKRPILSLIEWKYLLIIEKDRTKAETCFKQSI LFAELIGDLYLKGLIIEWNNKDLT

SeqID 223

MTEKTKAVETTDVALAIDTLVQNGLKALDEMRLNQEQVDYIVAKASVAALDAHGELALHAVEETGRGVFEDKATKN
LFACEHVNNMRHTKTGVGIEEDDVTGLTLIAEPGVVCGITPTTNPSTAI FKSLSISKTRNPIIFAFHPSAQESS
AHAARIVRDAIAAGAPENCVQWIEQPSIDATNALMNHGDIATILATGGNAMVKAAYS CGKPALGVGAGNPAYVEK
SANIRQAADIVMSKSFNDGMVCASEQAVIIDKEIYEFVEEFKSYHTYFVNKKEKALLEEFCFGAKANCSNAGAK
LNPNI VGKSAVWIAEQAGFTVPEGTNILAAECTEVSEKEPLTREKLSPVIAVLKAESTEDGVEKARQMVEFNGLGHS
AAIHTKDADLAREFGTRIRAIRVIWNSPSTFGGIGDVYNAFLPSLTLCGGSYGRNSVGDVNSAINLLNIKKVGRRRN
NMQWFKVP SKTYFERDSIQYLQKCRDVERVMIVTDHAMVELGFLDRIEQLDLRRNKVVYQIFAEVEPD PDITVMK
GTDLMRTFKPDTI IALGGGSPMDAAKVMWLFYEQPEVD FHDLVQKFMDIRKRAFKFPELGKKT KFAIPTTSGTGSE
VTPFAVISDKANNRKYPIADYSLTPTVAIVDPALVMTVPGFIAADTGMDVLT HATEAYVSQMANDYTDGLALQAIKI
VFDYLLERSVKDADEFAREKMHNA STMAGMAFANAF LGISHSMAHKIGA QFHTVHGRTNAILLPYVIRYNGTRPAKTA
TWPKYNYRAD EKYQDI AKLLGLPAATPEEAVESYAKAVYDLGTRLGIKMNFRDQGDIDEKEWKEKSRELAFLAYEDQ
CSPANPRLPMVDHMQEIIEDAYGYEERPGRRK

SeqID 224

VGIKVYKPTTNGRRNMTSLDFAEIT'TNTPEKSLLVSLKNKAGRNNNGRITVRHQGGGHRHYRLIDFKRNKDGVEAV
VKTIEYDPNRTANIALVHYTDGVKAYILAPKGLEVGQRIISGPEADIKVGNALPLANIPVGTVIHNIELQPGKGAEL

IRAAGASAOVLGQEGKYVLVRLQSCEVRMILGTCRATIGTVGNEQOQSLVNIGKAGRNRWKGVRPTVRGSMNPNDH
HGGGEGKAPVGRKAPSTPWGKPALGLKTRNKKAKSDKLIVRRRNQK

SeqID 225

MIEFEKPIITKIDENKDYGRFVIEPLERGYGTTLGNSLRRVLLSSLPGAAVTSIKIDGVLHEFDTIPGVREDVMQII
LNVKGLAVKSYVEDEKIIELDVEGPAETAGDILTDSDIEIVNPDHYLFTIAEGHSLKATMTVAKNRGYVPAEGNKK
DDAPVGTTLAVDSIYTPVKKVNYQVEPARVGSNDGFDKLTIEIMTNGTIIPEDALGLSARVLIIEHLNLFDTLDEVAKA
TEVMKETEKVNDEKVLDRITIEELDLSVRSYNCLKRAGINTVFDTLTKTEPEMMKVRNLGRKSLSEEVKIKLADLGLGL
KNDK

SeqID 226

MKKIRLSKFIMIVVILFLISVAASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIQKV
AWYVPAAKKTHKTAVVVHGFANSKENMKAYGWLPHKLGYNVLPMDNIAHGESHGQLIGYGWNDRENIKWTEMIIVDK
NPSSQITLFGVSMGATVMMASGEKLPQVNNIIEDCGYSSVWDELKFQAKEMYGLPAPFLLYEVSTISKIRAGFSY
GQASSVEQLKKNLALFIHGDKDNFVPTSMVYDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKYEK

SeqID 227

MSKVRGFELVSQFSNKELLPKRETAHAAGYDLKVAKKTVIEPGEITLVPTGIKAHMQPGEVLYLYDRSSNPRKKGIV
LINSVGVIDGDYNNQVNEGHIFAQMQNITDQAVILEEGERIVQAVFAPFLLADDDQATGMRTGGFGSTGK

SeqID 228

MKFGKGLGFLALLMSIVLILGACGKTGLGNSTGNSTKNVTKKSANLKLGVSIISTNNPYFVAMKDGIDKYASNKKI
SIKVADAQDDAARQADDVQNFISONVDAILINPVDSKAIIVTAIKSANNANIPIVILMDRGSEGGKVLTTVASDNVAAG
KMAADYAVKKLGKKAKAFELSGVPGASATVDRGKGFSVAKSKLDILSSQSANFDRAKALNTTQNMIOGHKDVQIIF
AQONDEMALGAAQAVKSAGLQNVLIVGIDGQPDADHAIKKGDISATIAQQPAKMGEIAIQAADHYKGKKVEKETISP
IYLVTKDNVEKYNW

SeqID 229

MGKKEKLILAYSGGLDTSVAIAWLKKDYDVIAVCMDEVGEGKDLDFIHDKALTIGAESYILDVKDEFABEHFVLPALQA
HAMYEQKYPLVSALSRIIAQKLIVEMAHQTGATTIAHGCTGKGNDQVRFEVAIAALDPELKVIAPVREWKWHREET
TFKANGVPIPADLDNPPSIDQNLWGRANECGVLENPNWQAPEEAFGITKSPEEAPDCAEYIDITFQNGKPIAINNQ
EMTLADLILSLNEIAGKHGIGRIDHVENRLVGIKSREIYECPAAMVLLAAHKEIEDLTLVREVSHFKPILENELSNL
IYNALWFSPATKAIYAVKETQKVVNGTTKVLYKGSKAKVVARHSSNSLYDENLATYTAADNFDQDAAVGFIKLWGL
PTQVNAQVNKG

SeqID 230

MAKVCYFTGRKTVSGNNRSHAMNQTKRTVKPNLQKVTVLIDGKPKKVWVSARALKSGKVERV

SeqID 231

MAKQKNWRRVGVGLTLASVATLAACGSKSASQDSNGAINWAIPTTEINTLDLSKVTDITYSNLAIGNSSSNFLRLDK
DGKTRPDLATKVDVSKDGLTYTATLRKGLKWSGSKLTAKDFVYSWQRLVDPKTASQYAYLAVEGHVLNADKINEGQ
EKDLNKLGVKAEGDDKVVIITLSSPSPQFIYYLAFTNFMPOKQEVVEKYGKDYATTSKNTVYSGPYTVEGWNGSNGTF
TLKKNKNYWDANKVKTKEVRIQTVKKPDTAVQMYKRGELDAANISNTSAIYQANKNNKDVTDVLEATTAYMQYNTTG
SVKGLDNVKIRRALNLATNRKGVVQAAVDGTGSKPAIAFAPTGLAKTPDGTDLAKYVAPGYEYNKTEAAKLKFEGLAE
SGLTKLKLTTADADVPAKNSVDYIKSTWEAALPGLTVEEKFVTFFKQRLDSRKQNFDIVSVWGGDYPEGSTFYG
LFKSDSQNNDGKFANKDYDAAYNKAISEDAKPEESAKDYKEAEKILFEQGAYNPLYFRSGKGLQNPCLKGVIRNTT
GLSIDFTTHAYKK

SeqID 232

MELLKTPPIFGICFSLILYTIGQHLFKKSKGFFLLQPLFFAMVSGIVILWLMSKGLGTDVKTFYTOAYKPGGDLIFWF
LNPATIAFAVPLYKKNVVKYVVEILSSLVIGMIVSLMLIVAISKMVGLSQVGIASMLPQAATTAIALPTAAIGG
NTAVTAMACILNAVIIYALGKKLVSFHLLNDSKIGAGLGLTSGHTVGAAFALELGELQGAMAIAVVVIGLVVDLV
IPIFSHLIGLL

SeqID 233

VTKYLKYSISFVALFLASIFLVACQNQNSQTKERTKQRPKDELVVSMGAKLPHEFDPKDRYGIHNEGNITHSTLLKR
SPELDIKGELAKKYKISKDGLTWSFDLNDDFKFSNGEPTADDVKFTYDMLKADGKAWDLTFIKNVEVVGKNQVNIH
LTEAHSTFTAQLTEIPIVPPKKHYNDKYKSNPIGSGPYMVKEYKAGEQAIFVRNPYWHGKKPYFKKWTWVLLDENTAL
AALESQDVMDIYATPELASKKVKGTRLLDIASNDVRGLSLPYVKKGVVKNSPDGYPVGNDVTSDBAIRKALTIGLNR
QKVLDTVLNGYGKPAYSIIDRTPFWNPKTAIKDNKVAKAKQLLTAKAGWKEQADGSRKKGNLKAEDFLYYPTNDQLRA
NLAVEVAEQAKALGITIKLKASNWDEMATKSHDSALLYAGGRHHAQQFYESHYPSLAGKGWNTNITFYNNPTVTKYLD
KAMTSPDLKANKYWKLAQWDGKTGASTLGDLPNVWLVS LNHTYIGDKRINVGKQGVHSHGHWSLLTNTIAEWTWDE
SAK

SeqID 234

MGQEP1IEYQNINKVYGENVAVEDINLKIYPGDFVCFIGTSGSGKTTLMRMVNHMLKPTNGTLLFKGKDISTINPIE
LRRRIGYVIONIGLMPHMTIYENIVLVPKLLKWSEEAKRAKARELIKLVLPPEEYLD RYPSSELSGGQQQRIGVIRAL
AADQDIILMDEPFGALDPITREGIQDLVKSLQEEMGKTIILVTHDMDEALKLATKIIVMDNGKMVQEGTPNDLLHHP
ATSFVEQMIGEERLLHAQADITPVKQIMLNNPVSITAECTITLTAITLMRQKRVD SLLVTDNGKLGIFIDLESLSKY
KKDRLVSDILKHTDFYVMEDDLRLNTAERILKRGLKYAPVVDHNNLKGIVTRASLVDMLYDIIWGD TETEDQ

SeqID 235

MKIDKKEFLALIASIILLIFASVTFFLFKD HGTQMDTVESSVNHVSDSQLTEAQDMLDKFEKKPSEKLLKDVELAL
NKLSNSSKKEALQKRFKKAKDKYLKDEADKKATKDATDLVEILEQAPSEENVLKAEEAVNKLTVKESKEALQKRIDT
VKTQYGLIGNQTPSSSVAETTEQGTANPASQDTSSVYNQNVAPTYEQPQTNNTPVTPGVNNTVPTPGTGTAPATNGT
GVAQ

SeqID 236

MTKDLLLELGLLELPAYVVTTPSEKQLGQKMVKFLEDHRLSFETVQTFSTPRRLAVRVKGLADQOTDLTEDFKGPSKK
IALDAEGNFSKAAQGFVRGKGLSVDDIEFREVKGEYVYVTKHETGKSAIDVLASVTEVLTETLFPVNMHWANNSFE
YIRPVHTLVVLLDDQALELDFLDIHSGRISRGRHFLGSDTETLSASSYEDDLRQQFVIADAKERQQMIVDQIHAIEE
KENISVEIDEDLLNEVLNLVEYPTAFLGSFDEKYLDVPEEVLVTSMKNHQRYFVVRDRDGKLLPNFISVRNGNAEHI
ENVIKNEKVLVARLEDGEFFWQEDQKLNIALDVEKLLKQVTFHEKIGSLYEHMDRVKVISQYLAEKADLSDEEK LAV
LRAASIKYFDLLTGMVDEFDELQGIMGEKYALLAGEQPAVAAAI REHYMPT SADGELPETRVGAILALADKFD TLLS
FFSVGLIPSGSNDPYALRRATQGIIVRILEAFGWDIPLDELVTNLYGLSFASLDYANQKEVMAFISARIEKMIGSKVP
KDIREAVLES DTYIVSLILEASQALVQSKSDAQYKVSIESLSRAFNLAEKVTHSVSDYSLFENNQEKALYQAILSL
ELTEDMHDNLDKLFALSPIINDFFDNTMVMTDDEKMKQNRLLALLNSLVAKARTVA AFNLLNTK

SeqID 237

MTFDTIDQLAVNTVRTLSIDAIQAANS GHPGLPMGAAPMAYVLWNKFLNVNPKTSRNWNTNRDRFVLSAGHGSALLYS
LLHLAGYDLSIDDLKQFRQWGSKTPGHPEVNHTDGEVATTGPLGGQIANAVGMAMAEAH LAAKFNKPGFDLVDHYTY
TLHGDGCLMEGVSQEAASLAGHLKLGLKLVLLYDSNDISLDGPTSQSFTEDVKGRFESYGWQHILVKDGN DLEAIAAA
IEAAKAETDKPTIIEVKTIIGFGAEKQGTSSVHGAPLGAEGITFAKKAYGWEY P DFTVPAE VVARFASDLQARGAKA
EEAWNDLFAKYEVEYPELA AEYKEAFAGQAETVELKAHDLGSSVASRVSSQQA IQQLSTQLPNLWGG SADLSASNNT
MVAAETDFQASNYAGRN IWFVREFAMAAAMNGIALHGGRVYGGTFFVF SNYLLPAVRMAALQNLPTVYVMTHDSI
AVGEDGPTHEPIEQLASVR SMPNLNVIRPADGNETNAAWQRAVSETDRPTMLVLTRQNL PVLEGTSELAQEGVNKGA
YILSEAKGELDGI IATGSEVKLALDTQDKLESEGIHVRVVSMPAQNI FDEQEASYQE QVLP SAVTKRLAIEAGSSF
GWGKYVGLNGLTLTIDTWGASAPGNRI FEYGYFTVENAVSLYKEL

SeqID 238

MTLQDQIIKELGVKPVINPSQEIRRSVEFLKDYLLKHSFLKTYVLGISGGQDSTLAGRLAQLAVEELRADTGENYQF
IAIRLPYGIQADEEDAQKALDFIKPDIALTINIKEAVDGGVRLNAAGVETD F NKGNIKARQRMISQYAVAGQYAG
AVIGTDHAAENITGFFTKFGDGGADLLPLFRLNKSQ GKQLLAE LGADKALYEKIPTADLEENKPGIAD EIALGVTYQ
EIDAYLEGKVVS DKSRIIENWWYKGQHKRHLPTITFDDFWK

SeqID 239

IKKESVIKLLKYAFGIIMGFII LAIVIGGLLFAYYVSRSPKLT DQALKSVNSSLVYDGN NKL IADLGSEKRESVSAD
SIPLNLVNAITSIEDKRFFKHRGVDIYRILGAAWNHLVSSNTQGGSTLDQQLIKLAYFSTNKS DQTLKRKSQEVWLA
LQMERKYTKEEILTFYINKVYMGNNGNYGMRTTAKSYFGKDLKELSLAQ LALLAGIPQAPTQYDPYKNPESAQTRRNT
VLQQMYQDKNISKEYDQAVATPVTDGLKELKQKSTPKYMDNYLKQVISEVKQKTGKDIFTAGLKVYTNINTDAQK
QLYDIANS DTYIAYPNNELQIASTIMDATNGKVI AQLGGRHQENISFGTNQSVLTD RDWGSTMKPISAYAPAI DSG
VYNSTGQSLNDSVYYWPGTSTQLYDWD RQYMGWMSMQTAIQQSRNVP AVRALEAAAGLDEAKSFLEKLG IYYPENYS
NAISSNNSSSDAKYGASSEKMAAAYS AFANGGTYYKPYVNKIEFS DGTNDTYAASGSRAMKETTAYMMTDMLKTVL
TFGTGTKAAIPGVAQAGKTGTSNYTEDELAKIEATTGIYNSAVGTMAPDENFVG YTSKYTMAIWTGYKNRLTPLYGS
QLDIATEVYRAMMSYLTGGYSADWTMPEGLYRSGSYLYINGTTTGTYS SSVYKNYQNSGQSSQSSSSSTSSEKQKE
DKNTANDANSSSPQVETPNNGNATT PNNSNQTVP GTGHGNGNGNNNTVPNGN

SeqID 240

MLDLKRIRTD FVVAKKLATRGVDQETLTTLKELDIKRRELLIKAE EAKAQRNVASAAIAQAKRNKENADEQIAAMQ
TLSADIK AIDAELADVDANLQSMVTVL PNTPADDVPLGADE DENVEVRRWGTPREFD FETKAHWDLGESLGILDWER
GAKVTGSRFLFYKGLGARLERAIYSFMLDEHAKEGYTEVIPPVMVNHDSMFGTGQY PKFKEDTFELADSPFVL IPTA
EVPLTNYRDEI IIDGKELPIYFTAMSPSFRSEAGSAGRDTRGLIRLHQFHKVEMVKFAKPEESYQELEKMTANAENI
LQKLNLPYRVITLCTGDMGFSAAKTYDLEVWIPAQNTYREISSCNTEDFQARRAQIRYRDEVDGKVRLHLHTLNGSG
LAVGRTVAAIL ENYQNE DGSVTIPEVLRPYMG NIDI IKPN

SeqID 241

VTISNQELTTLPLRGKSGKAYIGTYPNGERV FVKYNTTPILPALAKEQIAPQLLWARRTSNGDMMSAQEWLDGRTLT
KEDMGSKQIIHILLRLHKS RPLVNQLLQLGYKIENPYDLLMDWEKQTP IQIRENTYLSIVTELKRS LPEFRTEVAT
IVHGD IKHSNWVITTSGLIYLV DWD SVRLTDRMYDVAYILSHYIPQKHWDWLSYGYKDNEKVWSKIIWYQGF SYL
SQIIKCFDKRDM EHVNQEIYELRKFR ELIKKHNAS

SeqID 242

MKISQYNKWSIRRLKVGAAASVMIASGSIVALGQSHIVSADEMSQPKTTITAPTANTSTNVESSTDKALSKVTTMETSS
SEMPKMQNMMAKVEKTSKPKMMVATSVRKMMATPTPVAMTKTTSVDEVKKSTDTAFKQTVDPVPAHYVNAAGNGPFLA
GVNQTIPIYEAFFGGDGMRLRLILKSSSEGAKWSDNGVDKNSPLPLKGLTKGKYFYQVSLNGNTTGKEGQALLDQIKAN
DKHSYQATIRVYGAKDGKVDLKNMISQKMVTINIPHITTDMEVKNSLKMAFKEKVDPVPAKYVSAAKAGPFLAGVNE
TIPYEAFFGGDGMRLRLILKASEGAKWSDNGVDKNSPLPLKDLTKGKYFYQVSLNGNTAGKKQALLDQIKANGSHT
YQATITIIYGTGDKVDMNTILGQKTVMIHINVAKKDMNSTSMMKKDKMTMPMKKEMTSSKINTGMMMSNNKMSANM
QMSSQAQKSNDAKAGKMSMMSKNLPNTGETKQONVGVGLMGLSLAFATGLTALGLKKSQR

SeqID 243

MTHITFDYSKVLGQFVGEHELDYLPQVSAADAFRLQGTGPGSDFLGWMDLPENYDKEEFSRIQKAAEKIKSDSEVL
VVIGIGGSYLGAKAAIDFLNNHFANLQTAERKAPQILYAGNSISSTYLADLVEYVQDKEFSVNVISKSGTTTEPAI
AFRVFKELLVKKYQEEANKRIYATTDKVKGAVKVEADANNWETFVVPDNGGRFSVLTAVGLLPAAASCADITALM
EGANAARKDLSSDKISENIAYQYAAVRNVLYRKGYITEILANYEPSLQYFGEWWKQLAGESEGKDQKGIYPTSANFS
TDLHSLGQFIQEGYRNLFFETVVRVEKPRKNVTIPELTEDLDGLGYLQGDVDFVNKKATDGVLLAHTDGGVENMFVT
LPTQDAYTLGYTIYFFELAIGLSGYLNSVNPFDQPGVEAYKRNMFALLGKPGFEELS AELNARI

SeqID 244

MKEKQTAGRRLQEEFAPEFARYNDDILFGEVWAKEDHLTDKTRSIITISALISGGNLEQLEHHLQFAKQNGVTKEEI
ADIITHLAFYVGVWPKAWSAFNKAKEIWI

SeqID 245

AWRALEDAQKSGKVKSIGVSNFLEKDLENILKNGHVKPAVNOILAHIGNTPFDLIDYQCSKGIQVEAYSPIAHGQAL
KSDGIQKMAEKYGVSAQLCIQYLLQLNLIVLPKASSKEHLQSNLDFDFVISDEDMSILKSLMFDDYGEFSNFPVFS
EK

SeqID 246

MFRRSKNNSYDTSQTKQRFSIKKFKFGAASVLIGLSFLGGVTQGNLNIFEESIVAASTIPGSAATLNTSITKNIQNG
NAYIDLVDVKNGLIDPQNLIIVLNPSSYSANYIYKQAKYYSNPSEITTTGSATITFNILDETGNPHKKADGQIDIVS
VNLTIYDSTALRNRIDEVINNANDPKWSDGSRDEVLTLGLEKIKKIDIDNPKTQIDIDNKINEVNEIEKLLVVSPLDK
IKYSPEAKHRTVEQHAELDAKDSIANTDELPSNSTYNWKNHGPDTSTSGEKDGIVEVHYPDGTVDDVNVKVTTSK
KTDNTAPTTLTVTPEQQTQVKVDEDTFTVTAEDENEVELGLDDLKAKYENDIIGARVKIKYLTKEPNKKVMEVTIMKA
TLADKGAITFTAKDKAGNQAEPKTVTINVLPDDKIKYSPEAKHRTVEQHAELDAKDSIANTDELPSNSTYNWKNHGHK
PDTSTSGEKDGIVEVHYPDGTVDDVNVKVTVTSSKTDNTAPTTLTVTPEQQTQVKVDEDTFTVTAEDENEVELGLDDL
KAKYENDIIGARVKIKYLTKEPNKKVMEVTIMKATLADKGAITFTAKDKAGNQAEPKTVTINVLPDDKIKYSPEAKH
RTVEQHAELDAKDSIANTDELPSNSTYNWKNHGPDTSTSGEKNNAVVTYPDKSTDEVVPVKVTVVDPRDPAEKNDP
AGKDQTVKVGEPDPTKSLEAVPAGSTVAYKEPVDTKTPGEKNNAVVTYPDKSTDEVVPVKVTVVDPRDPAEKNDP
GKDQTVKVGEPDPTKSLEAVPAGSTVAYKEPVDTKTPGEKNNAVVTYPDKSTDEVVPVKVTVVDPRDPAEKNDP
KDQTVKVGEPDPTKSLEAVPAGSTVAYKEPVDTKTPGEKNNAVVTYPDKSTDEVVPVKVTVVDPRDPAEKNDP
DQTVKVGEPDPTKSLEAVPAGSTVAYKEPVDTKTPGEKNNAVVTYPDKSTDEVVPVKVTVVDPRDPAEKNDP
TTVPQGTPIISDEEITGLVKIPEGSNGVPKVVGDRPNTDVPGDYKVTVEVTYPDGTQDVAVTVHVTPKPVPDKDKYD
PTGKSQQVNGKGNKLPATGESATPFFNVAALTIISVGLLSVSKKKED

SeqID 247

MQILEDYDGRALPKLETDRILRLQRTVGDVPAMFDYVCLEEVAYPAGLSPIASLEDEYDYFENRYQNLEKAKLPSG
YGITVKGSDRIIGSCAFNHRREDDVFEIGYLLHPDYWGHGYMTEAVAALIEVGFLLNLHKKIEIRCYDYNKQSQRVA
EKLGFITLEATIRDRKDNQGNRCVNLIIYGLLRSEWE

SeqID 248

MSKELSPKYNPAEVEEGRYQTWLDQDVFKPSGDTEAKPYSIVIPPPNVTGKLHLGHAWDTTLQDIIIRQKRMQGFDT
LWLPQMDHAGIATQAKVEERLREQGISRYDLGREKFLDKVWEWKDEYAATIKSQWGMGLSVDYSRERFTLDEGLSK
AVRKVFVDLYNKGWIYRGEFIINWDPAARTALSDIEVIHKDVEGAIFYHMNYMLEDGSRALEVATTPETMFGDVAVA
VNPEDPRYKDLIGQNVILPIINKPIPIIADEHADPEFGTGUVKITPAHDPNDFAVGQRHNLQPVNVMMDDGTMMNELA
DEFNGMDRFEARKAVVAKLESGLNLVKIEKMTSHSVGHSERTGVVVEPRLSTQWFVKMDQLAKNAIANQDTEKVEFY
PPRFNDTFMSWMENVHDWVISRQLWWGHQIPAWYVNVNGEMYVGEDAPEGDGWTQDEDVLDTWFSALWPFSTMGWPD
TEAADFKRYFPSTSLTVTGDIIFFWVSRMIFQSLEFTGRQPFNSVLHGLIRDEEGRKMSKSLNGIDPMDVIEKYG
ADALRWFLSNGSAPGQDVRFSYEKMDASWNFINKIWNISRYILMNEGLTLDQARENVEKVVNSQVGNVTDRAWILHN
LNETVGKVTESFDKFEFGVAGHILYNEFIWEEFANWYVELTKEVLYSDNEDEKVVTRSVLLYTLQILRLHHPIMPV
TEEIFGQYAEBSIVLASYPQVNATFENQTAHKGVESLKDILRSVRNSRAEVNAPSKPITILVKTSDSELESFFKDN
SNYIKRFTNPETLETSSAITAPELAMTSIITGABIFLPLADLLNVEEELARLEKELAKWQKELNMVGKKLSNERFVA
NAKPEVVQKEKDKQTDYQTKYDATIARIEEMKKLNND

SeqID 249

MVEPIISIQGLHKSFGKNEVLKIDLDIHQGEVVVIIGPSGSGKSTFLRTMNLLEVPTKGTVTTFEGIDITDKNDIF
KMREKMGVMVFQQFNLFPNMTVLENITLSPIKTKGLSKLDAQTKAYELLEKVGLKEKANAYPASLSGGQQORIAIARG
LAMNPDVLLFDEPTSDALDPEMVGEVLTVMQDLAKSGMTMVIIVTHEMGFAREVADRVI FMDAGIIVEQGTPEVFEQT
KEIRTRDFLSKVL

SeqID 250

MNYKEIYQEWLENDLSLGDIKSDLEAIKGDSEIQRDFYKTLFETAGLRGKLGAGTNRMNTYVMVGKAAQALANTII
DHGPEAIARGIAVSYDVRYQSKEFAELTCSIMAANGIKSYIYKGRPTMCSYAIRALGCVSGVMVTASHNPQAYNG
YKAYWKEGSQILDDIADQIANHMDAITDYQQIRQIPFEEALASGLASYIDESIEEAYKKEVLGLTINDTNIDKSVRV
VYTPLNGVGNLPPREVLRRRGFENVYVPEQEMPDPTFTTVGYPNPEVPKAFAYSESLSGKSVADADILLATDPDCDRV
ALEVKDSKGEYIFLNGNKIGALLSYYIFSQRCALGNLPHHPVLVKSIVTGDLSKVIADKYNIEFTVETLTGFKNICGK
ANEYDISKDKTYLFGYEEISIGFCYGTFRVDKDAVSASMMVEMTAYYKERGQTLTLDVLQTIYDEFGYYNERQFSLEL
EGAEGQERISRIMEDFRQDPILQVGEMLRENSIDFKDGYKDFPKQNCLKYFNEGSWYALRPSGTEPKIKCYLYTTIG
CTEADSLSKLNAIESACRAKMNSTK

SeqID 251

MYREITAVEHDFRVSESNQTNLLQSSNWPVKVDNWSQLLGFFDGETQIASASILIKSLPLGFSMLYIPRGPIMDYS
NLDIVTKVLKDLKAFGKKQORALFIKCDPLIYLKMVNAKDFENSPDEKEGLIAIDHLQAGADWTGRTTDLAHTIQPR
FQANLYANQFGLDKMSKKTRQAIARTSKNKGVDIQFGSHELLEDFAELMKKTEDRKGINLRGIDYYQKLLDTPNNYSY
ITMASLDVAKRLEKIEKECQIAQSERIKSLELNREKKVKQHQTIDRLNKEIDFLKEAQKAYDRDIIPLAATLTLEF
GNTSENIYAGMDDYFKSYSAPIYTWFFETAQRAFERGNIWQNMGGIENDLSGGLYHFKSKFEPIIEBEFIGEFNIPVNR
LLYKASNYVYALRKKRNS

SeqID 252

MACTTILVGKKASYDGSTMIARTEDSVNGDFTPKKLKVMTSKDQPRHYKSVLSNFEVDLPDNPLPYTSVPDALGKDG
IWGEAGINSKNVAMSATETITNSRVLGADPLVSDGIGEEIDLTVLVPYIQSAREGVERLGAILLEKYGTYESNGIAF
SDTEEIIWWLETIGGHHWIARRVPDDVYVTNPNQLGIDHFEFNCCDDYMCSSDLKEFIEQYHLDLTSNEHFNPRYAF
GSQDKDRHYNTPRSWAMQRFNLNPEIEQDPRSLFI PWCQKPYRKITVEDIKYVLSHDYQDSVYDPYGPREGDAVSRAA
FRSVGINRTSQTSLQLRPNKSLETTGVQWLSYSGSMPFATMVPLFTQVETVPNYFSNTTKDASTDNFYWTNRLIAAL
ADPHFYQHEADIESYIERTMAQGHADINGVDREVAENKEIDFQKQKQMSDYIQKESQELLNRLIFDASNLMTNRFS
MGD

SeqID 253

MRKKFLLLSFVAMFAAWQLVQVKQVWADSKLKVVTTTFYPVYEFTKNVVGDKADVSMLIKAGTEPHDFEPSTKNIAA
IQDSNAFVYMDNMMETWAPKVAKSVKSKKVTTIKGTGDMLLTKGVVEEGEEHEGHEGHHHELDPHVWLSPERAIS
VVENIRNKFVKAYPKDAASFKNADAYIAKLKELDKKEYKNGLSNAKQKSFVTQHAAFGYMALDYGLNQVPIAGLTPD
AEPSSKRLGELAKYIKKYNINYYFEENASNKVAKTLADEVGKTAVALSPLEGLSKKEMAAGEDYFVSVMRRNLKVLK
KTTDVAGKEVAPEEDKTKTVETGYFKTKDVKDRKLTDSGNWQSVYPLLQDGTLDPVWDYKAKSKKDMTAAEYKYY
TAGYKTDVESIKIDGKKHQMFTVRNGKSQTFYKYAGYKILTYKKNRGVRYLFEAKEKDAGQFKYIQFSDHGKPN
KAHFHIFWGSSESQEKLFEEEMENWPTYFPAKMSGREVAQDLMSH

SeqID 254

MKLSKKLLFSAAVLTMVAGSTVEPVAQFATGMSIVRAAEVSQERPAKTTVNIYKLOADSYKSEITSNGGIENKDG
ISNYAKLGDNVKGLQGVQFKRYKVKTDISVDELKKLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVR
YLYVEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQDDAGYTTIGEEFKWF
LKSTIPANLGDYKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHYTIDEPTVDNQNTLKITFKPEKFKEIAELLKG
MTLVKNQDALDKATANTDDAAFLEIPVASTINEKAVLGKAIENFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRF
VKKDSTETQTLGGAFFDLLASDGTAVKWTDALIKANTKNYIAGEAVTGQPIKLSHTDGTFEIKGLAYAVDANAEG
TAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNKRPSIPNTGGIGTAIFVAIGAAV
MAFAVGKMKRRRTKDN

SeqID 255

MKKRQKIWRGLSVTLLILSQIPFGILVQGETQDTNQAALGKVIKKTGDNATPLGKATFVLKNDNDKSETSHETVEGS
GEATFENIKPGDYTLREETAPIGYKKTDKTWKVKVADNGATIEGMDADKAERKEVLNAQYPKSAIYEDTKENYPL
VNVEGSKVGEQYKALNPINGKDGRRREIAEGWLSKKITGVNDLKNKYKIELTVBGKTTVETKELNQPLDVVLLDNS
NSMNNERANNSQRALKAGEAVEKLIDKITSNKDNRAVLTASTIFDGTATVSKGVADQNGKALNDSVSWDYHKT
FTATTHNYSYLNLTNDANEVNILKSRIKPEAEHINGDRITLYQFGATFTQKALMKANEILETQSSNARKKLI FHVTDG
VPTMSYAINFNPISTSYQNQFNSFLNKIPDRSGILQEDFIINGDDYQIVKGDGESFKLFSDRKVPVTGTTQAAAYR
VPQNQLSVMSNEGYAINSGYIYLYWRDYNWVYPDPKTKKVSATKQIKTHGEPTTLYFNGNIRPKGYDIFTVGIGVN
GDPGATPLEAEKFMQSISSKTENYTNVDDTNKIYDELNKYFKTIVEEKHSIVDGNVTPMGEMIEFQLKNGQSFTHD
DYVLVGNDSQLKNGVALGGPNSDGGILKDVTVTYDKTSQTIKINHLNLGSGQKVVLTYDVRLKDNYSINKNFYNTNN
RTTTLSPKSEKEPNTIRDFPIPKIRDVREFPVLTSINQKMGGEVEFIKVNKDKHSESLGAKFQLQIEKDFSGYKQFV
PEGSDVTTKNDGKIYFKALQDGNKYLYEISSPDGYIEVKTKPVVTTFTIQNGEVTNLKADPNANKNQIGYLEGNGKHL
ITNTPKRPPGVFPKTGGIGTIVYILVGSTFMILTICSFRKQKL

SeqID 256

GAKKAGWTEYARMLEVRREQVDHVMIPKINQDLPIYAGPEEDNLQRGVGHLEGISLPIGGASTHAVLSGQRGMPAARL
FADLDKMKKGDFYFVTNLKETLAYQVDRIMVIEPSQLDAVSIEEDKDYVTLTCTPYMGSLSTVMGDLSTLTRENQL
GSLSFWMFKAMRILLLKFLKLRKPKACRLMSLISLLVASNLALERDS

SeqID 257

MSDVVEKQTAKSFIMNVNLGLALGTVIVLIPGAILGELMKALLPMWSGFATLIAATAVATSMMLGLVIGIMVGLNFKF
NPIQSASLGLAVMFAGGAATFLKGAIMLKGTGDIINMGITAAALGVLLIQFLSDKTKSFTLIVIPTVTLTLLVGGVGHV
LLPYVKMITTTMIGQGIIASLLGLQPVLMISILAMIFCFLIVSPITTVGIALAISLSGIGSGAANLGICAASFGLCMAG
WSVNSKGTALAHVLGSPKISMANVLAKPKIMLPMISSAAILGILGALFNIQGTTPASAGFGISGLIGPINALNLAKGG
WSVMNMLLIIFVAAPIILNFIFNYLFKVLKIIDPMDYKLDI

SeqID 258

MARPLVEQTADRLLHLILEREYFVGAKLPNEYELAEDLDVGRSTIREAVRSLATRNILEVRQSGSTYIISKKGVSED
PLGFSLIKDDTLRLTSDLFELRLLEPRIAELVAYRITDDQLQLLEKLVGDIEDAVHAGDPKHLLLDVEFHSMIAKYS
GNIAMDSLPLVINQSIHLINANYTNRQMKSDSLEAHREITKAIREKNPVAHADAMLHMHMSVRRSALKA

SeqID 259

MIKKNKVFLGVLLVLVVLGGGVLFYQSQFQKTTNQAALAIAYKDAKVAKKDVIHQKIDKEFENFRGSYEIEFNTKSA
EYSYHVDKGTGILERDMDNNGFSKSTSQSSSSSSQSKSHKISQEEAKKIAFKDANIEESEVSNLKIKEEIEENGKSVY
DIDFVDLKNKNEVDYQIDAETGKIIERSRDHMD

SeqID 260

LNRKKRYRLTVKKQNASIPRRNLNLLFFIIVLLFTVLILRLLEQMIGQQSFYMKKLTALTSTYTVKESKARGQIFDAKG
VVLVENDERPTVAFSRGNNISSQSIKELANKLSHYITLTFVASSDRAKRDYLLADKANYKKVVESLPDSKRYDKFGN
HLAESTVYANAAVAVPVSAINYSEDELKVVALFNQMNATPTFGSVKLSTGELSDDQIKKLDADKKELLGISVTSNWH
RRKKGTSLSLILGTISTEKAGLPREEVKYKKGYSINDRVGTSTYLEKQYEDDLQGIQIRKVVVNKKGKVVDNIT
QEGKSGRNKLKLTIDLNYQNKVESILKQYYGSELSSGRASFSEGMAYAVALEPSTGKVLAMAGLKNHGNLVDDSLGTI
AKNFTPGSVVKGATLSSGWENKVLRGNEVLVDQETANIRSWFTRGLTPISAAQALEYSSNTYMQVALRLMGQDYNT
GDALTDGRGYQEAAMAKLRKTYGEYGLGVSTGLDLPESEGYVPGKYSIGTTLMESFGQYDAYTPMQLGQYISTIANNGN
RLAPHVVSDIYEGNDSNKFQALVRSITPKTLNKLAIISDQELAI IQEGFYNNVNSGSGYATGTSMRGNVTTISGKTGT
AETFAKNVNGQTVSTYNLNAIAYDTNRKIAVAVMYPHVTDTTKSHQLVARDMIDQYISQFTGQ

SeqID 261

MTVFPKHFLWGGAVAANQVEGAFRTDGKGLSVQDVLNPGGLGDFTAKPDPNLKLEAIDFYHNYKNDIKLFAEMGFK
VFRSTIAWSRIFPNGDDAPNEAGLQFYDNLFDLELLKYNIEPLVTLSHYETPLHLAKTYNGWADRRLIAFFEKFAQT
VMERYKDKVKYWLTFNEVNSILHMPFTSGAIMTDKSQLSPQELYQAIHHELVASARVTKLGRSINPNFKIGCMILAM
PAYPMTSDPRDVLAAARQFEQHNLFSDIHVRGKYPTYIQSYFKNNGIKIKFEEGDDEEVLAQNTVDFLSFSYMSVTQ
AYDFENYQSGQGNILGGLTNPHLTTSSEWGWQIDPIGLRLVLNQQYERYQIPLFIVENGLGAKDQLIETLDGDTYVED
DYRIDYMNQHLVQVAKAIEDGVEIMGYTSWGCIDCVSMSTAQLSKRYGLIYVDRNDDGTGSLQRYKKKSFQWYQKVI
KTNGQSLFEHNR

SeqID 262

MATFQIKEKMFSLGGKFTITDQTGLPCYHVEGSLFPLPKTFKVFDEEGHLISQIEKKVLSFLPKFNVTLANGNHFTI
KKDFSFLKPHYTIEDLDMEVKGNFWDIDFQLLKDQNVIANISQQWFRMTSTYQVEVYNETYNDLTISLVIAIDYVKE
LEKNASN

SeqID 263

MKKITTLILASSLLLVATTSVKADDNFEMPTRYVKMSEKSAFYQRLQEKQKKAHTTVKTFNNSEIRHQLPLKQEKA
RNDIYNLGLISQESKGFQIRIDNAYSLENVSDIVNEAQALYKRYDLFEKIKSTRDKVQVLLASHQDNTDLKNFYA
ELDDMYEHVYLNESRVEAINRNIQKYN

SeqID 264

MKLKKFFEDLLAKLEYRPIQVFMHRFQSAEMDLSAIAVAYYLLVTAFFPLLVIAANIFPYFHINVSDDLQSLMQLNLPK
NIYEPASRLAVDAFSKPSGTGILGFASLTAFWTMSKSLTSLQKAINKAYGVDQHRDFVISRLVGVGTGLIILFLLTFV
LIFSTFSKPVQLIIVNMYDLGDTLTAWLLNLAQPVFTLTIFLGIGILYFILPNARIRKVRYPVPGTLFSTFVIGFFS
NLISQYVLNRVEKMVDIKTFGSVVIFILMLWFIFLAHIMILGAILNASVQEIATGKIESRRGDIMSLIQKSKEK

SeqID 265

MKLLYTDINHDMTIELVNQAAHAAEAGWRIFYIAPNSLSFEKERAVLENLPQEAFAITITRFAQLARYFTLNQPNQ
KESLNDIGLAMIFYRALASFEDGQLKVFGRLKQDASFISQLVDLYKELQTANLSILDLKYLHSPEKFEDLLAIFLVV
SDLLREGEYDNQSKIAFFTEQVRSGQLDVLKNTILIVDGFTRFSAEELIKSLSSRCQEIIGAYASQKAYKANF
TNGNIYSAGVDFLRYLATTFQTKPEFILSKWESKSGFEMISKNIIEGKHDFTNSSHILDDTAKDCITTIWECINQKDEV
EHVARAIRQKLYQGYRYKDILVLLGDVDSYKLQLSKIFEQYDIPYFQGAETMAAHPLVHFMDLSLRIKRYRFRAED
VLNLFKGTGIYGEISQDDLDYFEAYISYADIKGPKKFFTFDVFVGAKKFDLGRNLNTRQSLIAPLESFVKTKKQDGIKT

LNQFMFFLTQVGLSDNLSRLVGMSENEQEKHQEVWKTFTDILEQFQTI FGQEKLNLD EFLSLNLSGMMQAEYRMVP
 ATVDVVTVKSYDLVEPHSNQFVYALGMTQSHFPKIAQNKSLISDIERQLINDANDTDGHFDMITRENLKKNHFAALS
 LFNAAKQALVLTIPQLLNESEDQMSPYLIELRDIGVFPNHKGRQSLKEEADNIGNYKALLSRVVDLYRSAIDKEMTK
 EEQTFWSVAVRYLRQLTSKGIEIPIITDSDLTVTVSSDVMTRRFPEDDPLKLSSSALTTFYNNQYKYFLQYVLGLE
 EQDSIHPDMRHHGTYLHRVFEILMKNQGIESFEEKLNSAINKTNQEDVFKSLYSEDAESRYSLEILEDIARATATIL
 RQDSQMTVESEEEERFELMIDNTIKINGIIDRIDRLSDGSLGVVDYKSSAQKFDIQKFYNGLSPLVITYIDAISRDE
 VEQKPPIFGAMYLHMQEPKQDLSKIKNLDDLVTKNHQALTYKGLFSEAEKEFLANGKYHLKDSLYSEAEIATLQAHN
 QLLYKKASETIKSGKFLINPYTEDAKTVDDGQFKSITGFEDRHMARARALYKLPAGEKROGFLTLMQQEEENDDL

SeqID 266

MSETKVMALREAINVAMSEEMRKDEKVFLMGEDVGVYGGDFGTSVGMLEEFGAKRVRDTPISEAAIAGSAIGAAQTG
 LRPIVDLTFMDFVTIAMDAIVNQAKTNYMFGGLSTPVTFRVASGSGIGSAAQHSQSLEAWLTHIPGLKVVPAGTV
 NESKALLKSSILDNNPVIFLEPKALYKKEEVNMDPDFYIPLGKGDIKREGTDLTIVSYGRMLERVMQAAEEVAEEG
 INVEVDPRTLIPLDKELIIDSVKKTGKLILVNDAYKTGGFTGEIATMVARSEAFDYLDPHPIVRLASEDVPVPYSRV
 LEQGILPDVAKIKDAIYKVVNKGK

SeqID 267

MAFDVIMPKLGVDMQEGEILEWKKNEGDTVNEGDLLEIMSDKTNMBIEAEDTGVLLKIVHQAGDVVPVTEVIAYIG
 EEEGEEVGTSSPSADATITAEDGQSVSGPAAPSQETVAAATPKEELAAD EYDIVVVGGPAGYAAIRGAQLGGKIAI
 VEKTEFGGTCLNVGCIPTKTYLKNAEILDGLKVAAGRGINLASTNYAIDMDKTVAFKNSVVKTLTGGVRLGKANKV
 EIFNGLGQVNPDKSVVIGDKVIKGRNVVLATGSKVSRINIPGIESPLVLTSSDDILDRLREIPKSLAVMGGGVVGIELG
 LVWASYGVDVTVIEMADRIIPAMDKEVSLELQKILAKKGMKIKTSVGVSEIVEANNQLTLKLNNGEEVVADKALLSI
 GRVPQMNGLLENLEPELEMERGRIKVNAYQETSIPGIYAPGDVNGTRMLAHAAYRMGEVAAENALGGNKRKAHLDFTP
 AAVYTHPEVAMVGMTEEQAREQYGDILVGKNSFTGNGRATASNEAHGFVKVIAEPKYKEILGVHIIIGPAAAEELINEA
 STIMENELTVYDVAQSIHGHPTFSEVMYEAFLDVLGEAIHNPPKRK

SeqID 268

MGKYFGTDGVRGEANVELTPELAFKLGRFGGYVLSQHETDRPRVFVARDTRISGEMLESALIAGLLSVGIEVYKLG
 LATPGVSYLV RTEKASAGVMISASHNPALDNGIKFFGSDGFKLDDRELEIEALLDAKEDTLPRPSAQGLGLVDYP
 EGLRKYEFMESTGIDLEGMKVALDTANGAATASARNIFDLNADISVIGDQPDGLNINDGVGSGTHPEQLQSLVREN
 GSDIGLAFDGDSDRLIAVDENGEIVDGDKIMFIIGKYLSDKGQLAONTIVTTVMNLGFHKALDREGIHKAITAVGD
 RYVVEEMRKSGYNLGGEQSGHVIIMDYNTTGDGQLTAIQLTKVMKETGKKLSELA SEVTIYPQKLVNIRVENNMKDK
 AMEVPAIAEIIAKMEEEMDGNRILVRPSGTEPLLRVMAEAPTNEAVDYVDTIADVVRTEIGLD

SeqID 269

MKGQKIIALAGLVLSCHFALTACHTQEHKNSHHIKTKQVAKKKANKKKVSVKESHKKRKG VAGVDFPTDDGFLLT KD
 SKILSHPD SGIVVAHGNHSHFIFYSDLKGSKFSYLI PNANAKTNKKQAVRNFKAGAVAVNTLNDGYVFNPADIVSED
 ANGYVVRHGDHFIYPKASLSQQKQVQASRAVSR LGNQNNSHYRVNSSKIAGLHHPTSDGFLFNGQGIGKTPTTGIL
 VEHHNHLHFISFADLRKGGWGSIA DRYQPQKKVDSKKQSPSSKKPRTENTLPKD IKDKLAYLARELHLDISRIRVLK
 TLNGEIGFEYPHDDHTHVIMAKDIDL SKPIPNPHDDDEDHKKGHHDHSDHKHEEHEHTKSNKLSDEQKKLIYLA E
 KLGLNPNQIEVLTSEDGSIIFKYPHDDHSHTIASKDIEIGKPIPDGHHDDHSHAKDKVGMATLKQIGFDD EIIQDILH
 ADAPTFPFSNETNPEKMRQWLATVTKINIGQRTNPFQRFGLSLMPNIEVLGIGFTPINDMTPVLQFKKLQ LWMNTNT
 GITDYSFLDKMPLLEGLDISQNGIKDLSFLT KYKQLSLIAANNGITS LKPLAELPNLQFLVLSHNNISDLTPLSNL
 TKLQELHLDHNNVKNLSALS GKKDLKVLDSLNNKSADLSTLKTTSLETLLLN ETNTSNLSFLKQNP KVSNL TINNAK
 LASLDGIEESDEIVKVEAEGNQIKSLVLKKNQGS LKFLNVTNNQLTSLEGVNNYTSLETLSVSKNKLES LDIKTPNK
 TVTNLDFSHNNVPTSQKLKNEKNIPEAVAKNFP AVVEGSMVGNGSLAEKAAMASKEDKQVSDNTNHQKNTEKSAQAN
 ADSKKENPKTHDEHHDHEETDHAHVGH HHH

SeqID 270

MNKRVKIVATLGP AVEFRGGKKFGESGYWGESLDVEASA EKIAQLIKEGANVFRNF SHGDHAEQ GARMATVRKAEE
 IAGQKVGFLLDTKGPEIRTEL FEDGSD FHSYTTGT KLRVATKQGIKSTPEVIALNVAGGLDIFDDVEVGKQILVDDG
 KLGLTVFAKDKDTREFEVVENDGLIGKQKGVNIPYTKIPF PALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEV
 RAICEETGN GHVKLFAKIENQQGIDNIDEIIEADGIM IARGDMGIEVPFEMVPVYQKMIITKVNAAGKAVITATNM
 LETMTDKPRATRSEVSDVFN AVIDGTDATMLSGSANGKYPVESVRTMATIDKNAQTLLNEYGR LDDSSAFPRNKT D
 VIASAVKDATHSMDIKLVVTITETGNTARAI SKFRPADILAVTFDEKVQ RSLMINWGVI PVLADKPASTDDMF EVA
 ERVALEAGLVESGDNIIVIVAGVPVGTGGTNTMRVRTVK

SeqID 271

MTATKQHKKVILVGDGAVGSSYAFALVNQGI AQELGII EI PALFDKAVGDAEDLSHALAFTSPKKIYAATYADCADA
 DLVVITAGAPQKPGETRLDLVGKNLAINKSI VTQVVESENGIFLVAANPVDVLTYSTWKFSGFPKERVIGSGTSLD
 SARFRQALADKIGVDARSVHAYIMGEHGDSEFAVWSHANVAGVQLEQWLQENRDIDEQGLVDLFI SVRDAAYS IINK
 KGATYYGIAVALARITKAILDDENAVLPLSVYQEQYGDVKDVF IGQPAIVGAHGIVRPVNIPLNDAELQKMQASAE
 QLKDIIDEAWNPEFQEASKN

SeqID 272

MQDKNLVDVNLTSSEKTSFIDYAMSVIVARALPDVRDGLKPFVHRRILYGMNELGVTPDKPHKKSARITGDVDMGKYHP
 HGDSSLYEAMVRMAQWWSYRHMILVDGHGNGFSMDGDGAAQRYTEARMSKIALEMLRDINKNTVDQDNYDGSEREP
 LVLPARFPNLLVNGATGIAVGMATNIPPHNLGESIDAVKLVMDNPDVTTRELMEVIGPDPFTGALVMGRSGIHRAY
 ETGKGSIVLRSRTEIETTNGKERIVVTEFPYGVNKTKVHEHIVRLAQEKRIEGITAVRDESSREGVRFVIEVRDA
 SANVILNLFKLTSLQTNFSFNMLAIEKGVPKILSLRQIIDNYIEHQKEVIVRRTQFDKAKAEARAHILEGLLVALD
 HLDEVITTIIRNSETDTIAQAEILMSRFEISERQSQAILDMRLRLRLTGLERDKIQSEYNDLLALIADLADILAKPERVV
 TIIKEEMDEVKRKYADARRTELMIGEVLSELEDEDLIEEDVLITLSNKGYIKRLAQDEFRAQKRGGRGIQGTGVNND
 DFVRELVTSTHDTVLFFTNLGRVYRLKAYEIEPYGRTAKGLPIVNLKLDGEETIQTIIINARKEDVANKYFFFTTQ
 QGIVKRTSVSEFSNIRQNGLRRAINLKENDELINVLIDENEDVIIGTRTGYSVRFKVNAVRNMGRATGVRGVNLRRE
 GDKVVGASRIVNGQEVLIITEKGYGKRTEASEYPTKGRGCKGIKTANITAKNGPLARLVTTINGNEDIMVITDTGVII
 RTNVANISQTRSTMGVKVMRLDQEAQIVTVALVEQEIETDKSNIEDTKE

SeqID 273

MTIFDERELKERFTHENRVSFYEFVAKYDAQMVPMKAKGYRCIHSMERTVVFTFGEFTIRRRRWQKGEHWVVPVDE
 KLGLKKNVRSLEFMYQIASLATMMPYEKVIKVVQMMYICIVITKPTVVKAVKISRELLKEKEAYRFFDEDIPVDKEP
 VDMIYLEGDMVMKAREEGLDNRNVDLSHFVVHTGSQKVGSNRFVLQNKKEFVSLDNRQTRQKILDYLYNHFYIAPN
 TLLITNSDGGHGYTPYVFKETIAKALKVKQHEHFWDRYHVNEKIKSFFKLYPVELMTGAFQSIKQHDKEKLRVLDTT
 EALILMEEEMEGFNQFKRKLNNFQYTKSAELRGFSRAGIGVMESQHRKITYRMKKRGMWYTIQGAETMSQLIVLSY
 EGQLRDLFFGSWREDYQKYQLENLISAGKIKHEQNKINKRYDLQTLGRLRYGRHRL

SeqID 274

MAYLSKLSDDLPSLMDADSEQIYIPKVLFEHNDFKGLTYKEILLYSFLNRLREPLDFIQKGYDDNEDTYVHFVKVED
 LCELLNQSKTTVISLKKRLAQYGLIEEVKAGSHQPNRIYLTDKLVPIYKIG

SeqID 275

MTDNRFAQLKENFEKGSPPKRRVPTSRPIAAQKAPESYNKKGRYPFSLHQDVRYDKLEALVAYHGAKSASDYLERLIV
 QEWKMQRKCLKNKEK

SeqID 276

MFSWLEALYYTLIQAKVNRNLNALFLVSVVGYLCYQGIGIKLVKRTIRNFFQLMKGFIDRENKKCIKNKKEALVHSW
 KHRQDIDWKSTGKDKSKQLWNLMKRLATVAPSFLFLLGNVLFRLIYQLPFVKQDRKRFDEKMPLLYFKNYRSFVF
 MGIGFSFIAFILTNFYFVTVLRAAIRFLYFSIMTLRDNQSQVVSFNVDSLLIQNLFNARVFIAPILAVPIFLIGLVVA
 WRSWVNFQYRDYNHNEEGDDRFATVKEIHQQYKVPNKTEYTPGEGGVPLHETRKNLTGLTLKSQMLWQNRFTFS
 RYLTAERILGLLSTPSGDYIIDDSTTNLITMGITRSKGGEAHIAPIIDINSRAEIQPSLIADPKGEHYQSSYKTM
 RRRGYDVNVLSFQNMDSMSYNPLALALIAAAKKGYEYMTQTRVNAVAEATYRKTCPGSGNGNAKYWEDTSISLFNAT
 AMALMDRANETVRNGETDAWDTVTVRNIAKFLTDLGSEEVFVNDFGEIVENPDKNQVKKKSKITVYFDNLRKINQE
 QFSKFRDMADLNFRSSDFASEETKGNVFSMMSGINLFLQDNIAKLTSKNSIDLESVGFPRRLSIKFRSSSNVAMRN
 EYTHKTAKVTITSQAVWGKTTKQVIHVDAAATALIDGEGYLTYVIEPQLPDQFLVTIDFNHENNGGSAIRHKTQFQSA
 EKVKYKRGNVITLDDYTKKPVLDHIKVTVLNKKQDDNLLQKEDIDLISDNPKVIYLVTPPNRTEYNSIVSLFLDQLF
 NANYELALSNGRKCVNRILHILDEFTNIPAIHMDTKISIGLGNILYYLWIONLKQLVSEYGENTAETIRENCSLK
 VYIKSTAPATNEYFSKELGTRTITRRRRSSNILDEANPNVSIENPRQELLTPTQLSKLQEGEAVILRGVKGRDNAGR
 KITTDPIFLHEKTSIPYRYMFLQEEFDQSMALADIPVESGHRDLDLQDIAVGAQSTFNKIIDWRMALTDRTMRTNGKI
 PQLASRKQTIKALSQSQFTSPADLTQAVIAEVFDEEDDDDLFFVDDVM

SeqID 277

MNSNTKGHGFFRKSAYGLVCAIALAGAFTLATSQVSADQVTTQATTQTVTQNAETVTSTQLDKAVATAKKAQAVAV
 TTTPAVNHATTTDAQADLANQTQAVKDVTAQAQANTQAIKDATAENAKIDAENKAEAEVAKENKEGQAAVDARNKA
 GQAAVDARNKAKQQAQDDQKAKIDAENKAESQRVSQNLNAQNKAKIDAENKDAQAKANATNAQLQKDYQAKLAETKSV
 EAYNAGVRQRNKDAQAKADATNAQLQKDYQAKLALYNQALKAKAEADKQSINNVAFDIKAQAKGVDNAEYGNISMTA
 KTKPDGSEFENHDMIDGVKTIYGKLTGKVNHHYVANKDGSVTAFAVDSVTLYKYEYRNVAQNAAVNQNIIVFRVLTKD
 GRPIFEKAHNGNKTFEATLNLKTLQNLKYELKPHASSGNVEVFKIHDDWVHDTHGSALVSYYNNNDVAPNVVPIPERP
 TPPKPVKVTPEAEKPVPEKPVPEKLVPTLKTYPVKFIPREYKPEPITPETFTPEKFTPAQPKVKPHVSIPEKINY
 SVSVHPVLVPAANPSKAVIDEAGQSVNGKTVLPNATLDYVAKQNFSSQYKGIKASAEAIAGFAFVDQNEALAEALT
 KSIKASNGDDVSSLEMRHVLSDKDTLDQKLQSLIKEAGISPVGEFYMWTAQDPQAFYKAYVQKGLDITYNLSFKIKA
 NFTKGQIKNGVAQIDFGNGYTGNIIVNDVTVPEVHKDILDKEDGKSINNSTVKLGDEVITYKLEGVVPANRGYDLFE
 YKFVDQLQHTHDLYLRDKVVAKVVDVTLKDGTVIKKGTNLGEYTETVYNKTTGHYELAFKKEFLAKVSRESEFGADDF
 IVVKRIKAGDVYNTADLYVNGYKVKSEAVVTHTEKSKPVPEKQATPKAPAKGLPSTGEASMTPLTAIGATILSALG
 LAGFKKRQK

SeqID 278

MKQIKIITGLTVATLSAVGVNVYAEDITPTAPVNEPQVSSETAKTPQVTEQVNSAKVTADQAISDVNNQQIVVDEA
 QKQKQSQQNLVKATSTVTEAEKVAAEATPEVVKEAIKAVTEAKEAVTDAEANVDAQKTEQKANQEVQSQAKTVDE
 NVKVVDKESSEVKQAEGVVTTAQEAIDSKTANTNASEAEKAVTEKQTKLETAETNLTEAQKQDAKIAEEKRLAEQEV
 VNKQLAVTDTQTLLKKLVTEINNEKVSTSLNQAYFNQRDGWSWAGYGYNYTFAATGCVPSSSLAMVFTELARRQITPT
 EIANYLWNNNSNEFNKNYGGTSGKGLVQATKHFGFVPTHASQSAIVEALQAGHHVLAQVQDKFSPWGINYSHEIVL

RGYSNGNTYVYDYPNRRANIGWYPVANLWNEQSRDAIDTSSVGVPPFFKITTTQKMAQLEAQKAQVQSSSLNTAKNQLAKT
QDVLRTLEATPLKTPEAQAKLNQAKEALALAQADYTKAQEAVKLASQDLAVKEETLKNAQADLLTKQTALKDAQOTVL
VASQVKLADLKATLATVENNVKKAQATLTDAKAIVGQKQAKLLALQNA PKILADAQAKLVTAKNLANKMAILDEAV
AKLKS LQAVQAEAQKYHVVFAYKAVRDAKEQAKLAESYNHIIARGGEAIPVVDETDKITGYVDGSGQKAVANEVTL
ALTSNGAPLES PVNKENQNVTKSSQALPHTGEAGLSILSVLGVLITSLGLTSLKRRPH

SeqID 279

VRLTHVSLWMPKSRWSPLKLQLLRKGVIELEDELKTPYLDQYTDNLTA KVTKKSDDYQVYGRNKEVQSVIIISLLRRT
KNNPILVGEAGVGKSAIVEGITLAILRGQVPEPLKGLTVRSLELSSLMSEDDDEGFIKFKKIIHEMVATRGHNLLFV
DEFHTIIGAGSQNGQALDAGNVIPVLRGDIQLIGATTLEDEFHEYIETDRALERMMQPMVEEPTISQAITTIEQA
KVIYEKFGHIQISSDAVHQAIRLSVRYLTDRFLPKAFDLIDEAATIASVEGKSKVTEKDIAQVLDKDKTGIPVTTIL
KGDQERLEGFKERLMNRVKGQEDAEAVVDAVTIAQAGLQNEKRPLASFLFLGPTGVGKTEIAKATAEALFDDEAAM
IRFDMSEYKQKEDVTKLIGNRATRIKQGLTEGVKQKPYCVLLLEIEKAHSEVMDLFLQVLDGRLTDSSGRLISFK
NTIVIMTTNIGAKKIINKWELKGNFKDLTDRDRKQFEKSMDELQNEFRPEFLNRIENKLI FNLLERDVIEKIAEKN
LSEIADRMKRQNLTLSEYPSLIQYLSDVGTDVKNGARPLERLMKRKVLAPISVKSLQLDKSKQGYNVHLWVEGRAPD
GNHRQEQRIHMEIEGERDNFFS

SeqID 280

MAEENAOQPSLRGKSRRRERVEFARSRDILDVAHELMNMFRLDGNRYRWKEHDSMVITPATNQWYWFSSQRQGGDVIAL
VETIKEIGFNQAFEYLNNEGTFKEFTVNVQVKEPFSYYLEPYEQLFVEARRYLKENRGLSDDTIDFFYDKGVLAQANA
KVGDMIEPVLVFKNLDKNGQVVGAAQLGLVAAPDKYFGRGYLKQIMKNSQPYNGMHVDIGTPNRLVFAESSIDLMSY
YEIHKDSLSDVRLVLSLEGLKTGTIGRHLIQLRAEMERRPLSSSWTDEILAQGLDEAVKQGYFKDGKNSHLLTLAVDN
DVKGKQLIEELKDKSIPVIDATPPKAEGQSKMDWNAYLQETKATFSTEKYQEKIDHLISDVILGDETYLWHDDELV
NLGAGDSIIQAFHHQLEDRRYVINQAELYVEESSNDGATGYLSIEGHVLDKDGISDYLSQALTDKAEKVAFLETQ
ELPDIWDEIVNHYDKVFEEVVVYGLREKHADIIQEQLDLDPLVVPEAKEKSLEMNQETNTGGELFNRRNSSPLGED
SPGTAPQPVPEPTAQPDFTNVRHLHFTTDDGNMSNKA FRKNMRTLNLANTMRDSAQWYLSIADTTMSYVYKTPHEE
GVQVLSVHFGKKNWMLHTGVTVPYENWVDSLSEQFIDDIANSGHFKNLKFPALGTPDKLKVNLPLPEIESDTFVFN
DLSSVQKLNLDLSQALNPEDSLLLLLFRDEGLHQVPASLMRIKGDLEERLSHIDSGTVLGVYRERNQGLEQVSVNE
EYVKDSGQEMLSILQNKHYEEALDSGQEMVQTDGFSAEFTKVLDAVYHVGVPDDLARVPEGVLPVWQKYLEVSEEN
QWDLEQ MIDYADKNSLLVKDSAFYKEWKEDMIYKNDYHVRQLFAENWDNGVELPFRTEQLIDYKTFVTGLYEANQAH
HQRQESQLPYTKTEFDIYAPGGQLIKDNVHYAIGDETRPVSQMLGLGYRRLPGYQELAVIDNSILS QLENKELNQE
IASEANEHSLNSQEI PKEDNYPREAF TSPKQDIKKGLAQRVEEIVAEADTKILVSSIPQVQENLSVEGNLVGTPQAD
NRMLYTNLNEDFGQDYQLELAVYSPKRVDFLEDVQAPWTLALIRKEKKIGYLAYGSDWAKEFQIEEELEHLAAQIGDE
KVPEGLYKQAEVEAFIASHQGNESLQEPIPTIVAEFPDYTSASAYELSEHAFQKIREYTSQPEDLLEYMDFMSKFPQ
LSPRNVALIHEQWRGANAVATYEQWKAMGEALGIKPDDVVQTKATYVNKRGETKEVHVHQLSVKTKGEKSKITLFRP
LMVKMIPVLDENGQQLKNDKGNPKYKLLSEASLQEKALVKDGKLPVRQFQERDSKTGQPRFTTYKVFELSQTTLKPG
SYPKAMPNRHFNFNVDKVKTKEVLEGLCDYAEKIGVSLMKDDAHVLDNAKGA FYSEEQLILINPNNTPGKIATTI
ELAHATLHNPKEKQYKELPKGQKEFEAEMTSYLLSKHFGLDTSEKATHYMASWTDNLKALEDKQLADSLKRVHQTV
SKMLKQVEKYTNPHQLGRGKEHGLNFPKAPT KGSSR

SeqID 281

MDVSSSPNITFMLQYTEANPOYVDYTNREEAVKIDEELSLETNRQMIEGLTEDELTRI QEAVPETQLNFREYIDYMN
RSYATEEQSKELTAIFTQEADYLQKLRLIDLKKNKLESAYQNGSLLWQGVISFDNAFLAEQGLYDVATGQVDQKA
VMRDMPTLIQKEGLSDSAFWGNHNLNTDNIHIFGLSEVESNREKIFYQPRGRMEYKGNFSQKTINRFKSGVYHG
LLKEETRSNLLRKEQILANLKADFITSIYQKDKITSSAEKNFLEQAYNHLPLNKKWRYGNSARDFAVSKFFLDRLYD
SYLNNEGSAAYQEFLKETRDFLQTYEGVYSAEKNKIYEKLKRVGQGTIRTLAESKGYDLEHHLARRVMDLRERLANN
ILRSFREAAPIQDVQLEKNLESFVLNQQKILEQHPEASVVKSQAWQKLG YFVKAGEQPLEIIRPVYKSYDKHGK
GIGRPEFVSDTVYDISQLTENIQLKSLTLKDLSLFSSNELKELVDAAKLKTNPTE RERRELGT YRYALKLSILESSQ
KELQVRQKLLQVQPLASDQPFDFKQLIAQELQAIALQLTPNYKLS EDDKALKNRLKRQFEDSVALPVSKATPGA
IQLPIRQLWTELGLVHHIQDENILTLLKGTSTTKQAYIEELQTHISIFQLKYQINNRNKQISQLSDEATIKEMRIAN
AKGFSSELKRLYDTLQPSDDGQNQISQAVSKQLQERKVIKKAQLQQTQRSGKINTDFMRQLTASLNRSQQASKKALME
RARSDEREEQEERRQAQR

SeqID 282

MKKNKFLLVSIIVFIIIFVVPQNFQSLKNIFTQNDIASQLNIISSSPEEKNDGLGTAYQTQNE DLKSKSFDGQHQVIV
VNEKAQFTAEELSMRNGSWEKYDNLDLNRVGVAEAMLGKELMPKEARQDISSVKPTGWKNKKITFNGKQDYLYNRS
HLIGFQLSGENANVKNLFTGTALNANFNDDKSSMVYENEVANYIKKTNHHVRYRVTPLFKNVELVARGVRIEAS
IEDETISFDVYIFNGQPGYDIDYLTGSSEKIMTK

SeqID 283

VTKEIKIRSIPEKTWAQLHMISEEYFYP SFNEFMLAQLQRIVENGGDL DYDNKFAETLAVI KEQQAQILDQLLKNEI
KLLAYHAKQDIVEELTTDWLRFMDVDALAAERGAGGR

SeqID 284

LLYYFYIYLIKIVIGNGLKLSLICGLNWLKIVFKGQFYLFSAVFCGLLTYMPQDIQLFTVRVLELIIMLKVIIDVTH
TALS RDKFRMKTPLFLGVYVFFLAGNSYIKAHLLTEVMVNHLISFWLISLFFATLVIVIQPRLFKHYLLKKVIDKE
YLGIRKFTDSLPPFEINLYKDADEEDADKMRMLINQNVIKHPYQEVVELSFLNREVITAIGYKAVPFKEKETERTFIDD
DTIYYPIFTVHPFRNLEGGKSDFYHILMKLKLRSKAAFTKNGERLLIRDF

SeqID 285

MIRNEFYNQLINSEPIGFIDPFTDLGEFDSIQMKFKQPVNRNLVKNYSKGKPYNLSWQNKIEQMRVLYIKYQKSLKLED
EEQEVHNRVKNKSKKYVHEIVTITYLKLGFRFKEIEARVSLFNTRLRRNWKRSYVTTDNPEFYLLKDLQNGYCSPN
SFLPRSMKIN

SeqID 286

MNEIKCPHCGTAFAINESYHQLLEQIRGDAFDKEVSEERLEKERLILGEQAKNQLQEVVVEKDKEIAKLQYKVKQFL
TEKDNLLKDNEYQLAEQLNQKDMMLRDLNENQIDRLRLEHENSLOEALTKVERERDAIQNLHIEKEKDLALASVKS
DYEVLKAANEQVEFYKNFKAQOSTKAVGESLEHYAETEFNKVRHLAFPNAYFEKDNTLSSRGSGKDFIYREKDEND
LEFLSIMFEMKNESDDTIKKHKNEDEFKELDKDRREKSCEYAVLVMTLEADNDYNTGIVDVSHKYPKMYVIRPQFF
IQLIGILRNAALNTLKYKQELALMKEQNIDI THFEEDLDIFKNAFAKNYNSASKNFQKAIDEIDKSIKRMEAVKAAL
TTSENQLRLANNKLDDVSVKKLTRKNPTMKAKFDALKD

SeqID 287

MNHFELFKLKKAGLTNLNINNIINYLKKNLSLTSVRNMAVVSCKKNPTFFIENYKQLDLKKLRQEFKKFPVLSILD
SNYPLELKEIYNPPVLLFYQGNIELLSKPKLAVVGARQASQIGCQSVKKI IKETNNQFVIVSGLARGIDTAHVSA
KNGSSIAVIGSGLDVYPTENKKLQEYMSYNHLVLSEYFTGEQPLKFHFFERNRIIAGLCQGI VVAEAKMRSGSLI
TCERALEEGREVFAIPGNIIDGKSDGCHHLIQEGAKCTISGKDILSEYQ

SeqID 288

MTERTFEDIELDLKLFQIKLDNAENSKRLLQKLKNDVMELQIELLESCLKLGDAYLTESEEELEENNDFILTVNSETLS
LSYDNRINLVSKEIMDYENALDKLYYEKQSLMQKSNERKGG

SeqID 289

LFNKIGFRTWKSGKLWLYMGVLGSTIILGSSPVSAMDSVGNQSQGNVLERRQRDAENRSQGNVLERRQRDAENRSQG
NVLERRQRDAENRSQGNVLERRQRDAENRSQGNVLERRQRDVENKSQGNVLERRQRDAENKSQGNVLERRQRDAENR
SQGNVLERRQRDVENKSQGNVLERRQRDAENRSQGNVLERRQRDVENKSQGNVLERRQRDVENKSQGNVLERRQRDA
ENRSQGNVLERRQRDVENKSQGNVLERRQRDVENKSQGNVLERRQRDAENRSQGNVLERRQRDAENRSQGNVLERRQ
RDAENKSQVQGLIGKNPLLSKSIISRENNHSSQGSNKSQSFSSKKVSQVTNVANRPMLTNNSRTISVINKLPKTGDDQ
NVIFKLVGFGILLITSRCLRRNEN

SeqID 290

MKRLTYFYFKGYIKETIFGPLFKLLEASFELLVPIVIAKMIDETIPRGDRSSLLQLIGLIFFLAAGVVVAITAQYYS
SKAAVGYTRQLTEDLYQKVMSLGKKDRDELGTASLITRLTADTFQIQTGLNQFLRLFLRAPIIIVFGAIIAMAFSISPS
LTIWFLVMVVTFLFIIVFVMSRLNPIYLKIRSTDYLVKLTQQQLQGVVRVIRAFNQVDRESEAFNDINHYTNLQLK
AGRLSSLVPTPLTFLVNNITLVVLIWRGNLNIANHLSSQGMVALINYLQLILVELLKMFMVLTSINQSYISAKRIIA
VFERPSEIIDDKLEPKYSNKALEVQEMAFSYPNSSEKALS DITFSMNVGETLGIIGGTGSGKSTLVNLLHHIYKVQE
GDIDIIYHQGKSPDTISNWRTLVRVVPQNAQLFKGTIRSNLSLGLGKVSEEKLTALTAQAASDFVKEKDGQLDAPVE
SFGRNFGGQRQRLTIARALVQDKIPFLILDDATSALDYLTEARLFKAITKHFNQTNLIIVSQRINSIQNADRILL
DKGKQVGFNDNHQSLLAHNKVYSIYHSQNFKEEE

SeqID 291

MKFNEQSNSQAALLGLQHLLAMAYAGSILVPIMIASALGYNAEQLTLYLIATDIFMCGIATLLQLQLSKHFGVGLPVVL
GCAFQSVAPLSIIGAQQGSGYMFGALIASGIYVVLVAGIFSKVANFFPPIVITGTVITTIGLTLIPVAMGNMGDNAKE
PSLQSLTSLSVTIGVLLINIFAKGFLKSISILIGLISGTILAAFMGLVDASVVAEAPLVHIPKPFYFGAPRFEFTS
ILMMCIATVSMVESTGVYALSDITNDKLDKSKRLRNGYRSEGLAVLLGGLFNTFPYTGFSONVGLVQISGIRTRKP
IYFTALFLVILGLLPKFGAMAQMI PPSVLGGAMLVLFGMVALQGMKMLNQVDFEHNEHNFIIAAVSIAAGVGFNGTN
LFISLNPNTLQMFLTNGIVISTLTAVVLNIIINGLPKKLI

SeqID 292

MANTYDLISQRIEAQRQKLIADIVAVASSLGLNLKQSGGGHLYWDEHDSFHIYPQTNTFRWWSRSMGTNTIDLQV
IQEELTGKKPSFRETVNFLETGQFESVTVPVVRFPFKHYLAPYEHNFDFLGRQYLKEERGLSDETIDFALASGMS
SATLKKGDYFEPVIFKSFADGRMITGGSLQGIVENKVQHPERGRKQIMKHS DGLAGFHLDVGT PKRLVFSEAPID
LLSYELHKESELQNVRLVAMDGVKKGVISRYTADLLTDGQYSQTMPRESIRGAIDAINQTTRILKNNPNMITIAVDN
DEAGRNFIKELQEDGIPINVDLP PRKEHQSKMDWNYYLKQKKGLLKMPQTEGTQKAPEQVLEHEKMDRSQISSGSL
DDPQGSAPKPSKRDTFEQAVTSHPTFSYPLLQFSTEEAFNKNVNRVDGYHIASEEDIRNLNYYAPSLQQTANWYRDNL
DRQVTYMLKGDKKEIKALQVSFAKDKFAHLTGIRPIGKGLSAEKLDDFAKGRGSYPNLTLNNGFNDKIQVLPMIQEL
SQSKSFVFTDLEEVQKMRNLKASHAIQSNNRSILVVALKTIDDVTFPSSLLRGKKNLNDDLIQKAKENEVLGVLSKED
GNITVLSVNDKYIQDGGQALKDMIKNGELEPLQMETIQRHVPHENAYPKDSGDGGLTDDEETALGTNPFSDDSDGDG
TPDNVEKANGTDP TNASDNEVTRQOEANKRDFTLSEMIKAKNTAALNQHLQDGKIQYFSDSYTYKQYLEGMAHFNNYS

PRNIQLIMSOFPEASMSVASFQEWKRNGSVKKGEKAIYIQAPVSVMKDENGKPIILNPETGEKETITYFKPVPVFDI
KQVSPQEGKELNLPKAMGTIPEQLDKKEYYQNVYRSLRDISQNNKVPPIRFRELQEDGFYSPQTNIEIVIKKGMSYER
TLSTLIHEMAHSELHNKQSLTERFDGKLTRSTKELQAESIAVYVSSHGFDTSQESFFYLASWSKEKDGLANLTAQL
EIVQEEAKNLMERIDQQLSQYQTVTLNKETQQLTKQEMKKQTHPFYQSLAAAKTSRAQVTTQEKESVKKDNRPTMP

SeqID 293

MNSQETKGGHFFRKS KAYGLVCGIALAGAF TLATSQVSADQVTTQATTQTVTQNOAETVTSTQLDKAVDTAKKAAVA
VTTTTAVNHATTTDAQADLANQTQAVKDV TAKAQANTQAIKDATAENAKIDAENKAEAEERVA KANKAGQAEVDARNK
AGQAAVDARNKAKQQAODDQKAKIDAENKAESQRVSQNLNAQNKAKIDAENKDAQAKADATNAQLQKDYQTKLANIKS
VEAYNAGVRQRNKDAQAKADATNAQLQKDYQAKLALYNQALKAKAEADKQSINNVAFDIKAQAKGVNDNAEYGNISIMT
AKTKPDGSGFEFNHDMIDGVKTI GYGKLTGKVNHHYVANKDGSVTA FVDSVTLYKYEYRNVAQNAAVNQNVFRVLTK
DGRPIFEKAHNGNKTF AETLNLKTLQLNLKYELKPHASSGNVEVFKIHDDWVHDTHGSALVS YVNNNDVAVPNVPIEQ
PTPPKPEKVTPAEKPVPEKPVPEKLVTPVLKTYTPVKFIPREYKVPVPSTPETFTPEKFTPAQPKVKPHVSVPEKIN
YKVAVHPVQIPKATPTKKVLDENGQSINGKSVLPNATLDYVAKQNFSSQYKGIKASAEAIKAGFAFVDQPNELAELT
VKS IKASNGDDVSSLLEMRHVLSKDTLDQKLQSLIKEAGISPVGEFYMWTA KDPQAFYKAYVQKGLDIT'YNLSFKVK
KEFTKGQIKNGVAQIDFGNGYTGNIIVNDLTTPEVHKDVLDKEDGKSINNGTVKLGDEVYTKLEGWVVPANRGYDLF
EYKFVDHLQHTHDLYLKDKVVAKVAITLKDGTVIPKGTNLVQYTETVYNKETGRYELAFKADFLAQVSRSSAFGADD
FIVVKRIKAGDVYNTADFFVNGNKVKTETVVTHTPEKPKPVMPQKVTPKAPALPSTGEQGVSVLTVLGAALLSLLGL
VGFKKRQQ

SeqID 294

MNQIKIITGLT VATLSAVVGNVYAEDITPTAPVNEPQVSSETAKTPQVTESQVNSAKVTADQATSDVNAQKNVVNNA
QNQKNQAQKLVNAT'TTLNETQKLQVESTNQNVQQTVD SAKQRLSQTEANQKITQTEQVKAQNQVNAQQT VVVNNE
HDVATKTADV KQAQASVDTAKDAL'TNTIVNSDLNKAQSNVT'TKTADVKTATDAL'TKAQATDKLT'LNQKAKAQQIVDS
AKQNL SAKDTQLSQANAEVNHKFKTALGQSHYYNQ RDNAWAGVYGGHTFASTGCVPSALAMVYSDLSNRTITPREI
ADYLYNNTDEFNKRFGGTSGKGIISATKAFGYVTHLASKNAITEALKAGHHVVA AVQNNKFS PWGPPQYSHEIVLRG
SSNGNTYVYDPYNRDNNGFYSDRIWNEQSRDSIDTAGVGVPFFAIMTKNMANALTQSQALASQQVAQKQLNDAQA
KATGLNAVMTQTPIAQANLIKAQSNLKDAQKRLAEQAQASVKLANQDNVKKQADLTKAESKLKDAQKQLAAQAKLT'T
SKTKLNQLKQVLAEASQQVAQANQDYKQAKDNLTQKTAYLTNLRNAQANLIKAQSDVAQAKDNLANKIAKLQREVAY
LQELKTKAVDAQSQYQKVL SAYKSVLSAKASLKLAEKARLDDKGHEAVAVVDETGKITSYITSKHKIEMKSLVATK
TTDVKQVSVAKASVLPSTGDVQVSVALLGMLLTFSGFLGIRKQSKKVIN

SeqID 295

MISRKVALVTGASAGFGAAIVTKLVSDGYSVIGCARRMDKLKCFGEKFSEGYFYPLQMDITSRESVDKALESLPKNL
QSIDLLVNNAGLALGLDKSYEADFEDWMTMINTNVVGLIYLTRCILPKMVEVNRGLIINLGSTAGTIPYPGANVYGA
SKAFVKQFSLNLRADLAGTKIRVTNLEPGLCEGTEFSTVRFKGDHVRVEKLYEGAHAIQAEDIAN TVSWVASQPEHI
NINRIEIMPVSQTYGPQPVYRD

SeqID 296

MIYLDNAATTALTPSVIEKMTNVMTSNYGNPSSIH TFGQANQLLRECRQIIAEYLVNSREIIFTSGGTESNNTAI
KGYALANQLKGKHIITSEIEHHSVLHTMTYLSERFGFDITYLKPNHGQITAKDVQEALRDDTIMVSLMFANNETGDF
LPIQEIQLLRNHQAVFHVDAVQVFSKME LDPHSLGIDFLAASAHKFHGPKGVGILYCAPHHFDSLHGGDQEEKRR
ASTENIIGIAGMSQALTDATTNTLKNWTHISQLRTTFLDAISDLDFYLNNGQDCLPHVLNIGFPRQNNGLLLTQLDL
AGFAVSTGSACTAGTVEPSHVLTSLY GANS PRLNESIRISFSELNTQEEILELAKTLRKIIGD

SeqID 297

MSRKTFKHILSIGVCTLVLSMSLYYTEKAHAIAGPSDRQYVENPNPHIIVNVTGTDQNGNSILPHYIEVNVKMGQTL
SKEEILDYIARNLNSVGGESKNVQYSNIEFKESAYLKRQLDDGKTEEIAIDNDGVTVPKDGPNKFVIDVPV'TCTVT
PIVTETHEVWRGTPVAISHRIYFVEESSGKVLDEYTNLHTADSELNGYRVGDYITDYALSKSAYEAF LNSRLDKEGY
KLQHRISTNVQRNLQIDKLIFNYDFNEENIYYQIGNIRPLLSRSSAEVESDIITERYVSKNAKSLARTESTISIKM
VDAKTEQPLFNHTLTGYQLATVSHVYNRLFEENLIPTTKSGERYFIQNMKKTAEQEYTVYLSETPYSKENAPVISYD
ARPVDWDYHSGASGSLNQPNIIYTEEDSTEF LGNKPQAACYPNKQFACENTDSKYNYSYLEK

SeqID 298

MNPLIIGMNDKQAEAVQTTDGP LLIMAGAGSGKTRVLTHRIAYLID EKYVNPWNILAITFTNKAAREMRERAIALNP
ATQDTLIATFHSMCVRILRREADYIGYNRNF TIVDPGEQRTLMKRIIKQLNLDTKKWNERSILGTISNAKNDLLEI
AYEKQAGDMYTQVIACYKAYQEELRRSEAMDFDDLIMMTLRLFDQNKDV LAYYQORYQYIHVDEYQDTNHAQYQLV
KLLASRFKNCVVGADQSIYGWRGADMQNLIDFEKDYPQAKVVLLEENYRSTKKILQAANNVINHNKNNRPKKLWT
QNDEGEQIVYHRANNEQEEAVFVASTIDNIVREQGNKFKDFAVLRYRTNAQSRTIEEALLKSNIPYTMVGGTKFYSRK
EIRDVIAYLNLANTSDNISFERIVNEPKRGVGPGLTKIRSFAYEQNMSLLDASSNVMMSP LKGGKAAQAVWDLANL
ILTLRSKLDLSLTVTEITENLLDKTGYLEALQVQNTLESQARIENIEEFLSVTKNFDDNPEITVEGETGLDRLSRFLN
DLALIADTDDSATETAETVILMTLHAAKGLFFPVFLIGMEEGVFPLSRAIEDADELEEEERRLAYVGITRAEQILFLT
NANTRTLFGKTSYNRPTRFIREIDDEL IQHQLARPVNSSFGVKYSKEQPTQFGQMSLQALQARKSNSQPQVTAQ
LQALNANNSHETSWEIGDVATHKKWGDGTVLEVSGSGKTQELKINFPGIGLKKLLASVAPISKKEN

SeqID 299

MKLYVQLMVILTFSFAGEVLSTIFNLPVPGSIIGLLILLFLALKYKIIRLRHIDAVGNFLLANMTILFLPPAVGLMEH
FQDIKPYLFGIAIILGALFLNLTIGLVSQWIKKRYEGDYPEIGGKNGNFNE

SeqID 300

MIFVTVGTHEQQFNRLIKEVDRLKGTGAIDQEVFIQTGYSDFEPQNCQWSKFLSYDDMNSYMKEAEIVITHGGPATF
MSVISLGLKLPVVVPRRKQFGEHINDHQIQFFKKIAHLYPLAWIEDVDGLAEVLKRNIATEKYQGNNDMFCHKLEKII
GEI

SeqID 301

MVMKIIELKEATVQVSNGLAEMKTILDHVNLSIYEHDFITILGGNGAGKSTLFENVIA GTLMLSGGNIYIMGQDVTNL
PAEKRAKYL SRVFDPKMGTAPRMTVAENLLVAKFRGEKRPLVPRKITNYTEEFQKLIARTGNGLDRHLETPTGLLS
GGQOALSLLMATLKKPNLLLLDEHTAALDPRTSVSLMGLTDEFIKQDSL TALMITHHEDALKYGNRILVMKDGKI
VRDLNQAQKNKMAIADYYQLFD

SeqID 302

MEIKKKHRIMLYSALILGTILVNNSYQAKAEELTKTTSQIRDTQTNNIEVLQTESTTVKETSTTTTQODLSNPTA
STATATATHSTMKQVVDNQTONKELVKNGDFNQTNPVSGSWSHTSAREWSAWIDKENTADKSP IIQRTEQGQVSLSS
DKGFRGAVTQKVNIDPTKKYEVKFDIETSNAKAGQAF LRIMEKKDNTRLWLSEMTSGTTNKHTLT KIYNPKLNVSEV
TLELYYEKGTCSATFDNISMKAKGPKDSEHPQPVTTQIEESVNTALNKNYVFNKADYQYTLTNPSLGKIVGGILYPN
ATGSTTVKISDKSGKIIKEVPLSVTASTEDKFTKLDDKWNVDVTIGNHVYDTNDSNMQKINQKLD ETNAKNIKTIKLD
SNHTFLWKDLN LNNSAQLTATYRRLLEDLAKQITNPHSTIYKNEKAIRTVKESLAWLHQNFYNVNDIEGSANWDF
EIGVPR SITATLALMNNYFTDAEIKTYTDPIEHFVPDAGYFRKTLDNPFKALGGNLVDMGRVKIIEG LLRKDNTIIE
KTSLSLKNLFTTATKAEGFYADGSYIDHTNVAYTGAYGNVLIDGLTQLLP I IQETDYKISNQELDMVYKWINQSFLP
LIVKGELMDMSRGRSISREAASSHAAAEVFLRGFLRLANMSNEERNLDL KSTIKTIITSNKFYNVFN NLKSYSDIAN
MNKMLNDSTVATKPLKSNLSTFNSMDRLAYYNAEKDFGFALSLSHKSRTLNYEGMNDENTRDWYTGDMFYLYNSDQS
HYSNHFWPTVNPYK MAGTTEKDAKREDTTFKEFMSKHSKDAKEKTGQVTGTSD FVGSVKLNDHFALAA MFTNWDRTL
TAQKGWVILNDKIVFLGSNIKNTNGIGNVSTTIDQRKDDSKTPTTYTVNGKTIDLKQASSQQTDTKSVFLESKEPG
RNIGYIFFKNSTIDIERKEQTGTWNSINRTSKNTSIVSNPFTITISQKHDNKGDSYGYMMVFNIDRTSFDKLANSKEV
ELLENSSKQQVIYDKNSQTWAVIKHDNQESLINNQFKMNKAGLYLVQKVGNDYQNVYYQPQTMTKTDQLAI

SeqID 303

MHSFSNPGYPYDNAVTEAFFKYLKHRQINRKHYQNIKQVQLDCFEYIENFYNNYNPHTANLGLTPNQKEENYFNAIK

SeqID 304

VKKTYGYIGSVAAILLATHIGSYQLGKHHMGLATKDNQIAYIDDSKGKAKAPKTNKTMDQISAEEGISAEQIVVKIT
DQGYVTSBGDHYHFYNGKVPYDAI ISEELLMTDPNRYFRKQSDVINELDGYVIKVNGNYVYLKPGSKRKNIRTKQQ
IAEQVAKGTKEAKEKGLAQVAHLSKEEVAAVNEAKRQGRYTDDGYIFSPTDIIDDLGDAYLVPHGNHYHYIPKKDL
SPSELAAAQAYWSQKQGRGARPSDYRPTPAPGRRKAPIPDVTPNPQGQHQPNDGGYHPAPPRPNDASQNKHQRDEFK
GKTFKELLDQLHRLDLKYRHVEEDGLIFEPTQVIKSNAFGYVVPBGDHYHIIPRSQLSPLEMELADRYLAGQTEDND
SGSEHSKPSDKVEVTHTFGLGHRIKAYGKGLDGKPYDTS DAYVFSKESIHSVDKSGVTAKHGDHFHYIGFGELEQYELD
EVANVWKAKGQADELAAALDQEQGKEKPLFDTKKVS RKVTKDGKVGVMMPKDGKDYFYARDQLDLTQIAFAEQELML
KDKKHRYRDI VDTGIEPLRAVDVSSLP MHAGNATYDTGSSFVIPHIDHIHVVPYSWLTRDQIATVKYVMQHPEVRPD
VWSKPGHEESGVI PNVTPLDK RAGMPNWQIIHSAEEVQKALAEGRFATPDGYIFDPRDVLAKETFWVKDGFSFIPR
ADGSSLR TINKS DLSQAEWQQAQELLAKKNTGDATDTDKPK EKQQADKSNENQQPSEASKEEKESDDFIDSLPDYGL
DRATLEDHINQLAQKANIDPKYLIFQPEGVQFYNGELV TYDIKTLQQINP

SeqID 305

MKKGFFLMAMVVS LVMIA GCDK SANPKQPTQGMSVVT SFYPMYAMTKEVSGDLNDVRMIQSGAGIHSFEPSVNDVAA
IYDADLFVYHSH TLEAWARDLDPNLKKS KVDVFEASKPLTLDRVKGLDMEVTQGIDPATLYDPHTWTD PVLAGEEA
VNTAKELGR LDPKHKDSYTKKAKAFKKEAEQLTEEY TQKFKKVRSKTFVTQHTAFSYLAKRFGLKQLGISGISPEQE
PSPRQLKEIQDFVKEYNVKTI FAEDNVNPKIAHAIAKSTGAKVKTLSPLEAAPSGNKTYLENLRANLEVLVYQQLK

SeqID 306

LRKKQKLPFDKLALALMSTSI LLNAQSDIKANTVTEDTPATEQT VETPQPTAVSEEAPSSKETKTPQTPSDAGETVA
DDANDLAPQAPAKTADTPATSKATIRDLNDPSQVKTLQEKAGKGAGTVVAVIDAGFDKNHEAWRLTDKAKARYQSKE
DLEKAKKEHGT YGFWVNDKVAYYHDYSKDGKTAVDQEHGTHVSGILSGNAPSETKEPYRLEGAMPEAQLLLMRVEI
VNG LADYARNYAQAIRDAINLGAKVINMSFGNAALAYANLPDET KKA FDYAKSKGVSIVTSAGNDSSFGGKTRLP LA
DHPDYGVVGT PAAADSTLTVASYS PDKQLTETATVK TADQ QDKEMPVLSTNRFEPNKAYDYAYANRGTKEDDFKDVK
GKIALIERGDIDFKDKIAKAKAGAVGLIYDNQDKGFPIELPNVDQMPAAFISRKDG LLLKDNPKQTITIFNATPKV
LPTASGTKLSRFSSWGLTADGNIKPDIAAPGQDILSSVANNKYAKLSGTSM SAPLVAGIMGLLQKQYETQYPDMTKS
ERLDLAKKVLMS SATALYDEDEKAYFS PRQQGAGAVDAK KASAATMYVTDKDN TSSKVHLNNVSDKF EFTVTVHNKS
DKPQELYYQATVQTDKVDGKH FALAPKALYETSQKITIPANSSKQVTVPIDASRFSKDLLAQMKNGYFLEGFVRFK
QDPKKEELMSIPYIGFRGDFGNLSALEKPIYDSKDGSSYYHEANSDAKDQLDGDGLQFYALKNNFTALTTESNPWTI
IKAVKEGVENIEDIESSEITETIFAGTFAKQDDSHYYIHRHANGKPYAAISPNGDGNRDYVQFQGTFLRNAKNLVA

EVLDKEGNVWVTSEVTEQVVKNYNNDLASTLGSTRFEKTRWDGKDGDGVVANGTYTYRVRYTPISSGAKEQHTDFD
VIVDNTTPEVATSATFSTEDRRLLTLASKPKTSQPVYRERIAYTYMDEDLPTTEYISPNEGDGFTTLPEEAETMEGATV
PLKMSDFTYVVEDMAGNITYTPVTKLLEGHSNKPEQDGSQAPDKKPEAKPEQDGSQGPDKKTTETKPEKSSGQTP
GKTPQKGQPSRTLEKRSSKRALATKASTRDQLPTTNDKDTNRLHLLKLVMTTFFLGLVAHIFKTKRQKETKK

SeqID 307

FSVTYSQSERTVVSFGEITFSRSRWTFNGFETRIPVDEWLGLEKYKRYISIEFLYHVAKLATMMPYRQVCKVIDSTLQ
TIIITKDCVLKAVKFVEKLLKEKERYRFYLEPPERKKVKKLYVEGDGVMIKSTDSREERRYLDLTHFVIHTGSKKVS
TKRYELQDKHEILQLNYDKAKYNLLDYIYNNYEVDLDTILITNSDMGKGYTSRVFKELGKALKVKKHEHFWDIYHVK
EKLSSYLKRYPIELTDFALDAVKKYNKSDKLELVFDTVESLICDELEDQEFQKFKKKVLNNFKYIKPAHLRNLNRSNGI
GIMESQHRKITYRMKRRGMYWSKWGISMANMILERANGLRELEFFGSRWKVYSEYKEGSFSAGRLFKKTDELDDKFS
KPLLKNGRKWSITGIKTK

SeqID 308

KASSGDYGTREIITANKDKYSISKMCRWLNMPRSSYYYQAVESVSKTEFEETIKRIFLDSESRYGSRKIKICLNNE
GITLSRRRIRIRIMKRLNLVSVYQKATFKPHSRGKNEAPIPNHLDRQFKQERPLQALVTDLTIVRVGNRWAYVCLIID
LYNREIIGLSLGHKTAELVKQAIQSIPIYALTKVKMFHSDRGKEFDNQLIDEILEAFGITRSLSQAGCPYDनावस
TYRAFKIEFVYQETFSLEELALKTEKATLFCCTTFIKCCLFRFLPML

SeqID 309

MKTRNRKGGYLANANEYIDSKQAIHCLSVLEPQIRFEEGQPTGEIIAYKAWFSQKGLPPFMVKFENEVTLPAYMV
MVQFENLQACEVGFNVYFKADNLKEVK

SeqID 310

LSTFDSVTGRNHLAEYEGNLSEKFAILSHFDKLRNELQTPSIQLGEFDREMEAFSITLGNELLYLEANGSPYEL
KRELNQAEEMAVLELSRQLVAKFSTKLEELGIDLGSFQPDQVNIILDAVGRFRLKNADIALLLGGYPKASVSQLALAT
ELLQMGLSHDKVEFFLTSQQLLEDMRQVAFALHESLTREEAEQFETDRFRHTSLNFWREWRELLEKQEPFEMVEMSDV
SPLVREVLHHYPLGSRVYTKGQFEILSIEAADMDNLIRIELQNDFSYLIBQNPVLYFQNLAEIRQVHLHSRSEIVE
REEQPEEEWTLFSFMDEGTEDNEKEPEIVFESTDKVVTLDSPAQVSETISESVPETKEVIEAEQAIIVDFSPEDL
TNFYPKTARDKVVANLVAILRVKELESANQSATPNEQEILAKYVWGGLANEFFDEYNPKFSKEREELKTLVSDKEY
SDMKQSSLTAYYTDPLLRQMWSKLEQDGFSGGKILDPMTGNFFAAMPAHLREKSELGVELDTITGAIKQLHS
NVHIEVKGFFETVAFNDNSFDLVISNVPFANIRIADNQYDKPYMIHDYFVKKSLDLVHDGGQVAIISSTGTMDKRTEN
ILQDIRETTDFLGGVRLPDTAFKAIAGTSVTTDMLFFQKHLNKGQYQADDIAFSGSVRYDKDERIWLNPYFDGEYNAQ
VLGRYEIKNFNGGTLVKETTDNLIASVREALQHVKAAPRVIDKTEVMINSDVIARQVIDTTIPPEIRENLEQYSYGY
KGSTIYYRDNKGIRVGTKTEEISYYVDDEGNFQAWESKHSQKQIDRFNNLEVTDSALDVYVTEEPAKRGQFKGYFK
KAVFYEAPLSEKEVARIKGMVDIRNAYQEVIAIQRNVDYDKNEFNRLGNLNRTYDSFVKRYGFLNSPVNRNLFDS
DKYSLLASLEDESLDPSGKTVIYTKSLAFEKALVRPEKMKVEVSTALDALNSSIADGRGVDFDYMASIYQTASKAAL
IEELGDQIIPDPESYLKQQLTYVSRQEFSLGDIVTKLEVMDDLKQDNHDFNWAHYGNLLESVRPARVMLADIDYRI
GSRWIPLAVYKGFVQEAFFMGKNYDLTATEVEEVLVSPIDGTMEFTRFAYTYSTATDRSLGVAGSRYSRGRKIFEN
LLNSNQPTITTKQIQEGDKKKNVTDVEKTTVLRAKEAQIDLFQDFVASYPEAQQMIEDTYNSLYNRVTQSKYVDGSRL
EIDGLAQNISLRPHQKNAIQRIVEEKRALLAHEVSGKTLTILGAGFKLKGELGMVHKPLVYVPSLTAQFGQIMKF
FPTKKVYVTTKKDFAKARRKQFVSRIITGDYDAIVIGDSQFEKIPMSQEKQVTYIQDKLEQLREIKQGSDDSYTVKE
AERSIKGLENQLEELQKLDRTFIEFENLGIDFLVDEAHFKNIRPITGLGNVAGITNTTSKKNVDMEMKVRQIQ
EYGDRNVVFATGTPVSNISSELYTMMNYIQPDVLERVQVSNFDSWVGAFGNINSMELAPTGDYQPKKRFKKFVNL
PELMRIYKETADIQTSMDLDPVPEATVIAVESELTEAQKNYLEELVDRSDAIKSGSVDPVSDNMLKVIGEARKLAI
DMRLIDPAYTSLDNQKIMQVVDNVERIYREGKGDQATQMI FSDIGTPKSKEEGFDVYNELKALLVDRGIPKEEIAFV
HDANTDEKKNSLSRKVNSGEVRILMASTEKGGTGLNVQARMKAVHHLDPWRPSDIQQRNGRLIRQGNQHONVEIYH
YITKGSFDNYLWATQENKLRYIKQIMTSKDPVRSIEDIDEQTMATASDFKALATGNPYLKLMELENELTVLENQKRA
FNRSKDEYRHTISYCEKNLPVMEKRLRQYDRDIEKSQATKNQEFIMRFDNQTDNRSEAGDYLRKLITYNRSETKEV
RTLATFRGFELKMATRSPGEPLSDMVSLTISGDNQYSVSLDLKSDVGTIQRINNAIDHILEDKEKTEEMTNLKDKL
AVARVEVEKVFAKEEYQLVKAKYDVLAPLVEREADLEEIDVALSQFSSSDPCLKKDQQLVLDI

SeqID 311

MTTKCNHFLINQEKGEKYVFRKSKQYRTLCSVALGTVVMAFVALAGPMVQADEVGRTVATSVQTTETNPATNLKENQ
PSPIAEQKDSLAATGQSTGTVTVTVPDQVTKAQVQDKAKTEGIKAVQDKPMDLGNTVSAAEQTSQQLKKAEDATNQTT
TISKTVIEIYKSDKATYEAEEKWVEKRNEELTAAYDKAEQGTGTLNHSVDTTVSELKSQDQNAHVTVNTQTVKSGDGT
SVSGYQYVKSVAIDKKKNANLADYRTKKQAADAVVAKNQLIQKENEAGLAKAKAENEAIDRRNKEGQKAVDEANK
AGQAAVEQANQEKQKQANRAFEIATTTKRNKEREVAKKENAIDAYNAKEWIRYKRDLANISKGEEGYISEALAQ
ALDLNHGEPQVKHGAGTRNPDR.IISKGDAMLGGYSNILDSTGFFVYNHFKTGETLNFTYQNLKHARFDGKKITAITY
DITNLVSPGTNAVQLVVPNDPTEGFLAYRNDGAGNWRDCKMEFRVKARYFLEDGSQVTFTEKEKPGVFTHSSLNHND
IGLEYVKDSSGKFVPIHGSSVQVTNEGLARSLGSNRASDLKLPEEWDTTSSRYAYKGAIVSTVTSIGNIYTVTFGQGD
MPTQVGKTYWFALNTLPVAKTVTPYNPKTHVRPQLDPVPEPIKVTPEYTPPKIFTPEKPVTFTPKSVEKVPQPSLT
LTKVTLPTNLKLEPLPKAPQKPTVHYHDYLLTTTPAIAKEVMNVDKVNLHGKQVAKDSTVIYPLTVDVLSPNRSKIT
SLIFEDYLPAGYAFDMTKTQAENS DYDLTFDKNKNFVTLKAKD SLLQTLNKLKNSYQLSAPKLYGSVQNDGATYSN
SYKLLINKDTPNTYTVISNVVRIPTPGDGETTSRIRPKKDNEADGVILNDTVVALSTTNHYRLTWDLDDQYKGDTS

KDTIARGFLFVDDYPEEALDLVDKGTIVITTLTGKAVSGISVYSYTSLDKAPKELQDKLARANISPKGAFQVFEPDNH
QAFYDITYVKTGQSLALLTKMKVKDSLQYGTQVRYKNKAYQVDFGNGYETKEVNTVHPEPKQNLNKDKVDINGKAM
LVGSQNFYTLSDWLDQYRGLQADKSQIAQGFYFVDDYPEDVLLPDTKAIQIMTKDGKAVKGMIEKTYHQLSADAPKEL
QAALAKRNITPKGAFQVFMKDPQAFYKAYVTTGQNLITVNPMTVREAVYNSGKSYDNVAYQVDFGQAYETNIVTNH
VPTVNPHTSNTNKEGVSIEGKTVLPNTVNYKIVLDYSQYKNMIVTDDVLVKGFMVDDYPEEALTPHPDGTQVMDQ
NGKFVRGLSVRTYASLADAPKAVQEAMKSRNFIPKGAIQVFQADDPKTFEFTYVKTGQKLIVVTTTMTVKNERIQGTGG
QYENTAYQIDFGIAYVTETVNNVPKLEPQKDVIDLSQDKSLNGKALALDQVFNRYRLVGSILPRNRATAVEYSF
KDDYDEKHDEYKGVYKAYTLRDVTLKGTVLKQGTVEVTKYTLQSVDKAKGTIAIRFDTAFLENIADSEFQAEIYLO
MKRIASGDVENTVIHVSNGYNIRSNTVKTTPQEPSTPDNPPSPQPPVPTTESPVQASVLPSTGESQSLIALIGGG
LLLGLAYGLSKRKKKEKN

SeqID 312

MANNNFYNRDPFGNMDDIFNSLMGNMGGYNSSENKRYLINGREVTPEEFSQYRQTGKLPQOEIINNQNTPNTQVSADSV
LTKLGTNLTDQARQHLLDPVIGRNKEIQETAELARRTKNNPVLVGDAVGKTAVIEGLAQAIINGDVPAAIKKNKEI
ISIDISSLEAGTQYRGSFEENIQNIKEVKETGNIILFFDEIHQILGAGSTGDSGSKGLADILKPAISRGELTVIG
ATTQDEYRNTILKNAALARRFNEVKVNAPSAQDTFNILMGIRNLVEQHNNVLPDSVLKAAVDLSIQYIPQRSIPDK
AIDLIDMTAAHLAAQHPVTDLKSLEKEIAAQRDQKQEKAVNTEDFEEALKVKTRIEELQNIQDNHTEGQKVATINDI
AMSIERLTGVPVSNMGASDIERLKLGNRLKGVIGQNDAVEAVARIRNRAGFDDGNRPIGSFLFVGPTGVGKTE
LAKQLAFDMFGSKDAIVRLDMSEYNDRTAVSKLIGATAGYVGYDDNSNTLTERIRRNPPYSIVLLDEIEKADPQVITL
LLQVLLDDGRLTDGQNTINFKNVTIATSNAGFGNEAFTGSDKDLKIMERISPYFRPEFLNRFNQVIEFSLHLSKDD
LNEIVDLMLDEVNQITIGKKGIDLVDENVKSHLIDLGYDEAMGVRPLRRVIEQEIIRDITDYLLDHTDVKHLKANLQ
DGQIVISER

SeqID 313

MGRFKELLESKKALILHGALGTELESRGCDVSGKLWSDKYLIEDPAATQTIHEDYIRAGADIVTTSTYQATLQGLAQ
VGVSESQAEDLIRLTQVLAKAVREQVWKSILTKEEKSERIYPLISGDVGPYAAFLADGSEYTGlyDIYKEGLKNFHRH
RIELLLDEGVLLALETIPNAQEAELIELLVEDFPQVEAYMSFTSQDGKTSIDGSAVAGLAKAIDVSPQVVALGIN
CSSPSLVADFLQAIAEQTDKPLVTYPNSGETYDGASQSWQSSRDHSHLTLENTSDWQKLGAQVVGCCRTRPADIAD
LSEHLT

SeqID 314

MKIGIDKIGFATSQYVLEMTDLAIARQVDPEKFSKGLLLDSLSITPVTEDIVTLAASAANDILSDEDKETIDMVIVA
TESSIDQSKAASVYVHQLLEIQPFARSFEMKEACYSATAALDYAKLHVEKHPDSKVLVIASDIKYGIKSTGESTQG
AGSIAMLSQNPISILELKEDRLAQTRDIMDFWRPNYSVPVNGMFSTKQYLDMLKTTWKEYQKRNTSLSDYAAFC
FHIPFPKLALKGFNKILDNLDQKKAELENFEHSITYSKKIGNCYTGSlyLGLLSLLENSQNLKAGDQIAFFSYG
SGAVAEIFTGQLVDGYQNKQLQSDRMDQLNKRQKITVTEYEKLFTEKTILDENGANFNTYRTGTFSLSICEHQRIY
KKINN

SeqID 315

MKSAYIFFNPKSGKDEQALAEVKSylIEHDFQDDYVRIITPSSVEEAVALAKKASEDHIDLVIPLGGDGTINKICG
GVYAGGAYPTIGLVPAGTVNNFSKALNIPQERNLALENLLNGHVKSVDICKVNDYMISSLTGLGLADIAANVTSEM
KRKLGPFAFVGDAYRILKRNRSYSITLAYDNVRSRLRLLITMTNSIAGMPAFSPEATIDDGLFRVYTMHIIHFF
KLLLHLRQFRKGDFSQAKEIKHFHTNNLTISTFKRKKSAIPKVRIDGDPGDQLPVKVEVIPKALKFTIIPNSLP

SeqID 316

MTFTAKFIDQEWEPVPSGryHMIvGEFCPYAQRPQIARQLLGLDKHISISFVDDVPSDIGLIFSQPEQVTGAKSL
RDIYHLTDPTYKGPYTIPIILDKTDNRIVCKESADMLRLFTTDFSDLHQEDAPVLFSQETASLIDNDIKDINNMFQS
LMYKLAFLDKQADYDYSKEFFTFLDQKEHLIGQRPFLLGDNLSEVDIHFFTPLVRWDIAGRLLLLNQKALEDYPN
IFSWAKTLYNDFNLKTLTNPQSIKNYYLKGFGRAVRHHTIVPTGPNMVKWEK

SeqID 317

MKKKIILKSSVLGLVAGTSIMFSSAFADQVGQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYIDDAQKDF
KQTNPNGESIRVQAGDMVGASPANSGLLQDEPTVKTFTNAMNVEYGTGLGNHEFDEGLAEYNRIVTGKAPAPDSNNINI
TKSYPHAAKQETIVVANVIDKVNKQIPYNWKPYAIAKNIPVNNKSVNVGFIGIVTKDIPNLVLRKNYEQYEFLEAEET
IVKYAKELQAKNVKAIIVLAHVPATSKDDIAEGEAAEMMKVNQLFPENSVDIVFAGHNHQYTNGLVKGKTRIVQALS
QGKAYADVGRVLDTDTDQDFIETPSAKVVAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDN
VSPVGSILITEAQLAIAKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNQLQVVEITGRDLYKALNEQ
YDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEIINPDAKYKLVINDFLFGGGDGFASFRNAKLLGAIN
PDTEVFMAYITDLEKAGKKVSVPNKPKIYVTMKNVNETITQNDGTHSIIKKLYLDRQGNIVAQETVSDTLNQTKSK
STKINPVTTIHKKQLHQFTAINPMRNYGKPSNSTTVKSKQLPKTNSEYGSFLMSVFGVGLIGIALNTKKKHKM

SeqID 318

MAYIWSYLKRYPNWLWLDLLGAMLFVTVILGMPTALAGMIDNGVTKGDRGTGVYLWTFIMFIFVVLGIIGRITMAYAS
SRLTTTMIIRDMRNDMYAKLQEYSHHEYEQIGVSSLVTRMTSDTFVLMQFAEMSLRLGLVTPMVIMFSVVMILITSPS
LAWLVAVAMPLLVGVLVYVAIKTKPLSERQQTMLDKINQYVRENLTGLRVVRAFARENFSQKQFQVANQRYTDTSTG

MKKGQVNDTKQSYSLRKYKFGLASVILGPFIMVTSPVFADQTTTSVQVNNQGTGTSVDANSSNETSASSVITSNND
 SVQASDKVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYVSKETEVEKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNV
 KWISYKSPCGVRRYAAIESLDPSGGSETKAPTPTVNSGNSNNQEKIATQGNYTTFSHKVEVKNEAKVASPTQFTL
 DKGDRIFDYDQILTIEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFDIL
 ITNLIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGTDGNYKVAVSFADHKNEKGLYNIHLYYQEASGTLVGVTG
 TKVTVAGTNSSQEPIENGLAKTGVYNIIGSTEVEKNEAKISSQTQFTLEKGDKINYDQVLTA
 DGYQWISYKSYSGVRRYIPVKKLITTSSEKAKDEATKPTSYPNLPKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGE
 KIHVDQVLVVDGHQWISYKSYSGIRRYIEI

MENWKFFALSSILGHKMRAFLTLMGLIITIGVASVVLIMALGKGMKDSVTNEITKSQKNLQIYYKTKEDQKNEDNFGAQG
AFMQGSDTNRKEPIIQESWLKKIAKEVDGVSGYYVTNQTNAPVAYLEKKAKTVNITGVNRTYLGIKKFKIKSGRQFQ
EEDYNQFSRVILLLEEKLAQRLFQTNEAALNKVVTVKNKSYLVVGVYSDPEAGSGLYGSNSDGNAILTNTQLASEFGA
KEAENIYFHLNDVSQSNRIGKEIGKRLTDISHAKDGYDNDFDMTSIVKSINTQVGIMTGVIGAIAAISLLVGGIGVM
NIMLVSTVERTREIGLRKALKATRRKILAQFLIESMVLTTILGGLIGLLLAYGGTMLIANAQDKITPSVSLNVAIGSL
IFSAFITGII FGLLPANKASKALNPIDALRYE

MQYSEIMIRYGELSTKKKNRMRFINKLKNMEHVLSIYPDVSVKTDTRDRGHVYLNGTDYHEVAESLKEIFGIQAFSP
 SFKVEKNVDTLVKAVQEIIMTSVYKDGMTFKITAKRSDHSFELDSRALNHTLGDAVFSVLPNIKAQMKQPDINLKVEI
 RDEAAYISYENIRGAGGLPVGTSGKGMLMLSGGIDSPVAGYLAALKRGVDIEAVHFASPPYTPSPGALKKAHDLTRKLT
 KFGGNIQFIEVPFTEIQEEIKEKAPEAYLMTLTRRFMMRITDRIRENRLGLVIINGESLGQVASQTLESMQAINAVT
 ATPIIRPVDVMDKLEIIDIAQKIDTFDISIQPFEDCCTIFAPDRPKTNPKIKNTEBQYEKRMDEGLVERAVAGIMVT
 TIQPADSDDDDLDDLL

MARVKGGVVSRKRRKRVLKLAKGYYGAKHILFRTAKEQVMNSYYYAYDRRQKKRDFRKLWITRINAAARMNGLSYS
QLMHGLKLAEIEVNRKMLADLAVNDAAAFTALADAAKAKLKG

MFKASKKL VQKNKSNHFWL VFFITLILFLIGCYASLRFGAINFKTSD LITVLKNPLKNSNAQDVIFDIRLPRIIAAI
LVGAAMSQAGAIMQGVTRNAIADPGLLGINAGAGLALVVA YAPLGS MHYSTILIVCLLGSVISYLLVFTLSYTKQKG
YHQLRLILAGAMISTLFTSVGQVVTLTYFKFLNRTVIGWQAGLSQINWKMLIIIIAPIIILGLLISQLLAHQLTILSLN
ESVAKALGQKTQLMTAFTLLILVLTLASSAVALTIGTVSFIGLIIPHFIKLFIPKDYRLLLLPLIGFSGATFMIWVDLSS
RIINPSETPIISSIISIVGLPCFLWLIRKGNL

MIKRPIHLSHDFLAEVIDKEAITLDATMGNGNDTVFLAKSSKKVYAFDIQEEAIAKTKAKLTEQGISNAELIILDGHE
NLEQYVHTPLRAAIFNLGYLPSADKTVITKPHTTIKAIKNVLDILEVGGRLSLMVMYYGHDGGKSEKDAVIAFVEQLP
QNNFATMLYQPLNOVNTPPFLIMVEKLOSYLENEV

MRVHITSIYGQSPRSIALISQKLVDVGRQLGYDEMGIYFYNDHAETHGERSTRMDGIIAGLGRGDIVVFQVPTWNS
TEFDELFLDKLQAYGARIITFVHDIPLMFESNFYLLDRVIDMYNRSDVVILPTKAMHDYLIKGMTTSKVLYQEVW
DHPVNIDLPERPECQKVLFSFAGDIQRFPFVNDWKENIPLIYYGDGSRINSEANVHAQGWKDDVELMLSLSKRGGFGLC
WSEDERELVELVERRYSRNMASYKLSTFLAAGLPIIANHDISSRDFIKQHGLGFTVETLEEAVEKINNMEKETYDSYVEN
VEKIATLLLRNGYITKKLLIDAVHMLYR

[illegible]

MIDRKDTRNRFKLVSKYSPSGDQPOAIETLVDNIEGGEKAQILKGATGTGKTYTMSQVIAQVKNKPTLVIAHNKTLAQGLYGEFKEFFPDNAVEYFVSYYDYYQPEAYVPSSDITYIEKDSSVNDIDKLRHSATSSLLERNDVIVVASVSCIYGLGSPKEYADSVVSLRPGQEISRDQLLNNLVDIQFERNDIDFQRGKFRVRGDDVVEVFPASRDEHAFRIEFFGDEIDRIREIESLTGRVLGEVEHLAIFPATHFMTNDEHMEEAISKIQAEMENQVELFEKEGKLEAQRIRQRTEYDIEMLEMGYTNGVENYSRHMDGRSEGEPPFTLLDFFPEDFLIMIDESHMTMGQIKGMYNGDRSRKEMLVNYGFRLPALSALDNRPLRREEFESHVHQIVYVSATPGDYEMEQTDTVVEQIIRPTGLLDPEVEVRPSMGQMDLLGEINLRTEKGERTFITTLTKRM AEDTLDYLKEMGVKVKYMHSDIKTLTEIIRDLRLGLVDFVLGINLRLREGIDVPEVSLVAILDADKEGFLRNERGLIQDTIGRAARNSNGHVIMYADIKTDSMQRAMDETARRRRLQMDYNEKHGIVPQTIKKEIRDLIAITKSNDSDKPEKVV DYSSLSKKERQAEIKALQQQMQEAAELLDFELAAQIRDVILELKAID

MKHKLKAPTLLALLSIFVFVGGKVS AETVNIVSDTAYAPFEFKDSDQTYKGIDVDIVNEVAKRAGWNVNMTYPGFDAA
VNAVQSGQADALMAGTTVTTEARKKVFNFSDTYYDTSVILYTKNNNKVTNYKQLKGKVVGVKNGTAAQS FLEENKSKY
GYKVKTFDTS DLMNNSLSDSGSIYAAMDDQPVVQFAINQ GKAYAINMEGEAVGSFAFAVKKSGHDNLIKEFN TAF AQ
MKSDGTYNDIMDKWL GKDATKTS GKATGNANEKATPVKPSYKIVSDSS FAPFEYQNGKGKYTGFDMELIKKIAKQQG
FKLDISNPGFDAALNAVQSGQADGVIAGATITEARQKIFDFS DPYYTSSVILAVKKGSNVKSYQDLKGKTVGAKNGT
ASYTWLSDHADKYN YHVKA FDEASTMYDSMNSGSIDALMDDEAVLAYAINQGRKFETPIKGEKSGDIGFAVKKGANP
ELIKMFNNGLASLKKSGEYDKLVKKYLS TASTSSNDKAAKPVDESTILGLISNNYKQLLSGIGTTLSLTLISFAIAM
VIGIIFGNBVSPTSNTLRTISMIFVDIVRGIPILMIVA AFIWGI PNLIBSITGHQSPINDFVAATIALSLNGGAYIA
EIVRGGIEAVPSGOMEASRSLGISYGTKMQKVLIPQAVRLMLPNFINQFVISLKD TTIVSAIGLVELFQ TGTKI IAR
NYQSFRMYAILAIMYLVII TLLTRLAKRLEKRLK

MGDKPISFRDKDGNFVSAADVWNAEKL EELFNTLNPNRKLRLEREKLAKEKG

METYTLSTNTLNIPKIGFGTWQLTEGEEAYKAVTHALKVGYTHIDTAQIYGNESVGRAIRDSGLARESIFLTTKIWN
DKHDYHLAKASIDESLQKLGVDDYIDLILLIHWPNPKALRENDWKAGNAGTWKAMEEAYKEGKVKAI GVS NFMKHHLE
ALFETAIEIKPMVNQIILAPGCAQEDLVRFCCKNDILLEAYSPPFGTGAI FENESIKAI AEKYGKSV AQVALRWSLDNG
FLPLPKSATPKNIEANLDIFDFQLNEDDITTLIQLD SGIKPKDPDNVSF

MVKQGQGNVVAQNKKAHHDYTTIVETIEAGIVLTGTEIKSVRAARITLKDGYAQIKNGEAWLINVHITPYDQGNIWNQD
 PDRTRKLLLLKKREIEKISNELKGTGMTLVPLKVYLKDGFAKVLGLAKGKHDYDKRESIKRREQNRDIARQLKNYNS
 R

MDHFTKLWQDFSKLPNVVAIALGGSRSRGSDFDQSSDYDLYVYCAATPDITSRKRIILNKHCHYIELNNHYWELEDNGT
LNDGTDIDILYRNIDNFLSDLEDVVEHHNSRIGYTTCFWHNLINCQILYDPENQLQSLKERFEVSYPSQLQKQIIQ
NRNLLTGKLPSPYDKQIIKALKRQDFVSTHHRRTAFLDYSFYDIIFALNKLTHPGKRMISYAKKNATLLPKHFEENII
KLCHHNSNEHTVKETLNDIIMHLDVMLKENFQHFQIG

MKKIYYLGLACVSIILTLSCGESIERSLKGDRYVDQKLAENSSKEATEQLNKKTKQALKADKKAFPQLDKAVAKNEAQ
 VLIKTSKGDINIKLFPKYAPLAVENFLTHAKEGYINGLSFHRVIKDFMIQSGDPNGDGTGGKSIWNSKDKKKDSGNG
 FVNEISPYLYNIRGLAMANAGADTNGSQFFINQSQQDHSKQLSDKKVPKVIKAYSEGGNPISLDGGYTVFGQVISG
 METVDKIASVEVTKSDQPKKITITSIKVIKDYKFK

MKIGITAAAMEEELKLLVENLEDKSEQETVLSNVYYSGRYGEHELVLVQSGVGKVMSSAMSVAILVESFKVDALINTGSA
 GAVATGLNVGDVVADTLVYHVDLTAFGYDYGQMSMQPLYFHSDKTFVSTFEAVLSKEEMTSKVGLIATGDSFIAG
 QEKIDVIKGHFPOVLAVEMEGAAIAQAAQATGKPFVVVRAMSDTAAHDANITFDEFILIEAGKRSAOVLMAFLKAL

SeqID 335

MEKRLSLGALVLA STVLLAACGNVGGGASSTGT KIGKDIKVGYNWELSGNVSSYGNMKN GADLAVKEINAAGGVGG
KKLKVLSQDNKSENAEAAATVATNLVTKGANV IIGPATSGAAASSTPKVNAAAVPMIAPAATQDNLVYGS DGTKLTNQY
FFRATFVDNYQGKLLSQYATDNLKAKKVLFYD NSSDYSKGVAKSFKESYSGKIVDSMTFSAGDTDFQAS LTKLKGK
EYDAIVMPGYYTETGLIVKQARDLGISKPV LGPDGDFSPKFVQSATFVGASNVYYLTGFTTQGSTKAKAFHDHYVKA
YGEEPSMFSALS YDAVYMAAKSAKGAKTSIDLKKALAKL KDFKGVGTGKMSIDKNHNVVKSAYVVKLDDGKTSSVNI I
SAK

SeqID 336

MENHNSIKQTYGLMTT IAMIVGVVIGSGIYFKVDDILKFTGGDVFLGMVILVLG SFSIVFGSL SISELAIRTSESGG
IFSYYEKYVSPALAA TLGLFASFLYLPTLTAI VSWVAAYFTLGESSSLESQIILAAVYI LALSLMNI FAKRIAGGFQ
SLTTFFVKMIPLVLIALIGAFWSDKAPQLPQH LTAIQPSNVGWSVWSGLVPLYFAYD GWTIFVSI APEVKNPKNLPL
AFVIGPALILL SYLAFFYGLTQILGASFIMTTGNDAINYAANI IFGPSVGRLLS FIVILSVLGVANGLLLG TMRLPQ
AFAERGWI KSERMANINLKYQMSLPASLT VTAVAIFWLFVHF MVTKFNLLPGSDISEI AVVFNN TSLIILYVLVLSL
YLKKDIKNKFTGLVSPILAILGGLILFIGSLLSNFFT VLI FQCFCLLFCLICHYIYQKNPNKTHE

SeqID 337

LTEFNDDQHSNHDQKS FKEQILAELEEANRLRKL REEELYQKEQEAKEAARRTAQLMADYEAQRLKDEQE ARAKALE
TKQRL EEQE KARI EAKLLAEAREEERRQAEQALASQEEQVINQGM EPSRELD SGSKSSEFRTTENVPDIDLKADKT
DVATAVPNQETEEIFLVRATDIPT EGENVKLGETSELEPVAK EPIRVEDLSKEEDIALSAKNKHNKRERRQKADNV
AKRIARILISIIILVLLLTA FVG YRFVDSAIKP VDSNSNKFVQVEIPIGSGNKLIGQILEKAGVIKSATVFNYYSKF
KNYSNFGSGYYNLKKSMTLDQIAAELEKGGTAEPTK PALGKILITEGYTIKQIAKAIESNKIDTKTTSTPYKADDFL
KLVDDETFIKKMVAKYPNLLGSLPDKSKAIYQLEGYLF PATYNYKYD TTLEGLVEDMI STMNTKMAPYYNTIKAKNM
SVNDVLTLSLVEKEGSTDEDRRKIASVFYNRLSAGQALQSNIAILYAMGKLGDKTSLAEDAQINTSIKSPYNIYTN
TGLMPGPVDSPSISAIEATIKPASTDYLYFVADVKTGNVYAKDFETHKANVEKYINSQIN

SeqID 338

MSRMIPGRIRNQGI ELYEQGLVSLISQEGNLLKAKVGDCQIEYSLVTEETKCS CDF FARKGYCQH LAAL EHF LKN DP
EGKAILSKVRVQQESQ QETKKKTSFGSVFLDSL IINEDDTIKYQLSAQGEQNPYANDIWWTLKIRRLPDDRSYVIRD
IKAFLNTVRKEA Y YQIGKQYFETLSLIQFDETSQELIEFLWRLIPSHSSKIDLEFILPNQGRHLSL TRGFFEEGVTL
MNALENFSFESDFHQFNHLYFKELEGEDHLYQFKVIVHRQSTIELEI KEKDLKPLFANSYLFYRDTFYHLNLKQEKMV
TAIRSLPIEGDLAKHIHFDLDDQDKLAHLLDFKEIGLVDAPRSFSIHDFKVNFEFDINSQNEILLQMVFDYGN DLT
VHN RQELEQLTFASHFKHEEKIFKLLERYGFAPHFSTSHPAYSAQELYDFYTYMLPQFKKMGTVSLSAKLESYRLIE
RPQIDIEAKGSLLDISFDFSLL ENDVDQALVALFDNNPYFVNKSGQLVIFDEETKKVSATLQGLRARRAKNGHIEL
DNIAAFQLSEL FANQDNVSFSQHFYQLIEDLRHPEKFKIPGLSVSASLRDYQLTGVVRWLSMLDHYGFAGILADDMGL
GKTLQTISFLSTKLTRDSRVLILSPSSLIYNWQDEFHKFAPD VDAVAYGSKIRRDEIIAERH QVIITSYSSFRQDF
ETYSEGNYDY LILDEAQVMKNAQT KIAHSLSRSEFEVKNCFALSGTPIENKLEIWSIFQIILPGLLP GKKEFLKLNPK
QVARYIKPFVMRRRKEEVLPELPDLIEMNYPNEMTDSQKVIYLAQLRQIQESI QHSSDADLNRRKIEILSGITRLRQ
ICDTPRLFM DYD GESGKLES LHQLLTQIKENGHRALIFSQFRGMLDIAEREMVAMGLTTYKITGSTPANERHEMTRA
FNAGSKDAFLISLKAGGVGLNLTGADTVVLIDLWWNPAVEMQAISRAHRLGQKENVEVYRLITRG TIEEKILEMQET
KKHLVTTVL DGNETHASMSVDDIREILGVSK

SeqID 339

VLLTEIKKSP EGLYFDKKIDIKESLMERHSEIMDISDIQVSGHVYEDGLYLLDYNMAYDITLPSSRS MKPVVLSEK
QTINEVFIEAENVSTKKELVDQDLVLILEEDDINLEESVIDNILLNIPLRVLAAD EGVGEADLSGKNWSLMTEKQYE
EKQAKEKEKSNPFAALEGMFDS

SeqID 340

MEVKTAEWMHTFNQKIQSNKDYLSELDTPIGDGDHGGNMARGMTAVIENLDNNEFSSAADVFKTVSMQLLSKVGGA
SGPLYGS AFMGITKAEQSESTISEALGAGLEMIQKR GKAE LNEKTMVDVWHGVIEAIEKNELTEDRIDSLVDATKGM
KATKGRASYVGERSLGHIDPGSFSSGGLLFKALLEVGGV

SeqID 341

MQDKLMIRGARAHNLKNISVDIPRDKLVVVTGLSGSGKSSLA FDTIYAEGQRRYVESLSAYARQFLGNMEKPDVDSI
DGLSPAISIDQKTT SKNPRSTVGTVEINDYLRLLYARVGT PYCINGHGAITASSVEQIVDKVLALPERTKMQILAP
IIRKKKGQHKSTFEKI QKDGYVRVRIDGDIDHVT E VPELSKSKMHNIDIVDRLINKEGIRSLFDSVEAALRLSDG
YVVIDTMDGNELLFSEHYSCPECGFTVPELEPRLSFNA PFSGCTTCDGLGIKLEVDIDLVIPDKSKTLREGALVPW
NPISSNYYPTMLEQAMTQFDVMDT PFEKLSKAEQDLALYSGGEREFHFHYINDFGGERNIDL PFEGVVNNINRRYH
ETNSDYTRNV MREYMNELKCN TCHGYRLNDQALCVRVGGEEGLNIGQVSDLSIADHLELLETLRLSSNEQLIARPII
KEIHDRLSFLNNVGLNYLNLRSAGT LSGGESQRIRLATQIGSNLSGVLYVLDEPSIGLHQ RDNDRLIDSLKKMRDL
GNTLIVVEHDEDTMMAADWLIDVGP GAGAFGGEIVASGTPKQVAKNTKSITGQYLSGKKVIPVPSERRVGNRFL E I
KGAAENNLQNL DVKFP LKGFIAVTGVSGSGKSTLINSILKKAVAKKLN RNSDKPKGYVSL EGIEYVDRLIDIDQSPI
GRTPRSNPATYTG VFDDIRDLFAQTNEAKIRGYKKGRFSFNVKGRCESCSGDGIIKIEMHFLPDVYVPCVCHGTR
YNSETLEVHYKEKNIAQILDMTVNDAVTFFAAIPKIARKLQTIKDVGLGYVTLGQPATTL SGGEAQRMKLASELHKR
STGKSLYILDEPTTGLHADDIARLLKVLDRFVDDGNTVLVIEHNL DVIKTADHIIDLGP EGGIGGGQIVAIGTPEEV
AENPKSYTGYYLKEKLAR

SeqID 342

MWPEDRIASFRRTLLGWYDQEKRDLPWRRRTNPPYIIVWSEIMLQQTQVNTVIPYYKRFLWFPPQIKDLADAPEEQLL
KAWEGLGYYSRVRNMQKAAQQVMVDFGGIFPHTYDDIASLKGIGPYTAGAIASISFNLPEPAVDGNVMRVMARLFEV
NYDIGDPKNRKIFQAIMEILIDPDRPGDFNQALMDLGTDIESAKTFRPDESPIRFFNAAYLNGTYSKYPIKNPKKKP
KPMRIQAFVIRNQNQGQYLLKNTKGRLLGGFWSFPIIETSPLSQQQLDLFDDNQSNPIIWQTQNETFOREYQLKPQWT
DNHFPNIKHTFSHQWTIELIEGVVKATDLPNAPHLKWAATEDFSLYPFATPQKKMLETYLQKNA

SeqID 343

LIEITWTVKYITEFIATAFLIILGNGAVANVDLKGTKGNNSGWIIITAIGYGLGVMMPALMFGNVSGNHINPAFTLGL
AFSGLFPWAHVQYILAQILGAMFGQLVVMVYQPYFVKTENPNHVLGSFSTISALDDGQKSSRKAAYINGFLNEFV
GSFVLFFGALALTKNYFGVELVGKLVQAGYDQTTAATRISPYVTGSLAVAHLGIGFLVMTLVASLGGPTGPALNPAR
DLGPRIVHRLLPKQILGQAKEDSKWWYAWVPVLAPIVASILAVALFKLLYL

SeqID 344

MSSYWNYPPELKKNIDETNQLIQERIQVRNKDIEAALSQLTAAAGKQLRPAFFYLFSQLGNKENQDTQQLKKTAAASL
EILHVATLIHDDVIDDSPLRRGNMTIQSKFGKDIAYVTGDLLETFVFDLILESMADTFPMRINAKSMRKILMGELDQ
MHLRYNQQGIHHYLRASIGKTAELFKLASKEGAYFGGAKEVVRLAGHIGFNIGMTFQILDDILDYADKKTFNKP
VLEDLTQGVYSLPLLLAIEENPDIFKPILDKKTDMATEDMEKIAYLVVSHRGVDKARHLARKFTEKAISDINKLPQN
SAKKQLLQLTNYLLKRKI

SeqID 345

MFKIPLFKELKTDQWVKPFFKQYKVSILVIALFLGFMTFFSASALMFNSGYLISKASLPSNILLVYVPIVLTRAFIGI
GRPVFRYIERLTSHNWVLRMTSQLRLKLYHSLESNAIFMKRDFRLGDVMDGLAEDINYLNQNLYLRTIFPTIIAWLLY
SFIIITATGFFSLWFALMMLLYLAIMIFLPLWSILANGARQTREKELKNHLYTDLTDNVLGISDWIFSQRGQEYVAL
HERSESELMAIQKKIRSFNNRRALIVELVFGLAILVIWASNQFIGHRGGEANWIAAFVLTVPFPLSEAFAGLSAAA
QETNKYSDSIHRLNELSETYFETTQNLQPNKPYDFS VKNLSFQYKPQEKWVLHHLDDIKEGEKIAILGRSGSGKST
LASLLRGDLKASQGGKITLGGADVSIVGDCISNYIGVIQQAPYLFNTLLNNIRIGNQDASEEDVWKVLERVGLKEMV
TDLSDGLYTMVDEAGLRFSGGERHRIALARILLKDVPIVILDEPTVGLDPITEQALLRVFMKELEGKTLVWITHHLK
GIEHADRIIFIENGQLELEGSPOELSQSSQRYRQLKAADDGDL

SeqID 346

MKKLITEKKVNNVSTVNYLKLGLVSAMFAGGAFVALGSTQGVASASTFTAPQATHPKAERQLTDSEIYERAQKQVLPK
YIQGSLSGILNQHSTLYKQQAAVTPQVSSPKAERQLTDSEIYERAQKQVLPKYIQGSLSGILNQHSTLNA

SeqID 347

MEENMNKQLKSKTMLGTVALVSAFSFASTNADANTYNYAVDVDYLASAEIEIAQAHPASNTFPLGQCTWGVKEMATW
AGNWWGNGGDWAASAASAGYTVGTQPRVGSIVCWTDGSYGHVAYVTAVDPTNKIQVLESNYAGHQWIDNYRGWFDP
QNTATPGVVSYYIPN

SeqID 348

MKINQMKKDELFEFGYLIKKAIEVRKTRAGKDFIAFTFRDDTGEISGNMWDQAQTYNVEEFVAGKIVHMKGRREVYNGT
PQVNQITLNRNIKDGEPNDPRDFKEKPPINVDNVREYMEQMLFKIENATWQRVVRALYRKYNKEFFTYPAKTNHHAF
ESGLAYHTATMVLADSIGDIYPELNKSLMFAGIMLHDLAKVIELSGPDNTEYTTIRGNLIGHISLIDEELTKILAE
NIDDTKEEVTVLRHVILSHHGQLEYGSPVRPRIMEARIHIMIDNIDANMMMMTTALNRVNEGEMTNRIFAMDNRSFY
KPNIK

SeqID 349

MLVDKKWRFEDSASYFACPKCQNPLIKESNSLKCSDNHCDFDLKSGFYVNLGGKKIDEHYDKKSFENRQLVLENGYY
NHILEAISKVLNNSQFHSVLDIGCGEGFYSRQLVNKYEKTFLAFDISKDSIQLAAKSDQSRLVKWVSDLANLPIQ
DSSIDIILDIFSPANYPEFRVLSDDGILVKVVPVAEHVQELREKASQYLKQKDYSNQKILDHFRNFEEIIEQKVV
QSYNCSQQRQAFIDMTPLLFSDVKTIDWASISEITVGALIVIGKKRSVSK

SeqID 350

MCLICQRIEMIERNENPYFVKEYETGYLVLDGHQYFQGYCLFLSKKHVTELHELPRDWRNQYLSEMADEIVAKAF
RADKMNIESLGNDAHLHFHFLFPRKTGDLRNYGHNGKGPVWWYPPEKMYADSVRATGAETIEKLEKLLDVLG

SeqID 351

MFSDLRKKFVFLTMSILIVVVLFLFAVSNRYNQYWDEYDAYRIVKLVAKNLYLGGIPGDEPIALVTIDNQMKVQISN
NTDLTNDVIEKSSSLKLEQKKSRKWKSFYISKEYKDKTYTTIAIMDLASYEVPYARRFLILVFTIFGFCLLAAVSL
YLSRFIVGVPVETEMTREKQFVSDASHELKTPIAAIRANVQVLEQQIPGNRYLDHVVSSETKRMEFLIEDLLNLSRLDE
KRSKVNFKKLNLVLCQEVLLTYESLAYEEEEKCLNDTIEDDVWIVGEESQIKQILILLLDNAIRHLSLSKSEIQFSLK
QARRKAILTISNPSAISKEVMDNLFERFYQAKDDHADSLSFGLGLSIAKAIVERHKGRIRAYQEKDQLRLEVQLPI
DGFWTNTMIN

SeqID 352

LIILDKKSYDLLFYLLKLEEPETVMAIANALNQSRRKVYHLEKINDALPSDVPQIVSYPRVGILLTEKQKAACRLL
LDEVTDYSYVMKSSERLQLSLVSIVAKDRITIDRLMQLNDSRNTILNDLNLRLSELAEKEYNLQLQSTKCRGYFL
DGHPLSIIQYLYKLLDDIYHNGSSSFIDLFNHKLSQAFGASTYFSKEVLDYFHHYLFISQSRSLGKKINSQDQGQFMIQ
ILPFIIMAYRKMRLSPEVQTSLSNDSFSLVWQRKEYETAKELADELEENFQLSLDEIEVGLVAMLMLSFRKDRDNHLE
SQDYDDMRATLTSFLKELEERYHLHFVHKDILLRQQLLTHCKALLYRKRYGIFSVNPLTEHIKDKYEELFAITSSSVK
LLEKAWQIKLTDVAYLTIHLGGELRNSQQSPNKLKLVIVSDEGIAIQKLLLKQCORYLTNSDIEAVFTTEQYQSV
SDLMHVDMVSTSDALESRFPMLVVFVLTDDDIIRLIRFSKKGNCANSNQFTNELEKTIAQYVKEDSERYVLKSKI
EKLIHQELLQDVLPLQSTVC

SeqID 353

MKYFLDTADVSEIRRLNRLGIVDGVTTNPTIISREGRDFKEVINEICQIVDGPVSAEVTGLTCDEMVTAEAREIAKWS
PNVVVKIPMTEEGLAASVQLSKEGIKTNTVTLITVAQGLSAMKAGATFISPFVGRLEDIGTDAYALIRDLRHIIDFY
GFQSEIIAASIRGLAHVEGVAKCGAHIAITIPDKTFASLFTHPLTDKGIETFLKDWDSEFKKK

SeqID 354

MSHYSIKLQEVFRLAQFQAARYESHYLESWHLLLAMVLVHDSVAGLTFABEYSEVAIEEYEAATILALGRAPKEEIT
NYQFLEQSPALKKILKLAENISIVVGAEDVGTEHVLLAMLVKNKDLLATRIELVGFGRQDDGESVRMVDLRKALERH
AGFTKDDIKAIYELRNPKKAKSGASFSDMMKPPSTAGDLADFTRDLSQMAVDGEIEPVIGRDKEISRMVQVLSRKT
NNPVLVGDAVGKTAAYGLAQRIANGNIPEYELRDMRVLELDMMSSVAGTRFRGDFEERMNQIIADIEEDGHIILFI
DELHTIMGSGSIDSTLDAANILKPALARGTLRTVGATTQEEYQKHIEKDAALSRRFAKVLVEEPNLEDAYEILLGL
KPAYEAFHNVTISDEAVMTAVKVAHRYLTSKNLPDSALDDEASATVQMIMKKNAPSLLTEVDQAILDDDMKSASK
ALKASYKGGKRKPIAVTEDHIMATLSRLSGIPVEKLTQADSKKYLNLKELHKKRVIGQDDAVTAISRARRNQSGIR
TGKRPIGSFMFLGPTGVGKTELAKALAEVLFDDDESALIRFMSSEYMEKFAASHLNGAPPGYVGYDEGGELTEKVRNK
PYSVLLFDEVEKAHPDIFNVLLQVLDGVLTDSDRGRKVDFSNTIIMTSNLGATALRDDKTGVFGAKDISHDYAMQ
KRIMEELKKAYRPEFINRIDEKVVHLSLQDNMREVVKIMVKPLIILALKDKGMDLKFQPSALKHLAEDGYDIEMGAR
PLRRTIQQTQVEDHLSLELLANQVKEGQVIKIGVSKGKLKFDIAKS

SeqID 355

MVLDEKIKLAQLAQYLDLLESDIVLQADLGDNDNSQKVDFLDEIVAMSDRISLESTHLKRQPSFGIAKKGHESRVIF
SGLPMGHEFTSFILALLQVSGRAPKVEDIIRIKIGIEKTINLETVVSLTCHNCPPDVVQAFNIMAVLNPNIHTMTIE
GGMVQDEVKSKGIMSVPTVYKDQEEFTSGRATIEQLLEQLDGPLDAAFAADKGVYDVLVIGGGPAGNSAAIYAARKG
LKTGILAEATFGGQVETVGIENMIGTLYTEGPKLMAQIEEHTKSYDIDIKSQLATGIEKKELVEVTLANGAILQAK
TAILALGAKWRNINVPGEIEFRNKGVTYCPHCDGPLFEGKDVAVIGGNSGMEAAALDLAGVTKHVTVLEFLPELKAD
QVLQERAAKTDNLTILKNVATKDIVGEDHVTGLNYTDRDTNEEKHIDLEGVVFQIGLVPSTSWLKDSGIELNERQEI
VVDKFGSTNIPGIFAAGDCTDAAYQIIISMGSAGATAAIGAFDYLRQ

SeqID 356

MIKYQDDFYQAVNGEWAKTAVIPDDKPRGTGGFSDLADDIEALMLSTTDKWLADENKPSDTILNHFIAFHKMTADYQK
REEVGVSFVPLPIIEYKGLQSFSEFASKVAEYELEGKPNEFFPGVAPDFMNAQLNVLWAEAPGIILPDTTYSEDNE
KGKELLAFWRKSQEDLLPLFGLSEQEIKDILDKVLALDAKLAQYVLSREESSEYVKLYHPYNWEDFTKLAPELPLDA
IFQKILGQKPKDVIVPEERFWTEFASDYSESNEWELLKADLILSAANAYNAYLTDDIRIKSGVYSRALSQTPQAMDK
KKAAYYLASGPYNQALGLWYAGEKFSPEAKADVEHKIATMIDVYKSRLEKADWLAQSTREKAIMKLNVTIPHIGYPE
KLPEYTYTKKIIDPKLSLVENATNLDKISLAYGWSKWNKPVDREWHMPAHMVNAYYDPQQNQIVFPAAILQEPFYAL
EQSSSANYGGIGAVIAHEISHAFDTNGASFDEHGSILNNWWTDEDFEAFKKLTDKVVEQFDGLESYGAKVNGKLTVSE
NVADLGGVACALEAAQRESDFSARDFFINFATIWRMKARDEYMQMLASVDVHAPAQWRTNITVTNFEFHKFEFDVKD
GDNMWRPVEKRVIIW

SeqID 357

MSKILFFGEPLIRITPKENDYFADSIISTKLFYGGSEVNTARALQGFGQDTKLLSALPNNPIGNSFLQFLKAQGIDTH
SIQWVGERVGLYFLEDSFACRKGEVVYDRDHSSLHDFRINQIDFDQLFEGVSLFHFSGITLSLDESIQETITLLLLKE
AKKREITISLDLNRSKLISPKNAKILFSQFATFADICFGIEPLMVDSQDTTFFNRDEATIEDVKERMISLINHFDF
QVIFHTKRLQDEWGRNHYQAYIANRKQEFVTSKEITTAVNQRIGSGDAFVAGALYQLLQHSDSKTVIDFAVASASLK
CALEGDNMFETVTAVNKVLNQSKDIIR

SeqID 358

MKSRKKDKLVRLT'TLLVFGGLGVWFYNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAIL
ESSSGQSDLSKAPNYNLFGIKGEYKGSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELVSSQKYASVWKS
NTSSYKDATAALTGLYATDTAYASKLNQIETYSLDAYDK

SeqID 359

MADVKKVNNEDSRGQKQDLKAKLFHIKIGSVPLPVYVCLALLILLAGFLQKLVPNMLGGFAVILTMGWFLGTIGASI
PGFKNFGGPAILSLLVPSILVFFNLINKNVLESTNMLMKQANFLYFYIACLVSGSILGMNRKMLIQGLLRMIFPMLL
GMVCAMMVGTFFVGVILGLEWRHTLFYIVTPVLAGGIGEGILPLSLGYSSITGVASEQLVAQLIPATIIIGNFFAILCT
ALLNRLGEKKPHLSGQGQLVRLNKGEDMSDIADHSGPIDVKKMGGGVLTACSLFIFGHLLQQLTGFPGPVLMTVAA

AILKYINVIPRETQNGAKQLYKFISGNFTFPLMAGLGLLYIPLKDVVATLSIQYFIVVISVVFVTVISVGFFVSRFLN
MNPVEAGIISACQSGMGGTGDVAILSTADRMNLMPPAQVATRLGGAITVITMTAILRMLF

SeqID 360

RGKKAGKYTTSDGYIFDAKDIKKDTGTGYVIPHMTHEHWVPKKDLSESELKAAQEFLSGKSEANQDKPKTGKTAQEI
YEAIEPKAIVKPEDLLFGIAQATDYKNGTFVIPHKDHYHYVELKWFDEEKDLLADSDKTYSLLEDYLATAKYMMHPE
KRPKVEGWGKDAEIIYKEKDSNKADKPSAPTNDKSTSNSSDKNLSSAAEVFKQAKPEKIVPLDKIAAHMAYAVGFEDD
QLIVPHHDHYHNVPMAWFDKGGWLKKAPEGYTLLQQLFSTIKYYMEHPNELPKEKGWGHDSHDNKGSKNDKAKNYAPD
EEPEDSGKVTHNYGYFDVNKGSDEEEPEKQEDSESELDEYELGMAQNAKKYGMDRQSFEKQLIQLSNKYSVSFESFNY
INGSQVQVTKKDGSKVLVDIKTLTEVK

SeqID 361

MNRKKTVIIISALSVALFGTGVGAYQLGSYNAQKSDNSVSYVKTDKSDSKAQATAVNKTPDQISKEEGISAEQIVVKI
TDDGYVTSHGDHYHYNGKVPYDAIISEELIMKDPYSYVFNKADVINEVKDGYLIKVNGKYLYLKEGSKRTNVRTKE
QIQKQREEWKSGGSKGESGKHSSAKTQALSASVREAKASGRYTDDGYVFSPTDVIDDMGDAFLVPHGDHFIYIPKA
DLSPSELSSAAQAYWNRKTGRSGNSSKPSNSSSYIHASAPSGNVSTGRHANAPISIPRVTHANHWSKPAGNHATAPKH
HAPTTKPKINKDSALDKMLKRLYAQPLYARHVESDGLVYDPAQVNAFTAIGVSIIPHGNHFIHYKDMSPLELEATRM
VAEHRGHHIDALGKKDSTEKPKHISHEPNKEPHTEEHHAVTPKDKRKGKPNQIVYSAQEIIEBAKLVNTQHLMT
FLMPKILKKIQVQVMSFHI

SeqID 362

MAKFGFLSVLEELDKHLQYDFAMDWDKKNHTVEVTFILEAQNSSAIETVDDQGETSSEDIVFEDYVLFYNPVKSRF
DAEDYLVTIPYEPKKGLSREFLAYFAETLNEVATEGLSDLMDFLTDDSIIEFGLSWDTDAFENGRAELKETEFYPYP
RY

SeqID 363

MNTKQRFISIRKYKLGAVSVLLGTLFFLGGITNVAADSVINKPSDIAVEQQVKDSPTSANETPTNNTSSALASTAQD
NLVTKANNSPTETQPAESHSQATETFSVANQPVESTQEVSKTPLTKQNLAVKSTPAISKETPQNIDSNKIITVPK
VWNTGYKGEQTVVAIIDSGLDINHDLQNLNDSTKAKYQNEQQMNAKAKAGINYGKWMNKVIFGHNYVDVNTTELKE
VKSTSHGMHVTISIATANPSKKDTNELIYGVAPEAQVMFMRVFSDEKRGTPALYVKAIEDAVKLGADSLNLSLGGAN
GSLVNADDRLIKALEMARLAGVSVVIAAGNDGTFGSGASKPSALYPDYGLVGSPTAREAISVASYNNTTLVNKVFEN
IIGLENNRNLNNGLAAYADPKVSDKTFEVGKQYDYVFGKGNNDYKDKTLNGKIALIERGDIPTFKKVVNAINHGA
VGAIIFNNKAGEANLTMSLDPEASAIPIAFTQKEFGDVLAKNNYKIVFNNIKNKQANPNAGVLSDFSWSGLTADGQL
KPDLSAPGGSIIYAAINDNEYDMMSGTSMASPHVAGATALVKQYLLKEHPELKKGDIERTVQYLLMSTAKAHLNKDTG
AYTSRQOGAGIIDVAAAVQTGLYLTGGENNYGSVTLGNIKDKISFDVTVHNINKVAKDLHYTTYLNTDQVKDGFVT
LAPQQLGTFTGKTIRIEPGQTQTTITIDIDVSKYHDMKKVMPNGYFLEGYVRFTDPVDGGEVLSIPYVGFKGEFQNL
EVLEKSIYKLVANKEKGIFYFQPKQTNEVPGSEDTALMTTSSEPIYSTDGTSPILKALGSYKSIDGKWILQLDQKG
QPHLAISPNDQNDQDAVAVKGVFLRNFNNLRKAVYRADDVNLQKPLWVSAPQAGDKNYYSNGTENPKSTFLYDTEWK
GTTTGDIPLEDGKYKYVLTYYSVDPGSKPQOMVFDITLDRQAPTTLTATYDKDRRIFKARPAVEHGESGIFREQVCY
LKKDKDGHYNSVLRQGEDGILVEDNKVFIKQEKNGSFILPKEVNDFSHVYYTVEDYAGNLVSAKLEDLINIGNKNG
LVNVKVFSPELNSNVDIDFSYSVKDDKGNIIKKQHGGKDLNLLKLPFGTYTDFDLFLYDEERANLISPKSVTVTISEK
DSLKDVLVKVNLKKAALLVEFDKLLPKGATVQLVTKTNTVVDLPKATYSPTDYGKNIPVGDYRLNVTLPSPGYSTLE
NLDDLLSVVKEDQVNLTKLTLINKAPLINALAEQTDIITQPVFYNAGTHLKNNYLANLEKAQTLIKNRVEQTSIDNA
IAALRESRQALNGKETDTSLLAKAILAETIEKGNQYFVNASPLSQSTYINQVQLAKNLLQKPNVTQSEVDKALENLD
IAKNQLNGHETDYSGLHHMIIKANVLKQTSKYQNASQFAKENYNNLIKKAELLLSNRQATQAQVEELLNQIKATEQ
ELDGRDRVSSAENYSQSLNDNDSLNTTIPNPPNPQALIFKKGMTKESEVAQKRVLGVTSTQDNQKVKTNKLPKTGE
STPKITYTILLFSLSMLGLATIKLKSIRE

SeqID 364

MNNNEKKVKYFLRKTAYGLASMSAAFAVCSGIVHADTSSGISASIPHKQVNLGAVTLKNLISKYRGNDKAIATILLS
RVNDFNRASQDTLPQLINSTEAEIRNIIYQGQIGKQNKPSVTTHAKVSDQELGKQSRRSQDIKSLGFLSSDQKDIL
VKSISSSKDSQLILKFVTQATQLNNAESTKAKQMAQNDVALIKNISPEVLEEYKEKIQRASTKSQVDEFVAEAKKV
NSNKETLVNQANGKKQEIAKLENLSNDEMLRYNTAIDNVVKQYNEGLNITAAAMNLSIKQAAQEVAKQNLQKOYA
KKIERISSKGLALSCKAKEIYEKHSILPTPGYYADSVGTYLNNRFRDKQTFGNRSVWGTGQSGLDEAKMLDEVKKLL
KELQDLTRGTKEKDKPDVKPEAKPEAKPNIQVPKQAPTEAAKPALESPEALTRLTTWYNQAKDILLKDDQVKDKYVDIL
AVQKAVDQAYDHVEEGKFITTDQANQLANKLRDALQSLLELKDQKQVAKPEAKPEAKPEAKPEAKPEAKPEAKPE
AKPDVKPEAKPDVKPEAKPEAKPEAKSEAKPEAKLEAKPEAKPATKKSNTSGNLAAKKAIENKKYSKKLPSTGEAA
SPLLAIVSLIVMLSAGLITIVLKHKK

SeqID 365

MAKDIKFSADARSAMVRGVDILADTVKVTGLGPKGRNVVLEKAFGSPLITNDGVTTIAKEIELEDHFENMGAKLVSEVA
SKTNDIAGDGTATATVLTQAIIVREGLKNVTAGANPIGIRRGITAVSAAVEELKEIAQPVSGKEAIAQVAAVSSRSE
KVGEYISEAMGRVGNQGVITIEESRGMETELEVVEGMQFDRGYLSQYMTDNEKMSVSELENPYILITDKKISNIQEI
LPLLEEVLKTNRPILLIADDDVGEALPTLVLNKIRGTFFNVAVKAPGFGDRRKAMLEDIAILTTGGTVVTEDLGLDLK
DATMQVLGQSAKVTVDKDSTVIVEGAGDSSAIANRVAIIKSQMEATTSDFDREKLQERLAKLAGGVAIVKGAATET

ELKEMKLRIEDALNATRAAVEEGIVSGGGTALVNVEKVAALKLNGDEETGRNIVLRALEEPVRQIAYNAGYEGSVI
IERLKQSEIGTGFNAANGWVDMVTTGIIDPVKVTRSALQNAASVASLILTTEAVVANKPEPEAPTAPAMDPSMMGG
F

SeqID 366

VVENLEKPIGVSYKNSPMSKRTAIRMKKSSRFSILLYSVLSTLLAIANPLITYFANGLQTQONLYTGLMMTKGQIPY
SDVFATGGFLYYVTIALSYLLGSSIWLLIVQFIAYYVSGIYFYKLVYVVAQSEIVSIGMTLIFYIMNIVLGFQGMYP
IQWALPFMLISLWFLIKFCVDNIVDEAFIFYGILAAFSLFIDPQTILFWLCSFVLLTATNIKQKQSLRGFYQFLCVV
FGMLIAYTVGYFMFNLQIISSYIDKAIFYPPTYFARTNHSFLLSLAIQIVVLLGSGCLFGLWDFIQNRKKASYQIG
LNFIACIFLIYAIMAIFSRDFNLYHFLPALPFGLLLTSNKITILYQKVIDRRSHRRQYFSGKSLIVDLFVKKTYLPL
LLLVSLSIGLLIVYNTYQNVTLKERRDISHYLTTKIDRDGKIYVWDKVASIYSQTRLKSASQFVLPHINTAQKNNEK
ILKDELLQHGAKYFILNKNEKLPNELKSDIKKHYYQEVPLSNITHFVLYRFK

SeqID 367

MAKPTISPGMQQYLDIKENYPDAFLLFRMGDFYELFYDDAVKAAQILEISLTSRNKNAEKPIPMAGVPYHSAQQYID
VLVELGYKVAIAEQMEDPKKAVGVVVKREVVQVVTPTVVESTKPDSSANNFLVAIDSQDQQTFLGLAYMDVSTGEFQAT
LLTDFESVRSEILNLKAREIVVGYQLTDEKNHLLTKQMNLLLSYEDERLNDIHLIDEQLTDLAISAAEKLLQYVHRT
QKRELSHLQKVHYEIKDYLQMSYATKNSLDLLENARTSKKHGSLYWLLEDTKTAMGTRMLRTWIDRPLVSMNRIKE
RQDI IQVFLDYFFERNDLTESLKGVDIERLASRVSGKANPKDLLQLGQTLSPRIKMLQSFNQPELDIIVNKI
DTMPELESINTAIAPEAQATITEGNIKSGFDKQLDNRYTVMREGTGWADI EAKERAASGIGTLKIDYNKKDGY
FHVTSNLSLVPEHFRKATLKNSEYGTAEALAKIEGEMLEAREQSSNLEYDIFMRVRAQVESYIKRLQELAKTIAT
VDVLQSLAVVAENYHYVRPKFNDQHQIKIKNGRHATVEKVMGVQEYIPNSIYFDSQTDIQLITGPNMSGKSTYMRQL
ALTVIMAQMGGFVSADVDLPVFDALIFTRIGAADDLISGQSTFMVEMMEANQAVKRASDKSLILFDELGRGTATYDG
MALAQSIIEYIHDRVRAKTMFATHYHELTDLSEQLTRIVNVHVATLERDGEVTFHLKIESGPADKSYGIHVAKIAGL
PIDLLDRATDILSLEADAVQLIVSPSQEAVTADLNEELDSEKQQGQLSLFEEPSNAGRVIIELEAIDIMNLTMPQA
MNAIFDLKKLL

SeqID 368

MLKLDLKTKEIKAILIAFGVALYTFGFVKFNMANHLAEGGISGVTLLIHALFGVNPALSSLLLNIPILFILGARILGK
KSLLLTIYGTVLMSFFMFWQQIPVTVPLKNDMMLVAVAAGILAGTGSGLVFRYGATTGGADIIGRIVEEKSGIKLG
QTLFLFIDAIVLTSSLVYINLQOMLYTLVASFVFSQVLTVNENGVTYVRGMLITKESESAAATILHEINRGVTFRLG
QGAYSGREHDVLYVALNPSEVRDVKEIMADLDPDAFISVINVDEVISSDFKIRRRNYDK

SeqID 369

MKRSYAGRVRSEHIGTSITLKGWVGRRRLDGLLIFIDLRDREGIMQLVINPEEVAASVMATAESIRSEFVIEVSGV
VTAREQANDNLPTGEVELKVQELSVLNTSKTTPFEIKDGEIANDDTRMRYRYLDLRRPEMLENFKLRAKVTHSIRNY
LDNLEFIDVETPMLTKSTPEGARDYLVPSRVNQGHFYALPQSPQITKQLLMNAGFDRYYQIVKCFRDEDLGRDQPE
FTQVDLETSFSLSDQEIQDIVEGMIAKVMKDTKGLEVSPLPFRMAYDDAMNNYSGDKPDTRFDMLLQDLTEIVKEVDF
KVFSEASVVKAIVVKDKADKYSRKNIKLTETIAKQYGAQLAWLKYVDNTISGPVAKFLTAIEGRLTEALQLENNDL
ILFVADSLVANETLALRTRIAKELELIDYSKFNFLVVDWPMFEWSEEEGRYMSAHPFTLPTAETAHELEGLDA
KVRVAYDIVLNGYELGGSLRINQKDTQERMFKALGFSAESAEQVGFLLLEAMDYGFPPHGGLAIGLDRFVMLLAG
KDNIREVIAFPKNNKASDPMTQAPSLVSEQQLEELSLTVESYEN

SeqID 370

KEKGKLIKKEILENNTDIIPKIIKSPQNLILTSNRYNRVNIKIKNIKNFDDKGFELGFPLFEKGEILRKEGEITSAL
ELFDKARELGIFYVPALYNSYAMAFRKIKNYDDEILILQEGIERFKKSTLSSNINPKTIDRWSTRISRAKDLKCK

SeqID 371

LNKVKHHLAYGAITLVALFSCILAVMVIFKSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNE
APKSSSQSTEANSQQQVTASEEAAVEQAVVTENTPATSAQQAAYAVTETTYRPAQHQTSGQVLSNGNTAGAIQSAAA
AQMAAATGVPOSTWEHIIARESNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAIKAYRAQGLSAWGY

SeqID 372

MSNWDTKFLKKGFTFDDVLLIPAESHVLPNEVDMKTKLADNLTNLNIPITTAAMDTVTD SKMAIAIARAGGLGIIHKN
MSIVDQAEVVRKVKRSENGVIIDPFFLTDPDNTVSEAEELMQNYRISGVPIVETLENRKLVGIIITNRDMRFISDYKQL
ISEHMTSQNLVTAPIGTDLETAERILHEHRIEKLPLVDDDEGRSLGLITIKDIEKVIEFPKAAKDEFGRLLVAGAVGV
TSDTTFERAELFEAGADAVIDTAHGHSAGVLRKIAETRAHFENRTLIAGNIATAEGARALYDAGVDVVKVGIGPGS
ICTTRVVAGVGVPQITAIYDAAAVAREYKGTIIADGGIKYSGDIVKALAAGGNAVMLGSMFAGTDEAPGETEIFQGR
KFKTYRGMGSTIAAMKKGSSDRYFQGSVNEANKLVPEGIEGRVAYKGSVADIVFQMLGGIRSGMGYVGAANIKELHDN
AQFVEMSGAGLKESHPhdVQITNEAPNYSVH

SeqID 373

MTINHYKLRIPIYYTISFLLPFIIIVCILFTKNIIYWSPTTILASDGFHQYVIFNQALRNILHGSNSLFYFTFTSGLGL
NFYALSSYYLGSFSLPIVYFFNLKNMPDAIYLLTICKIGLIGLSMFVTLCKRHCKVNRVLLLVISTCYSLSMFSISQ
IEINMWLDVFILIPLVVLGVDQLLWERKPILYFLSLTALFIQNYFYGFMTAIFTSLYFIVQITRNTDSKVAFKQFLH

FTFLSLLAGMTSSIMILPTYFDLT'THGEKLT'KVS'KMFTENSWYMDLFAKNMIGAYDTTKFGSIPMIYVGLLPLLLSL
LYFTTIKEVPRRTRLAYGFLIIFVIASFYITPLDLFWQGMHAPNMF'LHRYSWVLSVLICLLAAECLEYLDNISWKKIL
GVNLILVSGFIITFLFKKHYYHLNLELLLLLTFLSAYIILTISFVSKQIPKLVFYPFLIGFVVLEMTLNTFYQLNS
LNDEWIFPSRQGYAKYNHSISKLVKTERNNSTFFRTERWLGQTGND'SMKYNYNGISQFSSIRNRSSSQVLDRLGFK
SDGTNLNLR'YQNNTLIADSLFGVKYNLTEYPFDKFGFIKKAQDKQTILYKNQFASQLAILTNQVYQDKPFTVNTLDN
QTTLNLQLSGLKETYFEHLIPNSVSGQTTLNKQVFVKKNKQGNTEITYNITIPKNSQLYVSMPPFINFNNEENKIVQI
SVNNGPFVPNTLDNAYSFFNIGSFAENSRIKVKFQFP'NDQVSFPIPHFYGLKLEAYQKAMTVINKRKVKVRTDHNK
VIANYTSPNRS'LSLFFTIPYDRGWKAYQNNKEIKIFKAQKGF'MKINIPKGGKGVTLIFIPYGFKFGVGLSITGIVLFT
VYYFKFGKNKIG

SeqID 374
WFMKHSV'GKRHNLVT

SeqID 375
MKDHLRCFLHYRSKNV'GKNGTRLKGGKPND

SeqID 376
DKQLFQCVQG'FQIRNLNGKKHGIKLIFIKNVKH

SeqID 377
NEEAIDGVSKL'GKKITILGNNSYLSS

SeqID 378
IKQWLLVMKKMTVL'CLKLLEILLCKTAILN

SeqID 379
RRISNNL'GVLKEATVIHAV

SeqID 380
ELCLKLSNVKPIYMP'WHFEQISLKKQVSRVYHALFE

SeqID 381
RSCFSRCYPRFNR'FRYHFLKPPWTRTNYCKRY

SeqID 382
RWFGRYDDGRKFS'FTNLL

SeqID 383
PLKSLSMTSRMKLL'RLRSQRKAM

SeqID 384
RHLRKRQKQNHLMNLC'FLCAVKKLKKDNLI

SeqID 385
KLFIQPIQENMKQPIE'ISNYAYAKLGLMKI

SeqID 386
YQYSSKKARKFGS'VWLKPK

SeqID 387
TLLFQIILL'LLSHLKKNIFLEWNMHATYN

SeqID 388
KKFYEIILATKYHTSVFKWSLKLKNKLTNTKKISEASSGKLEIHLEQQLNSMPKVTLALILLVDKSNALL

SeqID 389
LKQMFRRVLHLLFQVVLIAVRSLMKMVLKSSWDGVTCSLSLLMR'IIQYDYKVPLFQMMMLKGSVLVSKTKPRLTMMM
PLILEKYLKQ'TALVVAEYLVILFLKKPRDSF

SeqID 390
GRKINFSRPSRFE

SeqID 391
RVKYKKWEPLSISRSCY'EKSSSTSSRI

SeqID 392

TWSRCCIPRCYSWCKIRRSNQCFGRWTSSFG

SeqID 393

KENFVQRLRSLLKAISKNIITYSLVSLPLARHL

SeqID 394

SIINIKLEIYDICKPTISNRESIHGYRKLLPRLFLG DYLSKTLFQGFTSNHPNCRPIRL

SeqID 395

LSFRRSRRIGSSHSQI

SeqID 396

FIFKDRFKMRHFTD

SeqID 397

GLICACKAFISAILANLFCSSVIPIASCPENICAKPRTRFSSTSDIVLSPAKYIFKAPTVL SFIFRGTTIAEFN

SeqID 398

SSSLDTHYKHRELFIVADSLGSLWLILLVAYFV

SeqID 399

HLVPTQYHKQNLPLEYKRLNALVHK

SeqID 400

AHLHEGYHKYPLKRRNLYEFLRKL

SeqID 401

PLKELREHYIIPRKIRLQNFPHR

SeqID 402

KYTIAGSRVTQRRPSFSVTKV

SeqID 403

AAFSSPAAKNRAFITTRSS

SeqID 404

SMVKQISFSDHLISRFEGLCLRRFSVRFLRRSLSSVSNSTNNTSWL

SeqID 405

YHVLSRYHLNPLHVLQALYAHQEYVIVLIIHQRELFYRGQRQ

SeqID 406

AQPSSSTRISPKIDRFTP

SeqID 407

WNRTINYFLNNLQLVTNIKLPTRKIFQSQNKFLSFIKN

SeqID 408

VQEGHKIFPLQR

SeqID 409

QQSNNTANYSRPYKPWHKKKNGLSCRCFS

SeqID 410

FFDDTKVNIHWLEMFVCMCNIMWQCTNSSLWENYFTLPIKATGSIDSRYKTTCCRFYITFNTGHLSSKEKIWVLTC
SKGLV

SeqID 411

VYSLRIATLELERNLIDKRRGKPTDSRSIEFLEVSLAILSKKNKLIPDIMLEKTFPLVSSEAKSEDLKFKSAISLNL
ENCS

SeqID 412

GHSNGIKEGNGGIFPVFCIAITATRFRFTINGFCNRINPCLCHFIVTLLSCCNRS

SeqID 413

RIEKAIVPKPAISVLMIIISRMVLGTPEKEPVICSANGIISIVIATPADIEIQMSKADIKAKPVEKLCFENSLTELT
KAAPGTITISAPNIIIMLRCSNPKEYNKLALKATTELPRMVKRNPVCIRLSIKFRKYPKIKPVTAAENESNKELPKA
KEKLPAPQK

SeqID 414

PYSVTYAAPVICNGADLARRTAYAMSSSVTKPSDVEELVTIGDRTKRFSRLNPLGSINGRNKLPWTLFISAHRLPLIS
HRLSLKSIKLCN

SeqID 415

ANHNDKNNTISVKNKFSK

SeqID 416

SFCVFCCHSKKGSYPHPKQSSWSSRFNSRSHTNDITCPYRCSKSSCKGSIT

SeqID 417

TLGISFKIRGCHFSKAPFLGGKSPDFPLPG

SeqID 418

FNISNSSLGFGTSAKSASTSSANSLLIISCDKATHSLQMKTPLPAIIFFTSSWLLPQNEQ

SeqID 419

GVYKKQSLSLIFHQIHLIVYHFDLHDFVPPYYRE

SeqID 420

IFLRSVCGNSRQALGLTSYILHKLSSPKNGQGIALNTLSPSSSTSKNKSSKADNFIRKCLEILEISASVNRGPKVLQ
QLAHAVQSIS

SeqID 421

SRISTITIPIRISPTFLYREDFSSGLKGSFGLRLSSVKYFFPSKVYWRPKNIPAAASEKPRWKFTSCPRYPTTMGE
IKAPRLIPKTKILKPASRRSEFSYKLPPTISDTFGFNSPVPRIIRAIEMNRAV

SeqID 422

SFPRSNNLCAFKDKFKCRTSSRLDCL

SeqID 423

IHSFHRRKLNHHGKLNLYHLVLEKQPGLSSLLIMLYQSPDL

SeqID 424

LSFSIVSHLLTTIIIPLASCANPAIRLSYSRIPSSALITIRTTSESMARIERITEYFSVFSYTLPLRIPAVSII
VYSCPWLSTKLVSIA SRVVPATGLAITRSSPRMALIKLDFPTFGRPIKLRKRIISGFSFSSSTGRFSTIASNISPVPI
P

SeqID 425

CPSSDIAGINFTKNSGKIDKQTVT

SeqID 426

PFLRNHFHNNETSTKFFSDSTKSRIGNTCHRC

SeqID 427

ASTGSAANPQTTPGKLLQASIAPIVPQPVITKSAAPLLSKIAVSKPFC

SeqID 428

AMPKRCFIPPEYDEIFFLPTSPKPTSSSNLGISCLAFFLSTPFKVAI

SeqID 429

LLLILKNPDTTHNTTIKRQPNKPPKVLKRKTEKKSILMKRIPINHVAP

SeqID 430

NFKARPPGVVSGLPNITPTFSLNWLKIAIVFVLLMDADNLRIA

SeqID 431

KRVGICHYHVSQSSCFHNNKFSRYFTQFSFNIIVHSIFLSQYFSFW

SeqID 432

NSTTSASLISGLISSRSGRRVNEPSSFSASNDTKAGRPKVASTASRIAGTFIDFSRTEITCPGVTRYDGLSTRLPST
RI

SeqID 433

TRPLVEILVDKLPYKEANFSRNSCTLGYLAFVNTI

SeqID 434

RTRNAIRYPKASSGDYGTKREIITANKDKYSISKMCRLNMPRSSYYYQAVESVSKTEFEETIKRIFLDSESRYGSR
KIKICLNNEGITLSRRRIRRMKRLNLVSVYQKATFKPHSRGKNEAPIPNHLDROFKQERPLQALVTDLTYYVRVGNR
WAYVCLIIDLYNREIIGLSLGHKTAELVKQAIQSIPIYALTKVKMFHSDRGKEFDNQLIDEILEAFGITRSLSQAGC
PYDNAVAESTYRAFKIEFVYQETTFQSLEELALKTEKATLFCCTTFIKCCLERFLPML

SeqID 435

atggatgtat	cgtctagtc	gaatattaca	tttatgctgc	aatacacaga	ggctaatacct	60
caatatgtgg	actatactaa	cagagaagag	gctgtcaaaa	ttgatgaaga	attgtcctta	120
gaaacgaaca	ggcaaatgat	tgaaggatta	actgaagacg	agttgactcg	tattcaggaa	180
gctgtccctg	aaacgcagtt	gaatttttagg	gaatacattg	attatatgaa	ccgctcgtat	240
gcaactgaag	aacaatctaa	agaactaaca	gctatcttta	ctcaagaagc	agattatcct	300
cagaaactac	gattaatcga	tctaaaaaat	aagttggaat	cagcttatca	aaatggttca	360
cttctctggc	aaggagttat	ttcgtttgat	aatgcttttc	ttgcggaaca	gggattgtat	420
gatgttgoga	ctgggtcaagt	tgatcaaaaa	gcgattaagg	cagtgtatgcg	tgatatgatg	480
ccaacactta	tccagaaaga	gggcctttct	gattctgctt	tttgggtggg	gaatatccat	540
ctgaatacag	ataatatcca	tatccatttt	gggctttctg	aagttgaatc	taaccgtgag	600
aaaatattct	atcagccacg	tggacgtatg	gagtacaaag	gtaacttctc	tcagaaaacc	660
atcaaccggg	ttaaaagtgg	tgtgtatcat	ggattgtctg	aagaagaaac	aagatccaat	720
cttctcagaa	aagaacagat	tttagcta	ctcaaagcgg	acttcataac	atctatttac	780
cagaaggaca	agattacttc	ttcagctgaa	aaaaattttt	tggacaagc	ctacaatcat	840
ttgcgctaa	ataagaagtg	gcgctatgg	tctaatagcc	gagattttgc	ggtagtaag	900
ttctttcttg	atcgctat	agatttctat	ttaaacaatg	aaggtagtgc	tgctatcaa	960
gaatttttga	aagagactag	agattttctt	cagacttatg	aaggggttta	ttcagctgaa	1020
aaaaataaaa	tctatgaaaa	actacgtaaa	gttgatgggc	aaacgatcag	aacgcttgca	1080
gaatcaaaa	gatattgatt	agaacatcat	ttggcacgct	gtgtaatgga	tttaagagag	1140
cgttttagcca	ataatatctt	acgttcggtt	agagaagctg	caccccaaat	tcaagacgtt	1200
cagctggaaa	aaaatttaga	gagtttttct	gttttgaacc	agaagaaaat	tttagaacia	1260
catcctgaag	caagtgtgg	aaaaagtcag	aaagcttggc	agaagttagg	ctactttgtg	1320
aaggctggag	agcagccact	tgaaattata	aggccagctt	ataaatctta	tgataagcat	1380
ggtaaaaggta	taggacggcc	agaatttgta	tcagatactg	tttatgat	tagtcagcta	1440
acagaaaata	ttcagctgaa	aagtctaacc	ttgaaagacc	tctctctgtt	ttcttctaac	1500
gagttaaaag	agttagtaga	tgctgctaag	ttaaagacta	atccaacaga	gagagaacgc	1560
cgtgaattga	gtacctatcg	ttatgcgttg	aaacttagca	tattagaatc	tagtcagaag	1620
gaattgcagg	ttcgtcaaaa	gctactagaa	caggtacagc	cactagcgtc	tgatcaacca	1680
tttttagatt	tttaagaaaca	gttaatagct	caggaattac	aagctatagc	gctacaattg	1740
actcctaatt	acaagctatc	agaagatgat	aaagccttga	aaaatcgatt	gaagaggcag	1800
tttgaagata	gtgttgcgct	acctgtttca	aaagctactc	ctgggtgccat	acaacttctt	1860
attaggcaac	tttggactga	gctaggattg	gttcattcaca	ttcaagatga	aaacattcta	1920
acgcttctga	aaggagacatc	aacgacgaaa	caagcttata	tagaagaact	tcagactcat	1980
atctctattt	ttcagttgaa	atatcagatt	aacaatagaa	acaagcagat	aagccagtta	2040
tcggatgaag	caacaataaa	ggagatgagg	atagctaattg	ctaaagggtt	ctctgagcta	2100
aaacgtctat	atgatacatt	acagccatca	gatgatgggtc	aaaatcagat	tagtcaagct	2160
gtttctaaac	aattacaaga	acgaaaagtt	atcaaaaaag	ctcaattaca	acagacgcag	2220
agaagcggaa	aatcaataac	agacttcatg	cgacaattga	cagcttctct	taatcgttca	2280
caacaagcaa	gtaaaaaagc	attgatggaa	cgtgcacgta	gtgatgaacg	tgaggaaaca	2340
gaagaacgta	ggcaagctca	acgttaa				2367

SeqID 436

atgaattcta	acacaaaagg	tcacggattt	ttccgcaagt	caaaagcata	cggcttagta	60
tgtgctattg	cattagcagg	tgcatttaca	ttagctacta	gtcaagtgtc	tgctgatcaa	120
gttacaactc	aagcaacaac	tcaaacagta	acgcaaaatc	aagcagaaac	agtaacatca	180
actcaacttg	ataaagcag	agctacagct	aaaaaagcag	ctgtagctgt	tacaaccaca	240
cctgcagtta	atcatgcyac	aactactgat	gcacaagctg	atttagctaa	tcaaacacaa	300
gctgttaaag	atgttactgc	aaaagcacaa	gctaatacac	aagctattaa	agatgctact	360
gctgaaaatg	caaaaattga	tgctgaaaac	aaagcagagg	cagagcgtgt	tgcaaaagaa	420
aacaaggaag	gtcaagcagc	cgtagatgca	cgtaacaaag	caggtcaagc	agccgtagat	480
gcacgtaata	aagcgaaaca	gcaagcgcaa	gacgatcaaa	aagcaaaaat	tgatgctgaa	540

aacaaagcag	agtctcaacg	tgtaagtcag	ttaaagtcac	aaaataaagc	aaaaattgac	600
gcagaaaata	aagatgcgca	agctaaagca	aatgcgacta	atgcacaatt	acaaaaagat	660
tatcaagcta	aattagcgga	aatcaaatca	gttgaagctt	ataatgcagg	tgtacgtcaa	720
cgtaataaag	atgcacaagc	taaagcagat	gcgactaacg	cacagttaca	aaaagactat	780
caagctaaat	tagcacttta	taatcaagct	ctaaaagcta	aagcagaagc	agataaacag	840
tctattaata	atgttgcttt	tgatatcaaa	gctcaagcta	aaggtgttga	taacgctgaa	900
tatggaaact	caatcatgac	tgcaaaaaat	aaacctgacg	gaagtttcga	gtttaaccat	960
gatatgatcg	atgggtgtgaa	gacaatcggc	tatgggaaat	tgacaggtaa	agttaatcat	1020
cattatgttg	ctaacaagga	tggtctctgtg	acagcatttg	ttgattctgt	cactctttac	1080
aagtacgagt	atcgtaaatgt	tgctcaaaaat	gctgctgtta	accaaaatat	tgtatttaga	1140
gttttaacaa	aagatggctg	tcctatTTTT	gaaaaagctc	ataatggtaa	caaaactttt	1200
gcagaaactt	taacaaaaac	tttacaactc	aatctttaa	atgagcttaa	accacatgct	1260
tccagcggtg	acgtcgaagt	ctttaagatt	catgatgact	gggtacatga	cacacatggg	1320
tctgctttag	tgtcttatgt	taataataat	gaagctgttc	ctaattgtgt	catcccgaa	1380
cggccaactc	caccaaagcc	agtgaaggtt	acacctgaag	cagaaaaacc	agtacctgaa	1440
aagccagttg	agcctaaatt	ggtaacgcct	acattaaaaa	cttatactcc	agtcaaattt	1500
attccgcgag	aatacaaaacc	agaaccaatc	acctctgaga	cgtttaccct	tgagaaattt	1560
actccagctc	aaccaaaagt	gaaaccacat	gtgtctattc	ctgaaaagat	taactactca	1620
gttagtggtc	atcctgtttt	agttccagct	gctaactcct	caaaagctgt	cattgatgaa	1680
gcaggtcaat	ctgttaatgg	taaaaccgta	ttaccaaatg	caacattaga	ctatgttgct	1740
aaacaaaact	ttagtcaata	caaagggtatt	aaagcttctg	cagaagcgat	cgcaaaagg	1800
tttgcatTTG	tagatcaacc	aaatgaagcg	ttagctgaat	tgactgttaa	gtctatcaaa	1860
gcatctaattg	gtgatgatgt	atcaagcttg	ttagaaatgc	gtcatgtttt	atcaaaagat	1920
acttttagacc	aaaaaacttca	atctcttatt	aaagaggcag	gaatttagtcc	agttggtgag	1980
ttttacatgt	ggactgcaaa	agatccacaa	gctttttata	aagcttatgt	tcaaaaagga	2040
ctagatatca	cttataatct	atccttttaa	atcaaagcta	actttactaa	aggtcaaact	2100
aaaaatgggtg	ttgcacagat	tgattttggg	aatggatata	caggtaatat	tgtagtcaat	2160
gatgttactg	ttccagaagt	acataaggat	atacttgata	aagaggatgg	taaatcaatt	2220
aataatagta	cgggttaagtt	aggtgatgaa	gtgacctaca	aacttgaagg	atgggttgta	2280
ccagcaaacc	gtggttacga	tctttttgaa	tacaaatttg	tggatcaatt	acaacacaca	2340
catgatcttt	acttacgtga	taaagtgggc	gctaaagttg	atgtgacatt	aaaagatgg	2400
acagtcatta	aaaaagggac	taatttttag	gagtacacag	aaacagttta	caacaaaacg	2460
acaggtcatt	atgagcttgc	ctttaaaaaa	gagtttttag	ctaaggtttc	tcgtgaacta	2520
gaatttgggtg	cagatgattt	tattgtagtt	aaacgtatta	aggcagggtg	tgtttacaat	2580
actgctgatt	tatatgttaa	tggatataaa	gttaagtcag	aagcagttgt	gactcatact	2640
actgagaaat	caaaaccagt	tgaaccacaa	aaagcaactc	caaaagctcc	agctaaagga	2700
ctgccatcaa	ctgggtgaagc	tagtatgacg	ccacttactg	caattggagc	aattatctta	2760
tcagctctag	gcctcgcagg	ctttaaaaaa	cgtcaaaaat	aa		2802

SeqID 437

atgttttagtt	ggttggaagc	tctttattac	actctgatac	aactggcaaa	agtgaaccgg	60
ttgaatgctc	ttttcttagt	tagcgttggtg	ggttatcttt	gttaccaggg	aataaaactc	120
gtcagaaaaa	ccataagaaa	cttttttcag	ctgatgaagg	gtttcatagg	tgatagagag	180
aacatcaaga	aatgcatcaa	aaacaagaaa	gaggcactag	tccattcttg	gaaacatcgt	240
caagatattg	attggaaatc	aactggaaaa	gataagagta	aacagttatg	gaatcttatg	300
aagcgacttg	cgacagtTgc	tccttcattt	ttgttcttat	tattgggaaa	tgttctcttt	360
cgtctcattt	atcaactgcc	ttttgtaaag	caagacagaa	agcgatttga	caaggaaaatg	420
agcccttTgc	tctacttcaa	gaactatcgt	agttttgtgt	tcatgggaat	aggtttcagt	480
ttcatagcgt	ttattctcac	aaactatttt	gtgacggttt	taagggtcgc	tattcgtttt	540
ctatatTTct	caatcatgac	gttaagagat	aatagccaag	tcgttagctt	taacgttgat	600
agtttgctca	tccagaattt	attcaatgct	agggatattg	tgatagctcc	cattctagca	660
gtgccaatct	ttctcattgg	tttagtcgta	gcttgggcgt	ctgcttgggt	taactttgaa	720
cagtaccgtg	attataatca	taatgaagaa	ggggatgac	gctttgcgac	tgtcaaagaa	780
atccaccagc	aatatagaag	agttccta	aaaacggaaa	cttatccagg	tgaaggagg	840
gtgcccgTtc	ttcatgaaac	aagaaagaat	ttgacaggct	taacgcctaa	atctcaaatg	900
ctttggcaaa	accgtacctt	tagtcgctat	ttaacgaatg	cggaaaggat	tttagggctc	960
ttatcgacgc	cttcaggaga	ttattacatc	gatgatagca	ccacaaactt	gatcaccatg	1020
gggattactc	ggtcaggtaa	gggagaagct	catattgccc	ctattattga	tattaatagc	1080
cgtgcggaaa	ttcaaccgtc	actgattatt	gcagacccta	aaggggaaca	ttaccagtcc	1140
tcttataaaa	ccatgcgtcg	gcgtggctat	gatgttaatg	tcctttcttt	ccaaaacatg	1200
gattggTcca	tgtccataaa	ccttttagct	cttgcgattg	cagcagctaa	gaagggttac	1260
tatgaaatga	cacagacaag	ggttaatgcg	gttgacagaag	ccattttatcg	taaaacgaaa	1320
cctggtagcg	gtaatggcaa	tgcaaaatac	tgggaagata	cctccatttc	cctctttaat	1380
gccattgcta	tggccttaat	ggaccgtgct	aatgaaaccg	tcaggaatgg	tgaaccgat	1440
gcttgggata	cgtttacagt	tcgtaacatt	gccaaagttt	tgactgactt	gggttctgaa	1500

gaagtctttt	tcaatgattt	tggagagatt	gttgagaatc	ctgataagaa	ccaacaagt	1560
aagaagaaat	ctaaaaatcac	ggtttacttt	gataacttgc	gtaaaatcaa	tcaagaacaa	1620
ttttccaaat	ttagagatat	ggctgattta	aacttttaggt	cttctgactt	cgcttcagaa	1680
gaaactaagg	gaaatgtctt	ctctagcatg	atgtcaggta	ttaacttatt	cttgcaagat	1740
aatattgcta	aactaacctc	taaaaactct	attgacctag	aatcggttgg	tttcccacgt	1800
cgcttgtcta	tcaagtttgc	ttctagttcc	aatgtcgtta	tgcgtaacga	atacactcat	1860
aagacggcta	aggttaccat	tactagtcaa	gctgtttggg	gtaaaaccac	taaacaagtt	1920
atccacgtag	atgctgcaac	agctctgatt	gatggtgaag	gctatctaac	ctatgtgatt	1980
gaaccccgag	ttcctgatca	attcttggta	acaattgact	ttaatcacga	aaacaatggt	2040
ggttcagcta	ttcgtcacaa	aactttccaa	ttctcagctg	agaaagtcta	taagaaacgt	2100
ggtaacgtta	ttacgttggg	tgactacacg	aaaaaaccag	ttttggatca	tatcaaagtt	2160
actgttctca	acaagcaaga	tgataacctt	ctccagaaag	aagatattga	cctgatttat	2220
tcagataatc	ctaaagtgat	ttacttggta	acacctccaa	ataggactga	atataatagt	2280
attgtatctc	tgtttttggg	tcaattgttt	aatgccaat	atgagttagc	tctgtcaa	2340
ggtcgcaatg	gtgtcaatcg	aattcttcat	atcctcgatg	aattcacaaa	cattccagct	2400
attcctcaca	tgataccaa	gatttccatt	ggtcttggtc	aaaatattct	ctactatctc	2460
tggattcaga	acttgaaaca	gttagtcagt	gaatatggcg	agaatacagc	ggaaaccatt	2520
cgggagaact	gttctttgaa	agtttatatc	aaatctactg	ccccagcgac	caacgagtag	2580
ttcagtaaa	agttggggac	tcggaccatt	acacgtcgca	gaaggtcaag	taatattcta	2640
gatgaagcta	atccaaatgt	ttccattgaa	aatcctagac	aggaactctt	aacaccgaca	2700
cagctctcga	aactccaaga	aggggaagcg	gttattttgc	gtggtgttaa	aggtcgagac	2760
aatgcaggta	ggaaaatcac	aacggatccg	atcttcttgc	atgagaaaac	gagccttctc	2820
tatcgctaca	tgttcttaca	agaagaattt	gaccagtcga	tggtcttggc	agatattcca	2880
gtggaaagt	ggcatagggg	ccttgacctg	caagatatag	cagttagggc	acaaagcact	2940
tttaataaga	ttattgattg	gcggtatggc	ctaactgacc	gtatgagaac	aaatgggaag	3000
atacctcaat	tagcatcaag	aaaacaaacg	attaaagctc	taagtcaatc	tcaatttact	3060
tctccagcag	acctaacaca	agctgtgatt	gcagaggtat	ttgatgagga	agatgatgac	3120
gatcttttct	ttgtggatga	tgtcatgtaa				3150

SeqID 438

atgacagata	atcgcttttgc	ccaattaaaa	gaaaactttg	aaaagggatc	tcctaaaaag	60
cgagttccaa	cgtctcgccc	aatcgagct	caaaaagcgc	ctgagagcta	taacaaaaag	120
ggacggtatc	catttttcgct	ccaccaagat	gtgcgttatg	ataaattaga	agcattagta	180
gcttatcatg	gagctaagtc	tgcatacagat	tatctggaga	ggttgattgt	tcaggaatgg	240
gaaaagatgc	agcggaagct	taagaacaaa	gaaaaataa			279

SeqID 439

atggcatatt	tatcaaaatt	atccgatttg	gatccatcgt	tgatggatgc	ggattctgaa	60
caaatattata	ttcctaaagt	cttgtttgag	cataatgact	ttaaaggctt	gacctacaaa	120
gagattttat	tatattcttt	tttgttaaat	cgttttaagag	agccattaga	ttttattcaa	180
aaaggctatg	atgataatga	agatacctat	gttcacttta	aggtcgaaga	tttatgtgaa	240
ctactcaacc	agagtaagac	aaccgttatt	tccttgaaga	aaagggttagc	tcaatatggt	300
ttgatagaag	aagtgaagc	aggtagtcac	cagccgaatc	gtattttattt	aacagataaa	360
ttagttccat	atattaaggg	gtaa				384

SeqID 440

atgacaatct	ttgatgaaag	agagttaaaa	gaacgattta	ctcatgaaaa	taggggttagt	60
ttttatgagt	ttgtggctaa	atatgatgct	caaatggttc	ctgtgatgaa	agcaaagggc	120
tatcgatgta	ttcattcaat	ggagcgtaca	gtgggttttt	cttttgggga	attcacgatt	180
aggcgacgtc	ggtggcaaaa	aggagaacat	tgggtggtgc	cagttgatga	aaagctagga	240
ctgaaaaaga	atgttcgcta	ctctttagaa	ttcatgtatc	aaattgctag	tttagcaacc	300
atgatgcctt	atgaaaaagt	gattaagggt	gttcagatga	tgtattgtat	tgtgattacc	360
aaacctactg	ttgtgaaggc	cgtaagatt	agtcgtgaat	tgcttaaaaga	aaaggaagcg	420
tatcgttttt	ttgatgaaga	tataccagta	gataaagaac	cagttgatat	gatttatctt	480
gaaggagatg	gaagtcaggt	caaagctcga	gaagaaggat	tagataatcg	caatgttgat	540
ttgtctcatt	tcgtgggttca	tacgggtagt	cagaaagtag	gaagcaatcg	ctttgtctta	600
caaaaataaaa	aagagtttgt	gtcccttgat	aatcgtaaaa	cgcgtaaaaa	gattttggac	660
taccttttaca	atcatttttta	cattgcccga	aacaccttgc	ttattaccaa	ttcagatggt	720
ggccatggct	ataccccata	tgtttttaaa	gagattgcga	aagcactcaa	agtgaagcaa	780
cacgaacact	tttgggatag	gtatcatgtc	aatgaaaaga	tcaaaagttt	ttttaaactc	840
tatccagtg	aactgatgac	tggcgctttt	cagagcatta	aacagcatga	taaagaaaag	900
cttagaactg	ttttggatag	gacagaagca	ttgatactga	tggagaaga	aatggaaggg	960
tttaaccagt	tcaaacgaaa	gttgtaaaac	aattttcaat	atactaaatc	agctgaattg	1020
agaggtttca	gtcgtgcagg	aataggtgtt	atggagtcac	aacatcgaaa	aattacctat	1080
cggatgaaaa	agcgcgggat	gtattggaca	attcagggag	ctgagacgat	gagtcaatta	1140

attgtcctat	cgtatgaagg	acagctaaga	gatctcttct	ttggttcttg	gcgtgaagac	1200
tatcagaaat	atcaagagct	agaaaacctt	agtgcgggaa	aaatcaaaca	tgaacagaat	1260
aaaatcaata	agagatatga	tctccagaca	cttggctcggc	ttaggtacgg	taggcatcgt	1320
aatttatag						1329

SeqID 441

atggatgtat	cgtctagtcc	gaatattaca	tttatgctgc	aatacacaga	ggctaatacct	60
caatatgtgg	actatactaa	cagagaagag	gctgtcaaaa	ttgatgaaga	attgtcctta	120
gaaacgaaca	ggcaaatgat	tgaaggatta	actgaagacg	agttgactcg	tattcaggaa	180
gctgtccctg	aaacgcagtt	gaatttttagg	gaatacattg	attatatgaa	ccgctcgtat	240
gcaactgaag	aaacaatctaa	agaactaaca	gctatcttta	ctcaagaagc	agattatctt	300
cagaaactac	gattaatcga	tctaaaaaat	aagttggaat	cagcttatca	aaatggttca	360
cttctctggc	aaggagttat	ttcgtttgat	aatgcttttc	ttgcggaaca	gggattgtat	420
gatgttgcca	ctgggtcaagt	tgatcaaaaa	gcgattaagg	cagtgatgcg	tgatatgatg	480
ccaacactta	tccagaaaaga	gggcctttct	gattctgctt	tttgggtggg	gaatatccat	540
ctgaatacag	ataatatcca	tatccatttt	gggctttctg	aagttgaatc	taaccgtgag	600
aaaatattct	atcagccacg	tggacgtatg	gagtacaaag	gtaacttctc	tcagaaaacc	660
atcaaccggt	ttaaaagtgg	tgtgtatcat	ggattgctga	aagaagaaac	aagatccaat	720
cttctcagaa	aagaacagat	tttagctaat	ctcaaaagcg	acttcataac	atctatttac	780
cagaaggaca	agattacttc	ttcagctgaa	aaaaattttt	tggacaagc	ctacaatcat	840
ttgccgctaa	ataagaagtg	gcgctatggt	tctaattgcca	gagattttgc	ggttagtaag	900
ttctttcttg	atcgctattt	agattcctat	ttaaacaatg	aaggtagtgc	tgccatcaa	960
gaatttttga	aagagactag	agattttctt	cagacttatg	aaggggttta	ttcagctgaa	1020
aaaaataaaa	tctatgaaaa	actacgtaaa	gttgatgggc	aaacgatcag	aacgcttgca	1080
gaatcaaaag	gatatgattt	agaacatcat	ttggcacgtc	gtgtaatgga	tttaagagag	1140
cgttttagcca	ataatatctt	acgttcgttt	agagaagctg	caccccaaat	tcaagacggt	1200
cagctggaaa	aaaattttaga	gagtttttct	gttttgaacc	agaagaaaat	tttagaaca	1260
catcctgaag	caagtgtggt	aaaaagtcag	aaagcttggc	agaagttagg	ctactttgtg	1320
aaggctggag	agcagccact	tgaaattata	aggccagtct	ataaatctta	tgataagcat	1380
ggtaaaagga	taggacggcc	agaatttgta	tcagatactg	tttatgatat	tagtcagcta	1440
acagaaaata	ttcagctgaa	aagtctaacc	ttgaaagacc	tctctctgtt	ttcttctaac	1500
gagttaaaag	agtttagtaga	tgctgctaag	ttaaagacta	atccaacaga	gagagaacgc	1560
cgtgaattag	gtacctatcg	ttatgcgttg	aaacttagca	tattagaatc	tagtcagaag	1620
gaattgcagg	ttcgtcaaaa	gctactagaa	caggtacagc	cactagcgtc	tgatcaacca	1680
tttttagatt	ttaaagaaaca	gttaatagct	caggaattac	aagctatagc	gctacaattg	1740
actoctaatt	acaagctatc	agaagatgat	aaagccttga	aaaatcgatt	gaagaggcag	1800
tttgaagata	gtgttgcgct	acctgtttca	aaagctactc	ctgggtgccat	acaacttcct	1860
attaggcaac	tttggactga	gctaggattg	gttcatcaca	ttcaagatga	aaacattcta	1920
acgcttctga	aagggacatc	aacgacgaaa	caagcttata	tagaagaact	tcagactcat	1980
atctctattt	ttcagttgaa	atatcagatt	aacaatagaa	acaagcagat	aagccagtta	2040
tcggatgaag	caacaataaa	ggagatgagg	atagctaatg	ctaaagggtt	ctctgagcta	2100
aaacgtctat	atgatacatt	acagccatca	gatgatggtc	aaaatcagat	tagtcaagct	2160
gtttctaaac	aattacaaga	acgaaaagtt	atcaaaaaag	ctcaattaca	acagacgcag	2220
agaagcggaa	aaatcaatac	agacttcatg	cgacaattga	cagcttctct	taatcgttca	2280
caacaagcaa	gtaaaaaagc	attgatggaa	cgtgcacgta	gtgatgaacg	tgaggaacaa	2340
gaagaacgta	ggcaagctca	acgttaa				2367

SeqID 442

atgaattcta	acacaaaagg	tcacggatth	ttccgcaagt	caaaagcata	cggcttagta	60
tgtgctattg	cattagcagg	tgcatthtaca	ttagctacta	gtcaagtgtc	tgctgatcaa	120
gttacaactc	aagcaacaac	tcaaacagta	acgcaaaatc	aagcagaaac	agtaacatca	180
actcaacttg	ataaaagcag	agctacagct	aaaaaagcag	ctgtagctgt	tacaaccaca	240
cctgcagtta	atcatgcgac	aaactactgat	gcacaagctg	atttagctaa	tcaaacacaa	300
gctgttaaag	atgttactgc	aaaagcacaa	gctaatacac	aagctattaa	agatgctact	360
gctgaaaatg	caaaaattga	tgctgaaaac	aaagcagagg	cagagcgtgt	tgcaaaagaa	420
aaacaaggag	gtcaagcagc	cgtagatgca	cgtaacaaag	caggtcaagc	agccgtagat	480
gcacgtaata	aagcgaaaca	gcaagcgcaa	gacgatcaaa	aagcaaaaat	tgatgctgaa	540
aacaaagcag	agtctcaacg	tgtaagtcag	ttaaattgcac	aaaataaagc	aaaaattgac	600
gcagaaaata	aagatgcgca	agctaaagca	aatgcgacta	atgcacaatt	acaaaaagat	660
tatcaagcta	aattagcggg	aatcaaatca	gttgaagctt	ataatgcagg	tgtagctcaa	720
cgtaataaag	atgcacaagc	taaagcagat	gcgactaacg	cacagttaca	aaaagactat	780
caagctaaat	tagcaacttta	taatcaagct	ctaaaaagcta	aagcagaagc	agataaacag	840
tctattaata	atgttgcttt	tgatatcaaa	gctcaagcta	aaggtgttga	taacgctgaa	900
tatggaaact	caatcatgac	tgcaaaaact	aaacctgacg	gaagtttoga	gtttaaccat	960
gatatgatcg	atgggtgtgaa	gacaatcggc	tatgggaaat	tgacaggtaa	agttaatcat	1020

cattatgttg	ctaacaagga	tggctctgtg	acagcatttg	ttgattctgt	cactctttac	1080
aagtacgagt	atcgtaagt	tgctcaaaat	gctgctgtta	accaaaatat	tgtatttaga	1140
gttttaacaa	aagatggtcg	tcctatTTTT	gaaaaagctc	ataatggtaa	caaaactttt	1200
gcagaaactt	taaacaaaac	tttacaactc	aatctttaa	atgagcttaa	accacatgct	1260
tccagcggtg	acgtcggaag	ctttaagatt	catgatgact	gggtacatga	cacacatggg	1320
tctgcttttag	tgtcttatgt	taataataat	gatgctgttc	ctaagtgtgt	catcccagaa	1380
cggccaactc	caccaaagcc	agtgaaggtt	acacctgaag	cagaaaaacc	agtacctgaa	1440
aagccagttg	agcctaaatt	ggtaacgcct	acattaaaaa	cttatactcc	agtcaaattt	1500
attccgcgag	aatacaaaacc	agaaccaatc	acccctgaga	cgtttaccct	tgagaaattt	1560
actccagctc	aaccaaaagt	gaaaccacat	gtgtctattc	ctgaaaagat	taactactca	1620
gttagtggtc	atcctgtttt	agttccagct	gctaactcct	caaaagctgt	cattgatgaa	1680
gcagggtcaat	ctgttaaatg	taaaaccgta	ttaccaaatg	caacattaga	ctatgttgct	1740
aaacaaaact	ttagtcaata	caaaggtatt	aaagcttctg	cagaagcgat	cgcaaaaggt	1800
tttgcatattg	tagatcaaac	aatgaagcg	ttagctgaat	tgactgttaa	gtctatcaaa	1860
gcatctaattg	gtgatgatgt	atcaagcttg	ttagaaatgc	gtcatgtttt	atcaaaagat	1920
acttttagacc	aaaaaacttca	atctcttatt	aaagaggcag	gaattagtcc	agttggtgag	1980
ttttacatgt	ggactgcaaa	agatccacaa	gctttttata	aagcttatgt	tcaaaaagga	2040
ctagatatca	cttataatct	atccttttaa	atcaaagcta	actttactaa	aggtcaaatc	2100
aaaaatggtg	ttgcacagat	tgattttggg	aatggatata	caggtaatat	tgtagtcaat	2160
gatgttactg	ttccagaagt	acataaggat	atacttgata	aagaggatgg	taaatcaatt	2220
aataatagta	cgggttaagt	agggtatgaa	gtgacctaca	aacttgaagg	atgggttgta	2280
ccagcaaaacc	gtgggttacga	tctttttgaa	tacaaatttg	tggatcaatt	acaacacaca	2340
catgatcttt	acttacgtga	taaagtggtc	gctaaagttg	atgtgacatt	aaaagatggg	2400
acagtcatta	aaaaagggac	taatttagga	gagtacacag	aaacagttta	caacaaaacg	2460
acagggtcatt	atgagcttgc	ctttaaaaaa	gagtttttag	ctaaggtttc	tcgtgaatca	2520
gaatttggtg	cagatgattt	tattgtagtt	aaacgtatta	aggcagggtga	tgtttacaat	2580
actgctgatt	tatatgttaa	tggatataaa	gttaagtcag	aagcagttgt	gactcatact	2640
actgagaaat	caaaaaccagt	tgaaccacaa	aaagcaactc	caaaagctcc	agctaaagga	2700
ctgccatcaa	ctggtgaagc	tagtatgacg	ccacttactg	caattggagc	aattatctta	2760
tcagctctag	gcctcgagc	ctttaaaaag	cgtcaaaaat	aa		2802

SeqID 443

atgttttagtt	ggttggaagc	tctttattac	actctgatac	aactggcaaa	agtgaaccgg	60
ttgaatgctc	ttttcttagt	tagcggtgtg	ggttatcttt	gttaccaggg	aataaaactc	120
gtcagaaaaa	ccataagaaa	cttttttcag	ctgatgaagg	gtttcatagg	tgatagagag	180
aacatcaaga	aatgcatcaa	aaacaagaaa	gaggcactag	tccattcttg	gaaacatcgt	240
caagatattg	attggaaatc	aactggaaaa	gataagagta	aacagttatg	gaatcttatg	300
aagcgacttg	cgacagttgc	tccttcattt	ttgttcttat	tattgggaaa	tgttctcttt	360
cgtctcattt	atcaactgcc	ttttgtaaag	caagacagaa	agcgatttga	caaggaaatg	420
aagcccttgc	tctacttcaa	gaactatcgt	agttttgtgt	tcattgggaat	aggtttcagt	480
ttcatagcgt	ttattctcac	aaactatttt	gtgacgggtt	taagggtcgc	tattcgtttt	540
ctatattttct	caatcatgac	gttaagagat	aatagccaag	tcgttagctt	taacgttgat	600
agtttgctca	tcagaatttt	attcaatgct	agggatattg	tgatagctcc	cattctagca	660
gtgccaatct	ttctcattgg	tttagtcgta	gcttgccggt	ctgcttggtg	taactttgaa	720
cagtaccgtg	attataatca	taatgaagaa	ggggatgatc	gctttgcgac	tgtcaaagaa	780
atccaccagc	aataaagaa	agttcccta	aaaacggaaa	cttatccagg	tgaaggaggt	840
gtgcccgttc	ttcatgaaac	aagaaagaat	ttgacaggct	taacgcttaa	atctcaaatg	900
ctttggcaaa	accgtacctt	tagtcgctat	ttaacgaatg	cggaaaggat	tttagggctc	960
ttatcgacgc	cttcaggaga	ttattacatc	gatgatagca	ccacaaactt	gatcaccatg	1020
gggattactc	ggtcaggtaa	gggagaagct	catattgcc	ctattattga	tattaatagc	1080
cgtgcggaaa	ttcaaccgtc	actgattatt	gcagacccta	aaggggaaac	ttaccagtc	1140
tcttataaaa	ccatgcgtcg	gcgtggctat	gatgttaaat	tcctttcttt	ccaaaactag	1200
gattgggtcca	tgtcctataa	cccttttagct	cttgccgattg	cagcagctaa	gaagggttac	1260
tatgaaatga	cacagacaag	ggttaatgcg	gttgcagaag	ccatttatcg	taaaaacgaa	1320
cctggtagcg	gtaatggcaa	tgcaaaatac	tgggaagata	cctccatttc	cctctttaat	1380
gccattgcta	tggccttaat	ggaccgtgct	aatgaaacog	tcagggaatgg	tgaaaccgat	1440
gcttgggata	ccgttacagt	tcgtaacatt	gccaaagttt	tgactgactt	gggttctgaa	1500
gaagtctttg	tcaatgattt	tggagagatt	gttgagaatc	ctgataagaa	ccaacaagtg	1560
aagaagaaat	ctaaaatcac	ggtttaactt	gataacttgc	gtaaaatcaa	tcaagaacaa	1620
ttttccaaat	ttagagatat	ggctgattta	aacttttaggt	cttctgactt	cgcttcagaa	1680
gaaactaagg	gaaatgtctt	ctctagcatg	atgtcaggta	ttactttatt	cttgcaagat	1740
aatattgcta	aactaacctc	taaaaactct	attgaacctag	aatcggttgg	tttcccacgt	1800
cgcttgctca	tcaagtttgc	ttctagttcc	aatgtcgcta	tgcgtaacga	atacactcat	1860
aagacggcta	aggttaccat	tactagtcaa	gctgtttggg	gtaaaaccac	taaacaggtt	1920
atccacgtag	atgctgcaac	agctctgatt	gatgggtgaag	gctatctaac	ctatgtgatt	1980

gaaccccgagc	ttcctgatca	attcttggtgta	acaattgact	ttaatcacga	aaacaatggt	2040
gggttcagcta	ttcgtcacia	aacttttccaa	ttctcagctg	agaaaagtcta	taagaaacgt	2100
ggtaacgtta	ttacgttgga	tgactacacg	aaaaaaccag	ttttggatca	tatcaaagtt	2160
actgtttctca	acaagcaaga	tgataaccctt	ctccagaaaag	aagatattga	cctgattttat	2220
tcagataaatc	ctaaagtgat	ttactttggta	acacctccaa	ataggactga	atataatagt	2280
attgtatctc	tgtttttggg	tcaattggtt	aatgccaat	atgagttagc	tctgtcaa	2340
ggtcgcaagt	gtgtcaatcg	aattcttcat	atcctcgatg	aattcacaaa	cattccagct	2400
attcctcaca	tggtatacaa	gatttccatt	ggctcttggtc	aaaatattct	ctactatctc	2460
tggtattcaga	acttgaaaca	gttagtcagt	gaatatggcg	agaatacagc	ggaaaccatt	2520
cgggagaaact	gttcttttgaa	agttttatctc	aaatctactg	ccccagcgac	caacgagtag	2580
ttcagtaaaag	agttgggggac	tcggaccatt	acacgtcgca	gaaggtcaag	taatatttcta	2640
gatgaagcta	atccaaatgt	ttccattgaa	aatccttagac	aggaaactctt	aacaccgaca	2700
cagctctcga	aactccaaga	aggggaagcg	gttatttttgc	gtgggtgttaa	aggtcgagac	2760
aatgcaggtc	ggaaaatcac	aacggatccg	attttcttgc	atgagaaaaac	gagccttccct	2820
tatcgctaca	tgttctttaca	agaagaattt	gaccagtcga	tggtctttggc	agatattcca	2880
gtggaaagtg	ggcatagggg	ccttgacctg	caagatatag	cagtaggggc	acaaagcact	2940
tttaataaga	ttattgattg	gcggatggct	ctaactgacc	gtatgagaac	aatggggaag	3000
atacctcaat	tagcatcaag	aaaacaaacg	attaaagctc	taagtcaatc	tcaattttact	3060
tctccagcag	acctaacaca	agctgtgatt	gcagaggtat	ttgatgagga	agatgatgac	3120
gatcttttct	ttgtggatga	tgatcatgtaa				3150

SeqID 444

atgacagata	atcgcttttgc	ccaattaaaa	gaaaactttg	aaaagggatc	tcctaaaagg	60
cgagttccaa	cgtctcgccc	aatcgagct	caaaaagcgc	ctgagagcta	taacaaaaag	120
ggacgggtatc	catttttgcgt	ccaccaagat	gtgcgttatg	ataaattaga	agcattagta	180
gcttatcatg	gagctaagtc	tgcatcagat	tatctggaga	ggttgattgt	tcaggaatgg	240
gaaaagatgc	agcgggaagct	taagaacaaa	gaaaaataa			279

SeqID 445

atggcatatt	tatcaaaatt	atccgatttg	gatccatcgt	tgatggatgc	ggatttctgaa	60
caaatattata	ttcctaaagt	cttgtttgag	cataatgact	ttaaaggctt	gacctacaaa	120
gagattttat	tatattcttt	tttgttaaat	cgttttaagag	agccattaga	ttttattcaa	180
aaaggctatg	atgataatga	agatacctat	gttcacttta	aggtcgaaga	tttatgtgaa	240
ctactcaacc	agagtaagac	aaccgttatt	tccttgaaga	aaaggttagc	tcaatatggt	300
ttgatagaag	aagtgaagac	aggtagtcac	cagccgaatc	gtattttattt	aacagataaa	360
ttagttccat	atattaaggg	gtaa				384

SeqID 446

atgacaatct	ttgatgaaag	agagttaaaa	gaacgattta	ctcatgaaaa	tagggttagt	60
ttttatgagt	ttgtggctaa	atatgatgct	caaatgggtc	ctgtgatgaa	agcaaagggc	120
tatcgatgta	ttcattcaat	ggagcgtaca	gtgggttttta	cttttgggga	attcacgatt	180
aggcgacgtc	gggtggcaaaa	aggagaacat	tggtgtgtgc	cagttgatga	aaagctagga	240
ctgaaaaaga	atgttcgcta	ctcttttagaa	ttcatgtatc	aaattgctag	tttagcaacc	300
atgatgcctt	atgaaaaagt	gattaagggt	gttcagatga	tgtattgtat	tgtgattacc	360
aaacctactg	ttgtgaaggc	cgttaagatt	agtcgtgaat	tgcttaaaga	aaaggaagcg	420
tatcgttttt	ttgatgaaga	tataccagta	gataaagaac	cagttgatat	gattttatctt	480
gaaggagatg	gagtcattgg	caaagctcga	gaagaaggat	tagataatcg	caatgttgat	540
ttgtctcatt	tcgtgggttca	tacgggtagt	cagaaagtag	gaagcaatcg	ctttgtctta	600
caaaaataaaa	aagagtttgt	gtcccttgat	aatcgtcaaa	cgcgtcaaaa	gatttttgac	660
tacctttaca	atcattttta	cattgcccc	aacaccttgc	ttattaccaa	ttcagatggt	720
ggccatggct	atacccccata	tgttttttaa	gagattgcga	aagcactcaa	agtgaagcaa	780
cacgaacact	tttgggatag	gtatcatgtc	aatgaaaaga	tcaaaagttt	ttttaaactc	840
tatccagtg	aactgatgac	tggcgctttt	cagagcatta	aacagcatga	taaagaaaag	900
cttagaactg	ttttggatag	gacagaagca	ttgatactga	tggaaagaaga	aatggaaagg	960
tttaaccagt	tcaaacgaaa	gttggttaaac	aatttttcaat	atactaaatc	agctgaattg	1020
agaggtttca	gtcgtgcagg	aataggtgtt	atggagtcac	aacatcgaaa	aattacctat	1080
cggatgaaaa	agcgcgggat	gtattggaca	attcagggag	ctgagacgat	gagtcaatta	1140
attgtcctat	cgtatgaagg	acagctaaga	gatctcttct	ttgggttcttg	gcgtgaagac	1200
tatcagaaat	atcaagagct	agaaaacctt	agtcggggaa	aatcaaaaca	tgaacagaat	1260
aaaatcaata	agagatatga	tctccagaca	cttgggtcggc	ttaggtagcg	taggcacgt	1320
aatttatag						1329

SeqID 447

atggctgtcg	aaattattat	gcctaaactc	ggggttgata	tgcaagaagg	cgaaatcctt	60
gagtggaata	aacaggtagg	tgatgttgtt	aatgaagggtg	acgtcctact	tgaaattatg	120

tcagataaaa	caaatatgga	gattgaagca	gaagactcag	gtgttttact	aaaaatcaca	180
catgggaatg	gagatgttgt	tcctgtaact	gagacaattg	gctatatcgg	tgctgaaggt	240
gaagaagtaa	cagaagcatc	ttcttctgaa	aatacatcag	ttgaagaaaa	cgcgacacaa	300
gtaacttcag	aaccagaaaa	agttgaagaa	acatcagaac	caagtgtgcc	agcagctaca	360
agtgggtgaa	aagtacgtgc	cactcctgca	gctcgtaaat	tagcaagaga	gatgtctatt	420
gaccttgcac	tagtatctgg	aacaggggca	aatggctcgc	ttcacagaga	agatggtgaa	480
agcttcaagg	gtgctcaacc	acgtattaca	ccattggcac	gtcgaattgc	tgaagatcaa	540
ggagttgata	tagcagaaat	cactggcagt	ggtattcgtg	gtaaaaattgt	taaaaatgat	600
gttttggtg	ctatgtcacc	gcaagcagca	gaggctcctg	tagaaacgaa	agctacacca	660
acaacagaag	aaaaacaatt	accagaaggt	gttgaagtca	ttaagatgtc	tgcaatgcgt	720
aaggctatgt	ctaaagggtat	gactaactct	tacctcactg	ctccaagctt	tacacttaac	780
tatgacattg	atatgactga	aatgatggct	cttcgcaaga	aattaattga	tccaatcatg	840
gctaaaaacag	gcttgaaagt	cagctttact	gatttgattg	gaatggccgt	tggttaagaca	900
ttgatgaaac	cagagcatcg	atacctaaat	gcttcattaa	ttaacgatgc	acaagaaatt	960
gagcttcata	attttgttaa	tattggaatc	gcagttggct	ttgatgatgg	cttgattggt	1020
cctgttggtc	acaatgctga	tcaaattgtca	ctttctgact	ttgttatagc	atctaaagat	1080
gttattaaga	aaactcaaga	aggtaaatta	aaatcagctg	aaatgtcagg	ttcaacattc	1140
tcaattacta	acttaggtat	gtttgggtact	aagacgttta	acccaattat	caatcaaccg	1200
aactcagcaa	tccttggagt	aggcgctact	attccgactc	caacagtggg	tgatggtgaa	1260
attgtagctc	gaccaatcat	ggcaatgtgt	ttaacaattg	accaccgtat	tgttgatgga	1320
atgaatggcg	ctaagtttat	ggttgatcct	aagaacttaa	tggaaaaccc	atttggttta	1380
cttatttga						1389

SeqID 448

atgtctagtt	ttaatagaaa	aaaacttaag	tttttgggta	tatctttggc	gactctaaca	60
gccaccacag	ttaccctggt	tgccctgtgg	aatgagctca	agaactctgg	agataataaa	120
gttattaatt	gggtatattc	tactgaaatc	agtacattgg	acatttcaaa	gaatacagat	180
gcttattcaa	acttagctat	aggtaattca	ggcagcaatt	tacttagaat	tgataaagag	240
ggcaaaccaa	aacccgattt	agctaaaaaa	gtatccgttt	cttctgatgg	tcttacttat	300
actgctacac	ttcgtgataa	tttaaaatgg	tcagatggaa	gcaaactaag	cgctgaagat	360
tttgtttaca	catggcgagg	aatagttgat	cctaaaactg	catctgaata	tgcttacttg	420
gcgacagaat	cgcacctttt	aaatgctgat	aagattaatt	ctggagatat	taaagattta	480
aataaacttg	gtgtaacagc	taaaggcaat	caagtgcact	ttaaattgac	aagtcctatg	540
cctcaattta	aataattatt	agccttctct	aattttatgc	ctcaaaaaaca	atcgtatggt	600
gaaaaagttg	gtaaagatta	tggtacaaca	tcaaaaaatc	aaatttactc	aggtccttac	660
cttggttaagg	attggaatgg	ttcaaattgg	aaattttaaat	tagtcaaaaa	taaatattat	720
tgggattcta	aacatgttaa	aacaaatagt	gtcatagtcc	aaactatcaa	aaaaccagat	780
actgcagttc	aaatgtacaa	gcaagggtcag	attgatattg	ctgaaatatc	aggaacttct	840
gctatttata	accaaactgg	ttcgggttaa	gcattgacaa	atcagaaaaa	taggcaagct	900
ttgaatttag	cgactgatcg	taaagggtgt	gctaaagcgg	cagttgatac	aggttcaact	960
cctgctgaat	ctctgggtccc	taaaaaatta	gccaaattac	ctaattggtga	ggatctttcc	1020
aagtatactg	ccccagggtta	tacgtataat	acaagtaaag	ctcaaaaaact	ttttaaagaa	1080
ggctcttgctg	aggttgggtca	gtcatctctc	aagttaacaa	tcacagctga	ttcggactct	1140
ccagcagcta	aaaatgctgt	tgactatgtg	aaatctacat	gggagagtgc	tttgccctggt	1200
ctaactgttg	aagaaaaaatt	tgttactttc	aagcaacgcc	ttgaagatgc	aaaaaatgaa	1260
aatttttgatg	tcgtgctctt	ctcatggggg	ggagattatc	cagaaggatc	aactttctat	1320
gggttattca	cgactaattc	tgcgataaat	tatggtaaat	tttcttctaa	agagtatgac	1380
aatgcctatc	aaaaggcaat	tactactgac	gccttgaaac	caggagatgc	cgctaattgat	1440
tacaaaaactg	ctgaaaaaagc	tttatttgat	caatcatatt	ataaccagct	ttattaccta	1500
gggaaaaaag	gactccaaaa	ttctaaatta	aaggggttgg	taagaaattc	aactggtttg	1560
aatggttgatt	ttacttatgc	ttataagaca	gaataa			1596

SeqID 449

MDVSSSPNITFMLQYTEANPQYVDYTNREEAVKIDEELSLETNRQMIEGLTEDELTRIQEAVPETQLNFREYIDYMN
 RSYATEEQSKELTAIFTQEADYLQKLRLIDLKNKLESAYQNGSLLWQGVISFDNAFLAEQGLYDVATGQVDQKAIKA
 VMRDMMPTLIQKEGLSDSAFWGNIHLNTDNIHIFGLSEVESNREKIFYQPRGRMEYKGNFSQKTINRFKSGVYHG
 LLKEETRSNLLRKEQILANLKADFITSYQKDKITSSAEKNFLEQAYNHLPLNKKWRYGNSNARDFAVSKFFLDRLD
 SYLNNEGSAAYQEFLKETRDFLQTYEGVYSAEKNKIYEKLKRVGDGTIRTLAESKGYDLEHHLARRVMDLRERLANN
 ILRSFREAAPQIQDVQLEKNLESFSLVNQKKILEQHPEASVVKSQKAWQKLGYPVKAGEQPLEIIRPVYKSYDKHGK
 GIGRPEFVSDTVYDISQLTENIQLKSLTLKDLSLFSSNELKELVDAAKLKTNPTEERERRELGTYYALKLSILESSQ
 KELQVRQKLLQVQPLASDQPFDFKQQLIAQELQAIALQLTPNYKLSEDDKALKNRLKRQFEDSVALPVSKATPGA
 IQLPIRQLWTELGLVHHIQDENILTLKGTSTTKQAYIEELQTHISIFQLKYQINNRRNKQISQLSDEATIKEMRIAN
 AKGFSELKRLYDTLQPSDDGQNQISQAVSKQLQERKVIKKAQLQQTQRSKGINTDFMRQLTASLNRSQQASKKALME
 RARSDEREQEERRQAQR

SeqID 450

MNSNTKGHGFFRKSAYGLVCAIALAGAF TLATSQVSADQVTTQATTQTVTQNAETVTSTQLDKAVATAKKA AVAV
 TTTTPAVNHATT TDAQADLANQTQAVKDVTAQAQANTQA IKDATAENAKIDAENKAEAEVAKENKEGQA AVDARNKA
 GQAAVDARNKAKQQAQDDQKAKIDAENKAESQRVSQ LNAQNKAKIDAENKDAQAKANATNAQLQKDYQAKLAEIKSV
 EAYNAGVRQRNKDAQAKADATNAQLQKDYQAKLALYNQAL KAKAEADKQSINNVAFDIKAQAKGVDNAEYGNSIMTA
 KTKPDGSGFEFNHMDIDGVKTIYGKLTGKVNHHYVANKDGSVTA FVDSVTLYKYEYRNVAQNAAVNQNI VFRVLT KD
 GRPIFEKAHNGNKTF AETLNKTLQLNLKYELKPHASSGNVEVF KIHDDVHDTHGSALVS YVNNNDVAPNVV IPERP
 TPPKPVKVTPEAEKPVPEKPVPEKLVTP TLKTYTPVKFIPREYKPEPITPETFTPEKFTPAQPKVKPHVSIPEKINY
 SVSVHPVLVPAANPSKAVIDEAGQSVNGKTVLPNATLDYVAKQNF S QYKGIKASAEAIAGFAFVDQPN EALAE LTV
 KSIKASNGDDVSS LLEMRHVL SKDTLDQKLQSLIKEAGISPVGEFYMWTAKDPQAFYKAYVQKGLDITYNLSFKIKA
 NFTKGQIKNGVAQIDFGNGYTGNI VVNDVTVP EVHKDILD KEDGKSINNSTVKLGDEV TYKLEGWVVPANRGYDLFE
 YKFVDQLQHTHDL YLRDKVVAKVVDVTLKDGTVIKKGTNLGEYTTETVYNKTTGHYELAFKKEFLAKVSRESEFGADDF
 IVVKRIKAGDVYNTADLYVNGYKVKSEAVVTH TTEKSKPVEPQKATPKAPAKGLPSTGEASMTPLTAIGAILLSALG
 LAGFKKRQK

SeqID 451

MFSWLEALYYT LIQLAKVNRLNALFLVS VVG YLCYQGIKLVKRTIRNFFQLMKGFIGDREN IKKCIKNKKEALVHSW
 KHRQDIDWKSTGKDKSKQLWNLMKRLATVAPSFLFLLGNVLFRLIYQLPFVKQDRKRFDKEMKPLLYFKNYRSFVF
 MGIGFSFIAFILTNFYFVTVLRAAIRFLYFSIMTLRDSQVVSFNVD SLLIQNLFNARV FVIAPILAVPIFLIGLVVA
 WRSAWVNFEQYRDYNHNEEGDDR FATVKEIHQQYKVPNKTE TYPGEGGV PVLHETRKNLTGLTLKSQMLWQNRTFS
 RYLTAERILGLLSTPSGDYIIDSTTNLITMGITRSGKGEAHI APIIIDINSRAEIQPSLIADPKGEHYQSSYKTM
 RRRGYDVNVLSFQNMDSMSYNPLALALAAAKGYYEMTQTRVNAVAEAIYRKTKPGSGNGNAKYWEDTSISL FNAI
 AMALMDRANETVRNGETDAWDTVTVRNIAKFLTDLGSEEVFVND FGEIVENPDKNQQVKKKSKITVYFDNLRKINQE
 QFSKFRDMADLNFRSSDFASEETKGNVFSSMMSGINLFLQDNIAKLT SKNSIDLESVGFPRRLSIKFRSSSNVAMRN
 EYTHKTAKVTITTSQAVWGKTTKQVIHVDAATALIDGEGYLTYVIEPQLPDQFLVTIDFNHENNGGSAIRHKTFQFSA
 EKVKYKRGNVITLDDYTKKPVLDHIKVTVLNKQDDNLLQKEDIDLIYSDNPKVIYLVTPPNRTEYNSIVSLFLDQLF
 NANYELALSNGRKCVNRILHILDEFTNIPAI PHMDTKISIGLGONILY YLWIQNLKQLVSEY GENTAETIRENC SLK
 VYIKSTAPATNEYFSKELGTRTITRRRRSSNILDEANPNVSIENPRQELLTPTQLSKLQEGEAVILRGVKGRDNAGR
 KITTDPIFLHEKTS LPYRYMFLQEEFDQSMALADIPVESGHRDLDLQDIAVGAQSTFNKIIDWRMALTDRMRTNGKI
 PQLASRKQTIKALSQSQFTSPADLTQAVIAEVFDEEDDDDLFFVDDVM

SeqID 452

MTDNRF AQLKENFEKGS PKRRVPTSRPIAAQAPESYNKKGRYPFSLHQDVRYDKLEALVAYHGAKSASDYLERLIV
 QEWEKMQRKLKNKEK

SeqID 453

MAYLSKLSDDLPSLMDADSEQIYIPKVLFEHNDFKGLTYKEILLYSFLLNRLREPLDFIQKG YDDNEDTYVHFKVED
 LCELLNQSKTTVISLKKRLAQYGLIEEVKAGSHQPNRIYLTDKLVPYIKG

SeqID 454

MTIFDERELKERF THENRVSYFEYFAKYDAQMV PVMKAKGYRCIHSMERTVVF TFGFTIRRRRWQKGEHWVPVDE
 KLGLKKNVRYSLFMYQIASLATMMPYEKVIKVVQMMY CIVITKPTVVKAVKISRELLKEKEAYRFFDEDI PVDKEP
 VDMIYLEGDGVMVKAREEGLDNRNVDLSHFVVHTGSQKVGSNRFVLQNKKEFVSLDNROTRQKILDYLNHFYIAPN
 TLLLTNSDGGHGYTPYVFKETIAKALKVKQHEHFWDRYHVNEKIKSFFKLYPVELMTGAFQSIKQHDKEKLRTVLDTT
 EALILMEEEMEGFNQFKRKLNNFQYTKSAELRGFSRAGIGVMESQHRKITYRMKKRGMWWTIQGAETMSQLIVLSY
 EGQLRDLFFGWSWREDYQKYQELNLSAGKIKHEQNKINKRYDLQTLGR LRYGRHRNL

SeqID 455

MDVSSSPNITFMLQYTEANPQYVDYTNREEAVKIDEELSLETNRQMIEGLTEDELTRI QEAVPETQLNFREYIDYMN
 RSYATEEQSKELTAIFTQ EADYLQKLRLIDLKKNLESAYQNGSLLWQGVISFDNAFLAEQGLYDVATGQVDQKA IKA
 VMRDMPTLIQKEGLSDSAFWGNHNLNTDNIHIFGLSEVESNREKIFYQPRGRMEYKGNFSQKTINRFKSGVYHG
 LLKEETRSNLLRKEQILANLKADFITSIYQKDKITSSAEKNFLEQAYNHLPLNKKWRYG SNARDFAVSKFFLDRLD
 SYLNNEGSAAYQEFLKETRDFLQTYEGVYSAEKNKIYEKLKRVGDGTIRTTLAESKGYDLEHHLARRVMDLRERLAN N
 ILSRFREAAPQIQDVQLEKNLESF SVLNQKKILEQHPEASVVKSQKAWQKLG YFVKAGEQPLETIRPVYKSYDKHGK
 GIGRPEFVS DTVYDISQLTENIQLKSLTLKDLSLFSSNELKELVDAAKLKTNPTERERRELGT YRYALKLSILESSQ
 KELQVRQKLLQVQPLASDQPF LDFKKQLIAQELQATALQLT PNYKLSEDDKALKNRLKRQFEDSVALPVSKATPGA
 IQLPIRQLWTELGLVHHIQDENILTLKGTSTTKQAYIEBELQTHISIFQLKYQINN RNKQISQLSDEATIKEMRIAN
 AKGFSELKRLYDTLQPSDDGQNQISQAVSKQLQERKVIKKAQLQOQTORS GKINTDFMRQLTASLNRSQQASKALME
 RARSDEREQEERRQAQR

SeqID 456

MNSNTKGHGFFRKSAYGLVCAIALAGAF TLATSQVSADQVTTQATTQTVTQNAETVTSTQLDKAVATAKKA AVAV
 TTTTPAVNHATT TDAQADLANQTQAVKDVTAQAQANTQA IKDATAENAKIDAENKAEAEVAKENKEGQA AVDARNKA
 GQAAVDARNKAKQQAQDDQKAKIDAENKAESQRVSQ LNAQNKAKIDAENKDAQAKANATNAQLQKDYQAKLAEIKSV
 EAYNAGVRQRNKDAQAKADATNAQLQKDYQAKLALYNQAL KAKAEADKQSINNVAFDIKAQAKGVDNAEYGNSIMTA

KTKPDGSFEFNHDMIDGVKTIYGKLTGKVNHHYVANKDGSVTA FVDSVTLYKYEYRNVAQNAAVNQNVFRVLTKD
GRPIFEKAHNGNKTFAETLNKTLQNLKYELKPHASSGNVEVFKIHDWVHDTHGSALVS YVNNDNAVPNVPIPERP
TPPKPVKVTPEAEKPVPEKPVEPKLVPTLKTYPVKFIPREYKPEPITPETFTPEKFTPAQPKVKPHVSIPEKINY
SVSVHPVLVPAANPSKAVIDEAGQSVNGKT VLPNATLDYVAKQNFSSQYKGIKASAEAIKGF AFVDQPNELAE LTV
KSIKASNGDDVSSLLEMRHVL SKDTLDQKLQSLIKEAGISPVG EGYMWTAKDPQAFYKAYVQKGLDITYNLSFKIKA
NFTKGQIKNGVAQIDFGNGYTGNIVVNDVTPEVHKDILDKEDGKSINNSTVKLGDEVTYKLEGWVVPANRGYDLFE
YKFVDQLQHTHLDLYLRDKVVAKVVDVTLKDGTVIKKGTNLGEYTTETVYNKTTGHYELAFKKEFLAKVSRESEFGADDF
IVVKRIKAGDVYNTADLYVNGYKVKSEAVVTHTEKSKPVEPQKATPKAPAKGLPSTGEASMTPLTAIGATILSALG
LAGFKKRQK

SeqID 457

MFSWLEALYYTLIQLAKVNRLNALFLVSVVGYLCYQGIKLVKRTIRNFFQLMKGFIGDRENKKCIKNKKEALVHSW
KHRQDIDWKSTGKDKSKQLWNLMKRLATVAPSFLFLLLGNVLFRLIYQLPFVKQDRKRFDKEMKPLL YFKNYSFVF
MGI GSFIAFILTNFYFTVLRAAIRFLYFSIMTLRDN SQVVSFNVD SLLIQNLFNARV FVIAPILAVPIFLIGLVVA
WRS AWVNFEQYRDYNHNEEGDDRFATVKEIHQQYKVPNKTTETYPGEGGVPLHETRKNLTGLTLKSQMLWQNRFTS
RYLTNAERILGLLSTPSGDYYIDDSTTNLITMGITRSGKGEAHIAPIIDINSRAETQPSLI IADPKGEHYQSSYKTM
RRRGYDVNVLSFQNMDSMSYNPLALALIAAAKKGYYEMTQTRVNAVAEATYRKT KPGSGNGNAKYWEDTSISL FNAI
AMALMDRANETVRNGETDAWDTVTVRNIAKFLTDLGSEEVFVND FGEI VENPDKNQ QVKKKSKITVYFDNLRKINQE
QFSKFRDMADLNFRSSDFASEETKGNVFSMMSGINLFLQDNIAKLTSKNSIDLESVGFPRRLSIKFRSSSNVAMRN
EYTHKTAKTITTSQAVDWGKTTKQVIHVDAATALIDGEGYLT YVIEPQLPDQFLVTIDFNHENGSGSAIRHKTTFQFSA
EKVYKKRGVNTITLDYDTKKPVLDHIKVTVLNKKQDDNLLQKEDIDLIYSDNPKVIYLVTPPNRTEYNSIVSLFLDQLF
NANYELALSNGRKCVNRILHILDEFTNIPAI PHMDTKISIGLGQNILYYLWIQNLKQLVSEY GENTAETIRENC SLK
VYIKSTAPATNEYFSKELGTRTITRRRRSSNILDEANPNVSIENPRQELLTPTQLSKLQEGEAVILRGVKGGRDNAGR
KITTDPIFLHEKTSLPYRYMFLQEEFDQSMALADIPVESGHRDLDLQDIAVGAQSTFNKIIDWRMALTDRMRTNGKI
PQLASRKQTIKALSQSQFTSPADLTQAVIAEVFDEEDDDDLFFVDDVM

SeqID 458

MTDNRFAQLKENFEKGS PKRRVPTSRPIAAQKAPESYNKKGRYPFSLHQDVRYDKLEALVAYHGAKSASDYLERLIV
QEWKMQRKLNKEK

SeqID 459

MAYLSKLSDLDP SLMADSEQIYIPKVLFEHNDFKGLTYKEILLYSFLLNRLREPLDFIQGYDDNEDTYVHFKVED
LCELLNQSKTTVISLKKRLAQYGLIEEVKAGSHQPNRIYLTDKLVPYIKG

SeqID 460

MTIFDERELKERFTHENRVSFYEFVAKYDAQMV PVMKAGYRCIHSMERTVVFTFGEFTIRRRRWQKGEHWVVPVDE
KLGLKKNVRYSLBFMYQIASLATMMPYEKVIKVVQMMY CIVITKPTVVKAVKISRELLKEKEAYRFFDEDIPVDKEP
VDMIYLEGDGV MVKAREEGLDNRNVDLSHFVVHTGSQKVGSNRFVLQNKKEFVSLDNRQTRQKILDYLYNHFIAPN
TLITNSDGGHGYTPYVFKBIKALKVKQHEHFWD RYHVNKIKSFFKLYPVELMTGAFQSIKQHDKEKLRTVLDTT
BALILMEEEMEGFNQFKRKLNNFQYTKSAELRGFSRAGIGVMESQHRKIT YRMKKRGMYWTIQGAETMSQLIVLSY
EGQLRDLFFGWSWREDYQKYQELENLSAGKIKHEQNKINKRYDLQTLGR LRYGRHRNL

SeqID 461

MAVEIIMPKLGVDMQEGEILEWKKQVGDV VNEGDVLL EIMSDKTNMEIEAEDSGVLLKITHGNGDVVPVTETIGYIG
AEGEEVTEASSENTSVEENATQVTSEPEKVEETSEPSVPAATSGEKVRATPAARKLAREMSIDLALVSGTGANGRV
HREDVESFKGAQPRITPLARRIAEDQGV DIAEITGSGIRGKIVKNDVLAAMSPQAAEAPVETKATPTTTEEKQLPEGV
EVIKMSAMRKATSKGMTNSYLTAPSFTLNYDIDMTEMALRKKLIDPIMAKTGLKVSFTDLIGMAVVKTLMKPEHRY
LNASLINDAQEIEELHNFVNI GIAVGLDDGLIVPVVHNADQMSLSDFVIASKDVIKKTQEGKLKSAEMSGSTFSITNL
GMFGTKTFNPIINQPN SAILGVGATIP TPTVVDGEIVARPIAMCLTIDHRIVDGMNGAKFMVDLKNLMENPFGLLI

SeqID 462

MSSFNRKKLKFGLISLATLTATTVTLVACGNESKNSGDNKVINWYIPT EISTLDISKNTDAYSNLAIGNSGSNLLRI
DKEGKPKPDLAKKVS VSSDGLTYTATLRDNLKWS DGSKLSAEDFVYTWRRIVDPKTASEYAYLATESHLLNADKINS
GDIKDLNKLGV TAKGNQVTFKLTS PCPQFKYYLAFS NFMPQKQS YVEKVGKDYGTTSKNQIYSGPYLVKDWNGSNGK
FKLVKNKYWDSKHVKTNSVIVQTIKKPDTAVQMYKQGQIDFAEISGTS AIYNQTGSVKALTNQKIRQALNLATDRK
GVVKA AVDTGSTPAESLVPKKLAKLPNGEDLSKYTAPGYTYNTSKAQKLFKEGLAEVQSSSLKLTITADSDSPAACKN
AVDYVKSTWESALPGLTVEEKFTVFKQRL EDAKNENFDVVLFSWGGDYPEGSTFYGLFTTNSAYNYGKFSSKEYDNA
YQKAITTDALKP GDAANDYKTA EKALFDQSYNPFVYYLGKKGLQNSKLGLVRNSTGLNVDFTYAYKTE

SeqID 463

atgcttaaaa	aatcgcaactt	tttacagata	tttacacttt	gcttagccct	cttaacgatt	60
tctgggtgtc	aattaaccga	tactaaaaaa	cctggtcata	ccacaattaa	ggttgctgcc	120
caaagttcta	cagagtctag	tatcatggca	aatattgtca	ccgaattaat	tcatcacgaa	180
ttaggataca	acacaacttt	aataagcaat	cttgggttcc	ctacggttac	tcaccaagct	240
ttgctccgtg	gtgatgctga	cattgctgcc	acacgttata	caggaacaga	catcacagga	300

actcttggct	taaaagctgt	taaagacact	aaagaagctt	ctaagattgt	aaaaactgaa	360
ttccaaaaac	gctacaatca	aacttggtat	cctacttatg	gtttttctga	tacttatgca	420
ttcatgggta	ctaaagagtt	tgccagacag	aataaaatca	ccaagatctc	tgatctcaaa	480
aagttatcaa	caactatgaa	ggcaggggtt	gatagttcat	ggatgaatcg	cgagggagat	540
ggatacactg	atttcgctaa	aacatacggg	tttgaatttt	cacatattta	ccctatgcaa	600
attggcttag	tctatgatgc	agttgaaagt	aacaaaatgc	aatctgtatt	aggctactcc	660
actgacggtc	gtatttcgag	ctatgattta	gaaattttta	gggatgataa	aaaattcttt	720
cctccttatg	aagcctctat	ggttgtcaac	aattctatca	tcaaaaaaga	tcctaaacta	780
aaaaaattac	tccatcgact	cgatggtaaa	atcaatttta	aaacgatgca	aaaccttaat	840
tatatggtag	atgataaact	tttagaacct	tcagttgttg	ccaaacaatt	tttagaaaaa	900
aaccattatt	ttagaggaga	taaataa				927

SeqID 464

ttgaaaccgt	ccttcaaaaa	actattgcta	ctatttagta	ttatcaccat	tttatccatc	60
gctgtacac	cacatgcaaa	agcaagtggg	cgttcatgga	aaagttgggt	tatcgaacaa	120
tacttttggc	taaagcgca	taaaagttat	tataaagttc	aagatgaaag	ctcatttcaa	180
aagtacttaa	atgctagccg	tgaacaatct	gataaggggt	attacttaga	cccaaactct	240
gttaatggag	ggcttgttca	agagagactt	tttgatatgc	aagtctattc	ttggaatgac	300
aacggtaaa	ctaatacaaaa	gaccattttc	tatttagctg	gtggctctta	cttaataaat	360
ccaacgcctt	accatatacag	catgcttaag	acgctctcaa	ctagtcttga	tgcaaaaatt	420
attttaccag	tttatccaaa	aactcctcgt	tatacctatg	attatgctat	ccctagattg	480
gttaaccttt	atagacactt	tcatgaaaaa	aacgctaata	tcactttgat	gggtgattca	540
gctggcggag	gatttagcact	aggattagcg	catgcattgt	ctcaccaatc	agggcaagag	600
gctattcctc	aacctaaaaa	tattatcctc	ttatctccat	ggctagatgt	gacaatgaaa	660
catccagaaa	ttcccaaata	cgaagatact	gatcctatcc	tatctgcttg	gggtctcgca	720
cgtgtagggt	aaatttgggc	aatgggttct	aataatacta	accatacata	tgtagtcct	780
aaaaatgcc	ctgctactaa	actcgctcct	attacgttat	ttactggaac	acgagaaata	840
ttcttccag	atattcgca	ttatgctgca	caactccaag	cagctaatac	ccccgttaac	900
tatattgcac	aagagggaat	gaatcatgtt	tatccaattt	accctattga	agaagctaaa	960
acagcacagt	atcaaatgat	tgatatcatc	aataaaactc	cttaa		1005

SeqID 465

atgacaaaaa	aacatcttaa	aacgcttgcc	ttggcactta	ctacagtatc	agtagtgaca	60
tacagccagg	aggtatatgg	attagaaaga	gaggaatcgg	tcaaaacaaga	acaaaccag	120
tcagcttcag	aagatgattg	gttcgaagaa	gataatgaga	ggaaaacaaa	tgtttctaaa	180
gggaattcta	ctgttgatga	aacagttagt	gatttatttt	ctgatggaaa	tagtaataac	240
tctagttcta	aaaccgagtc	agtggtaagt	gaccctaacc	aagtcctcaa	agcaaaacca	300
gaggttacac	aggaagcaag	caattctagt	aatgatgcta	gcaaagtaga	agtacaaaa	360
caggatacag	cttcaaaaaa	ggaaaccata	gaaacatcaa	cttgggaggc	aaaagatttc	420
gtaactagag	gggtactttt	agtaggtttt	tcaaaatctg	gaattaataa	gttatctcaa	480
acatcacact	tagttttacc	aagtcattgc	gcagatggaa	ctcaattgac	acaagtagct	540
agctttgctt	ttactccaga	taaaaagacg	gccattgcag	aatatacaag	taggctagga	600
gaaaatggga	aaccgagtcg	tttagatatt	gatcagaagg	aaattattga	tgaggagaaa	660
atattttaatg	cttaccagtt	gactaaagct	actattccaa	atgggtataa	gtctattggt	720
caagatgctt	ttgtggacaa	taagaatatt	gctgaggtta	accttcctga	aagtctcgag	780
actaattcag	actatgcttt	tgctcacatg	tctttaaaac	aagtaaaagt	accagataac	840
ctgaaggta	ttggagaatt	agcttttttt	gataaccaga	ttgggtgtaa	gctttacttg	900
ccacgtcact	tgataaaaatt	agcagaacgc	gctttcaaat	ctaatacgtat	tcaaacagtt	960
gaatttttgg	gaagtaagct	taaggttata	ggagaagcaa	gttttcaaga	taataatctg	1020
agtaatgtta	tgcttccgga	tggacttgaa	aaaatagaat	cagaagcttt	tacaggaaat	1080
ccaggagatg	aacattacaa	caatcaggtc	gtattgcgca	caaggacagg	ccaaaatcca	1140
catcaacttg	cgactgagaa	tacttacgtc	aatccggaca	aatcattgtg	gcgtgcaacg	1200
cctgatatgg	attataccaa	atgggttagag	gaagatttta	cctatcaaaa	aaatagtgtt	1260
acagggttttt	caaataaagg	cttacaaaaa	gtaagacgta	ataaaaaact	agaaattcca	1320
aaacaacaca	atggcattac	tattactgaa	attgggtgata	acgcttttctg	caacgttgat	1380
tttcaaagta	aaactttacg	taaatatgat	ttggaagaag	taaagctccc	ctcaactatt	1440
cggaaaatag	gtgcttttgc	ttttcaatct	aataaactga	aatcctttga	agcaagtga	1500
gatttagaag	agattaaaga	gggagccttt	atgaataatc	gtattggaac	tctagacttg	1560
aaagacaaac	ttatcaaaa	aggtgatgct	tctttccata	ttaatcata	tcacgccatt	1620
gttcttccag	aatctgtaca	agaaatagga	cgttcagctt	ttcgacaaaa	tggtgcactt	1680
cacctgatgt	ttatcgga	taaggttaaa	acaattgggtg	aaatggcttt	tttatccaat	1740
aaactggaaa	gtgtaaatct	ctctgagcaa	aaacaattta	agacaattga	ggtccaagct	1800
ttttcggata	atgcccttag	tgaagtagtc	ttaccgcca	atttacagac	tattcgtgaa	1860
gaggctttca	aaaggaatca	tttgaaagaa	gtgaaggggt	catctacatt	atctcagatt	1920
gcttttaatg	cttttgatca	aaatgatggg	gacaaaacgt	ttggttaagaa	agtgggtgtt	1980

aggacacata	ataatttctca	tatgttagca	gatgggtgagc	gttttatcat	tgatccagat	2040
aagctatctt	ctacaatggt	agaccttgaa	aagggttttaa	aaataatcga	aggttttagat	2100
tactctacat	tacgtcagac	tactcaaaact	cagtttagag	aaatgactac	tgagggtaaa	2160
gcgttggtat	caaaatctaa	cctccgacaa	ggagaaaaac	aaaaattcct	tcaagaagca	2220
caatTTTTcc	ttgggtcggt	tgatttggat	aaagccacag	ctaaagctga	gaaggcttta	2280
gtgaccaaga	aggcaacaaa	gaatggctat	ttgcttgaga	ggagtattaa	caaagcggta	2340
ttagcttata	ataatagcgc	tattaaaaaa	gctaattgta	agcgccttga	aaaagagtta	2400
gacttgctga	cagatttagt	cgagggaaaa	ggaccattag	cgcaagctac	aatggtacaa	2460
ggagtttatt	tattaaagac	gcctttacca	ttgccagaat	attatatcgg	attgaacgtt	2520
tattttgaca	agtctggaaa	attgatttat	gcacttgata	tgagtgatac	tattggcgaag	2580
ggacaaaaag	atgcatatgg	taatcctata	ttaaatgttg	acgaggataa	tgaaggttat	2640
catgccttgg	cagttgcaac	tttagctgat	tatgaaggtc	tttatatcaa	agatatttta	2700
aatagttccc	ttgataagat	taaagcaata	cgtcagattc	ctttggcaaa	atatcataga	2760
ttaggatttt	tccaagctat	ccgaaatgca	gcggcagaag	cagaccgatt	gattcctaag	2820
acacctaagg	ggtacctaaa	tacagtccca	aattatcgta	aaaaacaagt	ggagaaaaat	2880
tcaaaaccag	ttgattataa	aacgcgcgatt	tttgataagg	ctttacctaa	tgaaaaggta	2940
gatgggtgata	gagtggtctaa	agggtcataat	ataaatgcgg	agactaataa	ttatgtagct	3000
gtaacaccaa	taagggtccga	gcagcaatta	cataagtcac	agtctgatgt	aaatttacct	3060
caacaagtt	ctaaaaataa	ttttatatac	gagattctag	gatacgtag	tttatgtttg	3120
cttttcttag	taactgctgg	gaaaaaagga	aaacgagcaa	gaaaaataa		3168

SeqID 466

atgaacaaaa	aaattgcccgg	gatcggccttg	gcttcgattg	cagtacttag	tttagctgca	60
tgtggacatc	gtgggtgcttc	taaatctggt	ggtaaactcag	atagcttgaa	ggttgcaatg	120
gtaacagata	ccggtggtgt	tgatgataaa	tcattttaacc	aatctggttg	ggaaggtagt	180
caagcttggg	gcaagaagaa	tggccttaaa	aaaggagctg	gttttgacta	tttccaactc	240
gcaagtgaat	ctgattatgc	aactaaactta	gatacagctg	tgtctagtgg	ttataaattg	300
atTTTcggtg	ttggatttttc	tcttcatgat	gctattgata	aagcagcaga	caataacaaa	360
gatgttaatt	acgtcatcgt	tgatgatgtt	attaaaggga	aagataatgt	tgcaagtgtt	420
gtctttgccc	ataatgaatc	agcttactta	gcaggatttg	cagccgctaa	aactacccaa	480
acaaaaacag	ttggcttttgt	aggtgggtatg	gaatctgagg	ttattaccgg	ttttgaaaaa	540
ggttttgaag	caggtgtcaa	atcagttgat	aaatcaatta	aaattaaagt	tgactatgct	600
ggttcattcg	gtgatgctgc	taagggttaag	acaattgcag	ccgcacaata	tgcttctggc	660
gcagatatgt	tttatcaagt	agctgggtgga	actgggtgcag	gtgtattcag	tgaagcaaaa	720
tcacgcaatg	aatctctaaa	agaagctgac	aaagtttggg	tattaggtgt	agaccgtgac	780
caagcagcag	aaggtaagta	tacttctaaa	gatggtaagg	cttctaactt	tgttttggct	840
tcacatcaatta	aagaagttgg	aaaatcagtt	gaattgattg	ctactaaaac	aagtaaaagg	900
aaattcccag	gtggtaatgt	aacaacttat	ggtttgaagg	atgggtggagt	tgatatagca	960
actacaaaacc	tttcagatga	cgccgttaaa	gcgattaaag	aggctaaagc	taaaattatt	1020
tcaggagata	tcaaagttcc	tagcaataaa				1050

SeqID 467

atgaggattc	aaacgacgaa	ccttgataaa	ggtggcgggtg	gaaaaagcag	tcacacctat	60
aacgaaggag	attgggtgtc	tagagttatg	gggaaacgag	tcttggtgat	tgatggggcc	120
agagaatgta	atttaacaca	ctcctttgat	gtgacgagcg	acaaaacaat	ctatgatatt	180
tttatcacag	gagaatatga	gatttgctga	atcaatgata	agcttagctt	aattagaggga	240
gatgaacgac	taactgatga	acagctagat	ttagccagtc	gaaataataa	ataccttcag	300
ttattcatgt	ggttcagtg	gcattatgag	gaactggccg	aacagtttga	tattatcttg	360
attgatactc	ataatgatga	aagtcttggt	actgccaat	gtattgccgt	ttctgatatt	420
gtcctagggg	tgactgatgc	gtcaactaat	ggatttcgtg	cctgggttagc	ccttaaaaaa	480
tttgtcgatg	acatcaagaa	tgaagctatt	gaggttatca	caaagaaaag	ctatgtgaag	540
gcagaagctt	atctgattgg	caataagatt	gagtattatg	gaaataatgt	gacagagact	600
tgtaagcaat	tcctggatgt	tgtgcaggaa	gatgaagctt	atttgggttc	aattcagaag	660
aaagaactga	tggccaaaag	tttagtcat	aatcagagtg	tctttgaaca	acgtgaacac	720
atgacagaaa	aacagaagca	agatcatcag	aaattttatg	ataatataga	atatgtctat	780
caaaatattt	taacgcgtact	agaaggagag	actaaatga			819

SeqID 468

gtgaaaaaag	ttgttttctt	gaaaaatactt	gttccgcttg	tctcttttgt	ctttcttatt	60
agcttgggtg	taacgatatt	agcaggtgtt	ttaggagcgg	ttgggtggtc	gcagtcaaat	120
tgtacgatag	aagttgtaac	ctcaacctct	acagactcgt	ccatatcttc	aggtgatggt	180
tcatttgatt	cttttgttaa	ggagcacaaa	gaggcttata	tcctgtcttg	gaaagctggg	240
ggcttcttac	catctgcctc	gattacgcag	accatgattg	aaaatggctt	taacttcacc	300
aatcctaagt	ggacctccct	ctggcaagcc	cataatatgg	gaggggttaa	aacgtctagt	360
aagagtaact	tccccgttac	cttagcaact	tatggccaag	atagtgttga	cctttcagga	420

acaaagccag	gagcaagagt	cggcgatggc	acaggtgggg	cttatacctg	gttttcaagc	480
tatgatgcag	ggattgtcgg	caaggcagag	tttatggccc	atcaaactct	ctataccaag	540
gcaattaaca	atatagatgg	gatagctaca	ctaagtgcga	ttgcggatgg	tggttgggcg	600
actgacggaa	cttataaaac	caagcttatt	gacatgtatc	ataagcttgg	taaaacctat	660
gaatggctgg	ataaggaagc	tatcagcgct	catgggtgata	aaccttataa	agcaaccaca	720
gcttcagctg	gagatgctgg	actatctgat	atttttacaa	gcaatagtaa	agattgtagt	780
gattcttctt	caggtgggtg	cactgatggg	acaggaacag	ttccagcaga	tgcgatagcg	840
tggggatata	ggcctgataa	cctaccagag	agtctgaagc	agtatatcat	tgatcctaaa	900
tcgcttggca	tggcttatgc	aaactcttct	ggctggttta	atccaggtag	tgattatcta	960
gctggacaat	gtgttaattt	aacaatcagt	cttggaaatc	acctctgggg	tcactcggga	1020
tctgtcagtg	gcaatggaaa	agaccaagct	gggtgcttgg	ccaatatctt	tggcaattca	1080
gtcaaaacga	ctcctaaaag	aggagctatc	ttttctaccc	aaaacggagg	tggcggttat	1140
ggccatactg	ggattgtgtg	ccatgtcttt	gaaaatggat	caatcttgat	tgtggaacaa	1200
aatacgccat	tactggggag	tgattatttc	aaaaaatctt	acacatggaa	ttaccgtatt	1260
tggacacctg	cccaacaaaa	agcagaagtc	attagttttg	cttacccata	tggtaaagaa	1320
cctaaacttg	gaaactaa					1338

SeqID 469

atgggaaaga	catttttgaa	agatatctat	cgatcaatta	cgacttcaaa	aggtagattt	60
tcacatcaat	tccttacttat	gatgttaggc	tcatttgctt	ttataggact	gaaggctctca	120
gcacctaata	tgcaaagaac	agcacaaaat	taccttgctc	atcatcatgt	tatggatatt	180
accgttttca	attcttgggg	acttgacaaa	catgatcaaa	ctgtttttaga	aagcttaaaa	240
ggatcacaa	ttgaattttc	ttacttttga	gatacaaccc	ctcaacagaa	tagtaaattct	300
tatcgattgt	attccaatac	caaaacaata	tcaacctttg	atcttgttaa	gggacgtctc	360
cctttaaata	aatcagaaat	tgctctctca	tttcagggaac	gaaaaaaata	tgcaatagggt	420
gataaaaatta	atttttaaaca	agataaaaaa	aaactgtttt	caaatacagg	tcctctaact	480
attgtagggt	ttgttaattc	taccgagatt	tggtctaaga	caaaccttgg	tagtttctcaa	540
acaggggacg	gcgacttaga	tagtttatgg	gtattagata	agacagcatt	tcactctcca	600
gtatatacaa	tggcaagggt	aaacttttaa	gatcttaggt	tgattaaccc	tttctcaata	660
agttacaaag	aaaaagtagc	gaaataccaa	gaaaagggtat	cgcgaaaatt	aaatattcac	720
aataaaaata	gatataccaa	aacaaaaaaa	gagagcctac	gtaaaatcga	tgaggaggaa	780
aaaagcctac	taaaagctca	aaaacaaatc	aatcggttag	ataatgatag	cctagcgatg	840
ccactatctc	aaagacaagc	tattcaaatg	aaaattaaac	aagaccgact	atctcttttg	900
aaacgaacaa	aagagcttct	aaaattgaga	cataacaccc	aaataatgga	atcgccctcaa	960
attattgtct	acaaccgtac	tacctttcct	ggaggacaa	gatataaac	ttttgactcc	1020
agtacaaata	gcacttctaa	aatcagtaat	cttttcccca	ttattttata	tttagtcgca	1080
gcatttagtaa	ccttaacaac	aatgactagg	ttcgctcgagg	aagaaagaac	caacgcaggc	1140
atattaaaag	cactaggcta	tagtgaccgc	caagttatct	ttaaatttat	tatttatgggt	1200
tttatagcag	gaacattagg	gactactttg	ggatcatttg	gagggcatta	tcctttacct	1260
cgtattattt	ctgatcatct	ttccaaagac	ctgactattc	caaacacaca	gtatcatctt	1320
ttcttaaaat	acagtttact	agcctttgtt	ttttcattat	taagcattgt	tcctccagtt	1380
tttgttatca	ctcgacgtga	gttgaaagaa	aaagcagcat	ttttattatt	accaaaccac	1440
ccagctaaag	gatctaaaat	agcttttagag	tatatcaatt	ggatttggaa	aaaactgtcc	1500
ttcacacaaa	aagtaactgc	tagaaaatatt	tttcgttaca	aacaaaggat	gattatgacc	1560
atatttggag	ttgctggatc	agtagcgctc	ttatttttcag	gtctaggaat	acaatcctcc	1620
ttaaagcaa	ccgtcaatga	acatttcggg	cgtattatgc	cctatgatat	attgctaaca	1680
tataacacaa	atgcttctcc	cccaaaaata	cttgaactac	tttcaaaaga	ttcaaaaata	1740
gacaaatacc	aaccaataca	ccttgaaaat	cttgacgaat	ccattcctgg	acaaattaat	1800
aaacagtcaa	tttccctatt	cataacagac	aaaaaacaat	tactaccttt	tattttattta	1860
caagaagcaa	caactaataa	gtcattgcac	ttgaataata	aagggtattat	tatttctaaa	1920
aaattagctc	aatttttatca	tgtaataacc	gggtgatttta	tccattttatc	tcattcacaa	1980
acacttcctt	ctagaaaatt	aaaaataaca	ggagttgtca	atgcgaatgt	tggtcactat	2040
atttttatga	caaaacaata	ctatcgaaact	attttttaaga	aagaaactaa	agataacgct	2100
tttttgggtt	agtttaaccac	acataaaaatc	gcaataaact	tagcagaaaa	acttttagaa	2160
attaatggag	ttgagtctct	tacgcaaaat	gctcttcagc	tagctagtgt	agaagccggt	2220
gtgcgttctt	tagatggctc	tatgactatt	ttagttgtcg	tatctttatt	gttagccatt	2280
gtaattctct	ataatctcac	taatattaat	ttagcagaac	gtaagcggga	gctatcaact	2340
ataaagggtat	taggttttta	taatgaagaa	gtaactttat	acattttaccg	cgaaccatt	2400
attttatcaa	ccatcggtgt	gattctaggg	accatttagcg	gtactttatt	acaccgtcaa	2460
atgatgttgc	taattggttc	agatcaaata	cttttgggtg	aaaaagtatc	accaactaca	2520
tttataatac	caataagcgt	agtagtcatc	attctaataa	gtctatgttt	tatagttaac	2580
catcaattaa	aaaaactcaa	tatgttagat	gccttgaaat	cagtagatta	g	2631

SeqID 470

atgaataaaa	gaaaattatt	aacagtttta	tcaattgcat	cagttgcagt	tttatcaagt	60
------------	------------	------------	------------	------------	------------	----

gttacttttg	cagatgaaat	aactccatct	gatccaacag	caccatcaac	accccttatt	120
actccaaccc	cagtagatcc	tggaacacca	actgatacga	caaaacctag	tactccagta	180
gatcctggaa	cgccaactga	tacgacaaaa	cctagtagctc	cagtagatcc	tggaacacca	240
actgatacga	caaaacctag	tactccagta	gattcagggga	cttcgactaa	tccctcagat	300
tcagaagcaa	caaatacaaa	tctaggtaca	aaaccaacag	atgtagttaa	gccagagaca	360
cctaaaatcc	ctgaagtgcc	gtcaacagta	actccagatg	tgattgacaa	ggtagacaaa	420
gaaacaggta	atattacgat	taaaccaatt	caaatcagcc	ctgataaaaac	gattattgga	480
acacaaaatg	gtaatgtcat	tattcgagat	agttcaggca	gccacttagt	atctgcaagt	540
gaagttgggtg	gtcgacttaa	tgaagatggg	acagtaacaa	ttaaagattc	gtcagggaaa	600
acaaaaacac	tccctcgtac	tggagaagct	aaaggattct	taagcattat	tgggtgccaca	660
atcctatctt	ttgtagctta	tttattcaag	cagagagtaa	ctttaaatta	a	711

SeqID 471

atgagacctt	tcgttagaaa	aaagatgtac	aaaaaaggta	aatttttgggt	cattgcagggt	60
atcgttacta	tttttaggtgg	tagtgcaatt	cttgggtcaag	atgtcaaggc	agaacaggca	120
gaagcagcaa	cttcaacgat	ctcagagaaa	actgatagca	gtcagactat	ttcggatact	180
tccaagttaa	cgttacctgt	taattcctcg	gaggctatga	aaaatagtgc	agagccttta	240
ataaaaacag	gctttgctac	atctgttttc	tctaactcta	gagagatagc	agctacccca	300
gtcaaaacct	ttgatgctag	ttcaaaagt	gttgtaaaag	ctagtactgc	tgagcactca	360
gcaaatcaaa	caaattctaa	tgttaatcaa	gtagctaatg	atagtgaagt	tattactcaa	420
caaaattcaa	caaagcaatt	acaaaaagt	acttactctg	ctcatgttca	agatattgga	480
tggcaaaagt	cggttgataa	tgcaacagtt	tcaggaacag	taggacagga	aaagcagggt	540
gaggcaataa	aattgtctat	taaagcccct	gaaggaaata	caggaaaact	tagctataaa	600
acttatgtta	aaggacaagg	ttggcaacct	tcagtagaga	gtgggtcaagt	tagtggtact	660
gttgggtcaga	gtagacctat	tgaagcacta	agcattaacc	ttactgataa	tttacaaaaa	720
ttatatgatg	tctattatcg	tggtcatggt	caagatcatg	ggtggatggc	ttggggctaaa	780
aatggagctt	acgctgggac	tttgggaatg	tcaaagcgcc	ttgaagctta	cgaagttaaag	840
tttaccctta	aaggacaatc	tgttttaaca	ccaactatac	ttaaggaaga	gagacctgtc	900
ttaaattatc	aggttaagggt	aggccaaaat	ggttggcaat	ctaataaact	tgaaggacaa	960
atggcgggaa	ctttaggaga	atccaaagcc	ctagatggag	taaaattcac	tcttagcacc	1020
ttgaagtatg	gggacattct	ctatcgtact	catgtacaag	ataaagggtt	gggagaaatt	1080
ttaggtagtc	aaacaagtaa	ggattatcaa	ggaaaaagac	tagaagctat	tcaattggac	1140
ttaagtggga	atttaaaaca	aaattatgat	atttattatc	gcgctcacgt	ccaagataaa	1200
ggttggatgg	cttggcaaaa	aaataatagt	gtagcaggta	cagtcggaga	atcgaaacgt	1260
ttagaggctt	tggaagtaaa	actagtagct	aaagcttcag	attttagttc	ccaaacaaat	1320
cattcattct	tagaaatgaa	gcacccctgga	ttaagtatct	aaacttatct	tcaaaaagat	1380
ggttggaaac	caacggtttt	ggaaggccaa	ttaggaggta	gtattggact	ttcaaaatct	1440
ataaaagcca	tcaaaactaa	cttaggtagt	acagctctag	gaaatataga	atatagaact	1500
tttcttaatg	gttcagggtt	gcaaactgtt	gttaattcag	ggagagaaag	taatgtacca	1560
aatgaatctc	aacaagtaga	agctattcag	atgcgattga	cagggtctgct	atcgaaaacc	1620
tatagtgtga	tgtatcgagt	tcacatgcaa	gattatgggt	ggcaggattg	gacttataac	1680
aatgacatcg	ctggtagtac	taaccaagga	aaacgaattg	aagcaatcga	aattaaatta	1740
gttgagactg	ctaaaatacc	tataactgtc	caaacgacct	ataaggggaa	tggaaactat	1800
aatgtacgag	tgacaaatgt	tattagtcct	gggaatttaa	aaattgctat	ttgggtcagat	1860
aaaaacaatc	aggatgcat	taagtggat	accgtcacac	ccaaaaatca	tgaagctaga	1920
ttgacattta	atgttacaaa	tcataagagac	aatgttaaat	actttatcca	tgtttatcag	1980
gaaaatgctt	ctaatacaaa	acaattattg	gtaaaaactt	ctctacaagt	cgcacattca	2040
aattataata	ctccttactt	tagccaacgt	gatgggaagg	gggcaagtgc	aagatatgggt	2100
atggcaactt	taggagaaac	tggttgtgta	ccaacttctc	tagctatgat	tttgtcttct	2160
ttgaaaggag	aaactgtttt	accaacgcaa	attgcagatt	acctttaacca	taagacagtt	2220
gaatttaate	gtggtgttca	aggaacaact	tctagaggaa	tcttaaaagc	agccaaagaa	2280
tggggtgtaa	cagcaactgc	attaggaact	caagctaacc	ttgtacaagc	gttgaaggat	2340
ggttatcatg	tcctagcggc	agtacaaaat	aatgtttttg	ttcttcatgg	aagtcatgaa	2400
atcgttctca	aaggatataa	taacggactg	acacatgtct	ctgaccttta	cacacgttcc	2460
ttgtctgggt	ggtatccaat	ttcacaactt	tggaaagaac	agagctatta	tagtgaggat	2520
agaattgata	ttggagaacc	ttttgtcaag	gtaacagatg	cctaa		2565

SeqID 472

atggcaagaa	tcccttatca	gaaaacactt	attttttgtg	tagccgttat	tattgctatt	60
tttatttttg	gattatctaa	ggatttagca	caatctaaag	ggcaaaagggt	tgcaataaat	120
aatactgtaa	aaacagcacg	tgtggttgca	aacggagata	ttttgctgca	cgatgtacta	180
tatgccagtg	cgcgccaacc	cgacggcact	tataatttta	ctccttattt	taaagaggta	240
aaatcttgga	ttgagagcgc	tgatttagcg	attggtgatt	atgaagggac	gattagttca	300
gaatatcctt	tagcaggcta	tcccttattt	aatgctccta	atgagattgc	aactactatg	360
aaagaaaactg	gatatgatgt	cgttgactta	gcacataatc	atattctgga	ttcacaactg	420

gcagggtgcta	tcaatactgt	caagactttt	aatcgtatgg	gattggatac	tattgggggtt	480
tatttaaagg	atagaaataa	agaagatatc	ttaattaagc	gtgtaaagtg	tataaaaaatt	540
gctatttttag	gttatttcgta	tggctacaat	ggtatggaag	ctaagtgttc	aaagagtgac	600
tatgaaaaac	atatgtctga	tttagatact	aaaaagatta	agcaagatat	taaaaaggct	660
gaaaaagaag	cagatatcac	cattgtcatg	ccacagatgg	ggatagaata	tcaaaaaaaaa	720
cctactacag	aacaagtaat	gctttatcac	agtatgatta	aatggggggc	agatattata	780
ttcggaggag	accctcacgt	tgttgaaccg	tctgaagtga	taaaaaaaga	tggccagaaa	840
aaatttatta	tttactctat	gggaaatttt	atttcaaatac	agcgttttaga	aacagttgat	900
gatatctgga	cagaaagagg	attattaatg	gatgtaacaa	tagagaaaaa	aggtcaaaaa	960
acagtaatta	aaaaagttaa	ggcgcatcca	acactagtag	aagcaaaagc	aaatggccgt	1020
tatgttgaag	aaggctttcc	agcttatgat	tataggacgc	tagtttttaga	ggatttatatt	1080
gaagggtgga	agaaacgttc	tacgattgat	cagactatga	aagataaagt	tgataaaagca	1140
tataaggaga	tgaatgagtt	agttaatttg	aagtggtaa			1179

SeqID 473

atgaaacatt	tctttgatta	caagacaatg	tctgtcgcac	gtaaactcag	cattagtttt	60
atcgctgtta	tctatttggg	aagtatttta	ctttcacttc	caatttttca	atatgctaac	120
gcccctaaaa	cacattacat	tgatcacctt	ttcacgactg	tttcaatggg	atgtgtaact	180
ggtttatctg	tttttcttat	cagtaagggt	tataacgggt	gggggcagat	tgtagctatt	240
ttactcatgc	aaacaggggg	acttgggtta	gtaacactaa	tgtcgttgtc	ttactatacc	300
ctaagacgta	aaatgtcgtt	aaatgatcag	acccttttgc	agtcagcgat	aacttataac	360
agttcgacag	atttaaaaaa	atatctctat	atgattttta	aagtaacttt	aacttttagaa	420
gttttagcag	ccagcatttt	agccatagat	tttattcctc	gatttggttt	gggtcatggg	480
atctttaata	gtatattctt	agctgtctca	gccttttgta	atgccgggtt	tgataatcta	540
ggggcaacga	gcttagctca	atttaaaacta	aatccttttg	ttaacattat	cgtttgtttc	600
ttgattattt	caggaggact	tggatttgcc	gtatggaag	atttaattga	agctactata	660
caaacatctc	acaagggacc	aaaattaatc	aagacatttc	caaaacgcct	cagcaaccat	720
tctaaactgg	ttttaaaaac	aacaaccatt	attttactaa	caggaaactt	gctttcttgg	780
ttgtagaggt	ttggaaattt	tagaacaatt	gctaatttat	ctctacctaa	acaactaatg	840
gtcagctttt	tccaaacagt	tacgatgcgt	accgctggat	tttcaactat	tgattatacc	900
caaactgatt	tcgcaaccaa	ccttggttat	attatccaaa	tgtaatttgg	aggagctcct	960
gggtggaacgg	caggaggatt	taaagtcaat	gttatcgcca	ttttactctt	actattttaag	1020
gccgaactga	gtggccaaag	ccaagtgaat	tttcattatc	gaacaattcc	ttccagtatt	1080
attaaacaaa	cactatcgat	tttaactttc	ttttttatca	tacttattag	cggctatctc	1140
cttcttctgg	aactcaatcc	ccatatagat	cctttttctc	ttttctttga	ggcatctagt	1200
gccttagcaa	ccgtgggtgt	gacaatgaac	actaccaatc	aattaagtct	gggcggtcga	1260
attgtaatta	tgttcctcat	gtttatttgg	cgagtcgggc	caattaccgt	actgctatca	1320
attcttcaga	aaaaagagaa	ggaaattcac	tatgctgaaa	cagaaattat	tctaggttag	1380

SeqID 474

atgtagacg	aattaaaagc	aatcataaaa	agcccaaaat	tatggattac	gatggctggg	60
gttgactga	ttccaacgct	atataatgtt	atctttctaa	gctcaatgtg	ggatccttat	120
gggaatacta	aaaattttacc	tgtggcagtc	gttaaccaag	ataaatcggc	taaaattaaat	180
ggaaaaacta	tttcaatttg	caaagatatg	gaggacaatt	tgtctaaaaa	tgatagctta	240
gatttccatt	ttacaacagc	taaaagagat	gaaaaagaat	tagaaaaggg	tcactattat	300
atgggtatta	cctttcctaa	agatccttct	agaaaaagca	caactctcat	gacagaaaaa	360
ccagaaagg	taaatattac	ttataaaact	actaaggggc	gtagttttgt	agcttcaaaa	420
atgagtga	cagcagctaa	taaactaaaa	gatgaggtag	cagaatctat	tacagggact	480
tatactgaat	cagtttttaa	aaatatgggt	tctatgaaaa	caggtatcaa	taaagctgct	540
gatgggagtc	aagaattatt	aatgggttct	aataagctac	aggatgggag	ccaaaccttg	600
acaagtaatt	tagatgtttt	agcaagctct	agtcaaactt	tttctggagg	agctaataaa	660
ctaaatagtg	gaataaacct	ttatacagat	gggtgggga	ccctatctaa	cgggttagaa	720
acattatcag	atgggtgttac	tgccttacaca	acaggtgtgc	ataagttgag	tgaaggtagt	780
caaaaattag	atgataagtc	tcaagcattg	gtggaaggat	cagaaaaagt	gacggatggg	840
ttacaacaat	tgtcacaagc	aactcaacta	aaaccagagc	aagaacgtac	tttgacgaac	900
ctttcagatg	gattaaagaa	tctaaatcag	attattacaa	atttacaatc	gacagcaact	960
actgatagcg	atactaatag	taagttattt	aattttttat	caactattga	atcaagtaga	1020
aaggctttga	tgaatacggc	tgctgctgat	aaacaaaagc	aatgactgc	ggtacaatca	1080
acgtcagctt	ttaaaagttt	aacctctgaa	caacaatctc	aatcacctc	agcggttact	1140
ggaacaccta	cttcagctga	gacaattgca	gcaaatattt	cttcaaatat	agaaaaatag	1200
aaaactgtgc	ttagtgaagc	atctagttca	gcccttctta	ataatggatc	acaaaatctt	1260
caaaactttgt	caggaacagc	taacaattta	gtattaaaag	ctatctcaga	tttagataaa	1320
attcaaaaaat	tgccaacggc	tactaagcag	ttatatcaag	gtagtcaaac	cttgacaaaa	1380
ggaatcacgg	attatacgaa	tgctgtaggg	caattacgca	aagggtgcagt	aacttttagat	1440
agtaaattcca	atcaattgat	ttcaggaaca	caaaaagcaa	gtcaggggagc	tcaaacttta	1500

gatagtaa	cggaatca	attgagac	ggagcgga	gcggggca	atagctagt	ggtctgata	ga	1560
attgcagat	gttctaata	agcttgct	gggaggac	atcagttgat	agtggttga	ca	1620	
gagttgtcag	gtggtgtttc	tcaattat	caagttct	ttggggag	ctggaccag	ttg	1680	
tccatgggtt	ctgtaaata	agataatgc	caaatgcag	tatctagccc	agtcactat	caag	1740	
catgaagatt	atgatagcgt	tgatacga	aatggttga	aatgttatt	ttggcaccat	ca	1800	
gttgcgttga	tggtggtagc	tttatcagcc	aatgttatt	ttggcgaag	cttatctggc		1860	
aaagagccag	ctaactggtt	tagttgggct	aaaaataaa	tattaatcaa	tggtattcatt		1920	
gcaactctag	cagcaactat	cttatttttt	gcagttcaat	tcataggtct	taaaccagat		1980	
taccctggaa	aaacctactt	tattatccta	ttgacagcat	ggactttgat	ggcattagta		2040	
actgctttag	tggtgatggga	taataggtat	ggttccttct	tgctcgttatt	aatattatta		2100	
ttccagcttg	gttcaagcgc	aggaacttac	ccaatagaat	tgagtcctaa	gttctttcaa		2160	
acaattcaac	catttttacc	gatgactttac	tctgtttcag	gattaagaga	gaccatctcg		2220	
ttgacgggag	acgttaacca	tcaatggaga	atgctagtaa	cttttttagt	atcatcgatg		2280	
atacttgctc	ttcttattta	tcgtaaacia	gaagattaa				2319	

SeqID 475

MLKKSFLQIFTLCLALLTISGCQLTDTKKPGHTTIKVAQSSSTESSIMANIVTELIHHELGYNTTLISNLGSSTVT
 HQALLRGDADIAATRYTGTDTITGTLGLKAVKDTKEASKIVKTEFQKRYNQTYPTYGFSPTYAFMVTKEFARQNKIT
 KISDLKKLSTTMKAGVDSSWMNREGDGYTDFAKTYGFEFSHYPMQIGLVYDAVESNKMOSVLGYSTDGRISYDLE
 ILRDDKKFFPPYEASMVVNNSSIKKDPKLLKLLHRLDGLKINLKTMMQNLNMYDDKLLLEPSVVAQKQFLEKNHYFRGDK

SeqID 476

LKPSFKKLLLLFSIITILSIACTPHAKASGRSWKSWFIEQYFWLKRDKSYKQVDESSFQKYLNASREQSDKGYLYD
 PNSVNGGLVQERLFDQVYSWNDNGKANQKTIIFYLAGGSYLNNTFYHISMLKTLSTSLDAKILPIYPKTPRYTYD
 YAIPLRLVNLRYHFHEKNANLTLMGDSAGGGLALGLAHLASHQSGQEAIPQPKNIILLSPWLDVMTMKHPEIPKYEDTD
 PILSAWGLARVGEIOWANGSNNTNHTYVSPKNAPATKLAPITLFTGTREIFFPDIRDYAAQLQAANHPVNYIAQEGMN
 HVYPIYPIEEAKTAQYQMIDIINKTP

SeqID 477

MTKKHLKTLALALTTSVSVTYSQEVYGLEREESVQEQTQSASEDDWFEEDNERKTNVSKGNSTVDETVSDLFSDGN
 SNNSSSKTESVSDPKQVPKAKPEVTQEASNSNDASKVEVPKQDTASKKETIETSTWEAKDFVTRGDTLVGFSKSG
 INKLSQTSHLVLP SHAADGTQLTQVASFAPTPDKKTAIAEYTSRLGENGKPSRLDIDQKEIIDEGEIFNAYQLTKLT
 IPNGYKSIGQDAFVDNKNIAEVLNLPESLETISDYAFAHMSLKQVKLPDNLKVI GELAFFDNQIGGKLYLPRHLIKLA
 ERAFKSNRIQTVEFLGSKLVIGEASFQDNNLSNVMLPDGLEKIESEAFGNPGDEHYNNQVLRTRTGQNPQHQLAT
 ENTYNPNPKSLWRATPMDYTKWLEEDFTYQKNSVTGFSNKGKQKVRNKNLEIPKQHNIGITITEIGDNAFRNVDFQ
 SKTLRKDYDLEEVKLPSTIRKIGAFQSNNLKSFEASEDLEEIKEGAFMNNRIGTLDLKDCLKIKIGDASFHINHIIHA
 IVLPESVQEIGRSAFRQNGALHLMFIGNKVKTIGEMAFLSNKLSEVNLSEQKQLKTIEVQAFSDNALSEVVLPPNLQ
 TIREEAFKRNHLKEVKGSSSTLSQIAFNADFQNDGDKRFGKKVVRTHNNNSHMLADGERFIIDPKLSSTMTVDLEKVL
 KIIIEGLDYSTLRQTQTQFREMTTAGKALLSKSNLRQGEKQKFLQEAQFFLGRVDLDKATAKAELVTKKATKNH
 LLERSINKAVLAYNNSAIKKANVRLEKELDLLTDLVEGKGPLAQATMVQGVYLLKTPPLPEYYIGLVNVDKSGK
 LIYALDMSDTIGEGQKDAYGNPILNVEDNEGYHALAVATLADYEGLYIKDILNSSLDKIKAIRQIPLAKYHRLGFF
 QAIRNAAAEADRLIPKTPKGYLNTVPNYRKQVEKNSKPVYDKTPIFDKALPNEKVDGDRVAKGHNNINAETNNYVAV
 TPIRSEQQLHKSQSDVNLPTSSKNFIYEILGYVSLCLLFLVTAGKKGKRARK

SeqID 478

MNKKIAGIGLASIAVLSLAACGHRGASKSGGKSDSLKVAMVTDTGVDKSFNQSGWEGMQAWGKKNGLKKGAGFDY
 FQSASESDYATNLDTAVSSGYKLIFGIGFSLHDAIDKAADNNKDVNYVIVDDVIKGDNDVASVVFADNESAYLAGIA
 AAKTTKTFTVGFVGGMESEVITRFEKGFEAGVKSVDKSIKIKVDYAGSFGDAAGKGTIAAAQYASGADIVYQVAGGT
 GAGVFSEAKSRNESLKEADKVWLVGVDRDQAAGKYTSKDGKASNFLASSIKEVGKSVELIATKTSKGKFPGGNVT
 TYGLKDGGVDIATTNLSDDAVKAIKEAKAKIISGDIKVPSK

SeqID 479

MRIQTNLNDKGGGKSSHTYNEGDWLSRVMGKRVLLIDGARECNLTHSFDVTSDKTIYDIFTTGEYEICRINDKLSL
 IRGDERLTDEQLDLASRNKYLQLFMWFSEHYEELAEQFDIILIDTHNDESLVTANCIASDIVLGVTDASTNGFRA
 WLALKKFVDDIKNEAIEVITKKSIVKAEAYLIGNKIEYYGNVNTETCKQFLDVVQEDAEAYLGSIQKKELMAKSLVIN
 QSVFEQREHMTKQKQDHQKFYDNIEYVYQNIILTVLEGETK

SeqID 480

VKKVFLKILVPLVSLVFLISLGITILAGVLGAVGGSQSNCTIEVVTSTSTDSSISSGDSIDSFVKEHKEAYILSW
 KAGGFLEPASITQTMIEGNFNFTNPNGTSLWQAHNMGGVKTSSKSNFPVTLATYGQDSVDLSGKTPGARVGDGTGGA
 YTWFFSSYDAGIVGKAEFMAHOTLYTKAINNIDGIATLSAIADGGWATDGTYKTKLIDMYHKLKGTYEWLKDEAISAH
 GDKPYKATTASAGDAGLSDIFTSNKDCSDSSSGGATDGTGTVPADAIAGWYRPNLPESLKQYIIDPKSLGMAYAN
 SSGWFNPGSDYLAGQCVNLTLISLGNHLWGHSGSVSGNGKDQAGAWANIFGNSVKTTPKRGAIYSTQNGGGGYGHTGI
 VCHVFENGSLILIVEQNTPLSGADYFKKSYTWNRYIWTTPAQQKAEVIFAYPYGKEPKLGN

SeqID 481

MGKTFWKDIYRSITTSKGRFSSILLMLLGSFAFIGLKVSAAPNMQRTAQNYLAHHHVMDITVFNWSGLDKHDQTVLE
SLKGSQVEFSYFVDTPQQNSKSYRLYSNTKTIISTFDLVKGRPLPNKSEIALSFQERKKYAIQDKINFKQDKNKLFS
NTGPLTIVGVFNSTEIWSKTNLGSSTQTDGDLDSYGVLDTAFHSPVYTMARVTFKDLRLINPFSISYKEKVAKYQE
KVSRLNIHNKIRYTKTKKESLRKIDEEKSLKKAQKQINRLDNDSLAMPLSQRQAIQMKIKQDRLSLLKRTKELLK
LRHNTQIMESPQIIVYNRRTFPGGQGYNTFDSSTNSTSKISNLFPIILYLVAALVTLTMTREVFVEERTNAGILKAL
GYSDRQVIFKFIIYGFIAGTLGTTLGIIGHYLLPRIISDIISKDLTIPNTQYHLFLNYSLLAFVFSLLSIVLPEVFV
ITRRELKEKAAFLLLPKPPAKGSKIALEYINWIWKKLSFTQKVARNIFRYKQRMIMTIFGVAGSVALLFSGLGIQS
SLKQTVNEHFGRIMPYDILLTYNTNASPPKILELLSKDSKIDKYQPIHLENLDESIPGQINKQSISLFTDKKQLLP
FIYLOEATTNKSILHNNKGIIISKKLAQFYHVNTGDFIHLSSHSTLPSRKLKITGVVNANVGHYIFMTKQYRYRTIFK
KETKDNAFLVKLTCHKIANNLAEKLEINGVESLTQNALQLASVEAVVRSLDGSMITLVVVSLLLAIVILYNLTNIN
LAERKRELSSTIKVLGIFYNEEVTLYIRETIILSTIGVILGTISGTYLHRQMMLLIGSDQILFGEKVSPTTFIPIPSV
VVIILISLCFIVNHQLKKNLMLDALKSVD

SeqID 482

MNKRKLLTVLSIASVAVLSSVTFADEITPSDPTAPSTPLITPTPVDPGTPTDTPKPSPTPVDPGTPTDTPKPSPTPVD
GTPTDTPKPSPTPVDSTSTNPSDSEATNTNLGTPKPTDVVKPETPKIPEVPSTVTPDVIDKVDKETGNITIKPIQISP
DKTIIIGTQNGNVIIRDSSGSHLVSASEVGGRLNEDGTVTIKDSSGKTKTLPRTEAKGFLSIGATILSFVAYLFKQ
RVTLN

SeqID 483

MRPIVRKKMYKKGKFLVIAGIVTILGGSAILGQDVKAQEAEAAATSTISEKTDSSQTISDTSKLTLPVNSSEAMKNSA
EPLIKTGFAATSVSSNPRIEAAATPVKTFDASSKVVKASTAEHSANQTNNSNVQVANDSEVITQQNSTKQLPKVITYSA
HVQDIGWQKSVDNATVSGTVGQEKQVEAIKLSIKAPEGITGKLSYKTYVKGGQWQPSVESGQVSGTVGQSRPIEALS
INLTDNLQKLYDYVYRVHVQDIGWMAWAKNGAYAGTLGMSKRLEAYEVKFTLKGQSVLTPITLKEERPVLNLYQVKVG
QNGWQSNKLEGQMAGTLGESKALDGVKFTLSTLKYGDILYRTHVQDKGWEILGSGTQSKDYQGRLEAIQLDLGSLN
KQNYDIYYRAHVQDKGMAWQKNSVAGTVGESKRLEALEVKLVAKASDFSSQTNHSPLEMKHPGLSYQTYLQKDGW
KPTVLEGQLGGSIGLSKSIKAIKLNLGSTALGNIYRTFNLGSGWQTVVNSGRESNPNESQQVEAIQMRITGLLSK
TYSVMYRVHMQDYGWQDWTYNNDIAGSTNQGKRIEAEIKLVETAKIPITVQITTYKGTGNYNVRVTNIVISPGLNKIA
IWSDKNNQDDLKWTVTVPKNHEARLTFFVTNHRDNGKYFIHVYQENASNQKQLLVKTSLOVAHSNYNTPYFSQORDGR
WASRRYGMATLGETGCVPTSLAMILSSLKGETVLPQTADYLYHKTFEFNRGVQGTTSRGILKAAKEWGVTTATALT
QANLVQALKDGYHVLAAVQNNVFLVHGSHEIVLKGYNGLTHVSDPYTPSLSGWYPISQLWKEQSYSEDRIIDIGEP
FVKVTD

SeqID 484

MARIPYQKTLIFCVAVIIAIFILGLSKDLAQSKGQKVANNNTVKRTARVVANGDILLHDVLYASARQPDGTYNFTPYF
KEVKSWSIESADLAIGDYEGTISSEYPLAGYPLFNAPNEIATTMKETGYDVVDLAHNHILDSQLAGAINVTKTFNRMG
LDTIGVYLKDRNKEDILIKRVNGIKIAILGYSYGYNGMEANVSKSDYEKHMSDLDTKKIKQDIKKAKEADITIVMP
QMGIEYQKKPTTEQVMYLYHSMIKWGADIIIFGHPHVVEPSEVIKDDGQKKFLIYSMGNFISNQRLTVDDIWTERRGL
LMDVTIEKKGQKTVIKKVKAHPTLVEAKANGRYVEEGFPAYDYRTLVLLEDYIEGGKKRSTIDQTMKDKVDKAYKEMN
ELVNLKW

SeqID 485

MKHFFDYKTMSVARKLSISFIAVILLGSILLSLPIFOYANAPKTHYIDHLFTTVSMVCVTGLSVFPISKVYNGWGQI
VAILLMQTGGLGLVTLMSLSYYTLRRKMSLNDQTLQLQSAITYNSSDTLKKYLYMIFKVTLTLEVLAASILAIIDFIPR
FGLGHGIFNSIFLAVSAFCNAGFDNLGATSLAQFKNLPLVNLIVCFLLISGGLGFVWVKDLIEATIQTSHKGPKLIK
TFPKRLSNHSLVLKTTTIIILLTGTLSSWLLBFGNFRTIANLSLPKQLMVSFFQTVTMRTAGFSTIDYQTQDFATNL
VYIIQMLIGGAPGGTAGGFKVTVIAILLLLFKAELSGQSQVTFHYRTIPSSIIKQTLISILTFFFIILISGYLLLEL
NPHIDPFSLFFEASSALATVGVTMNTTNQLSLGGRIVIMFLMFIGRVGPITVLLSILQKKEKEIHYAETEIIIG

SeqID 486

MLDELKAIKSPKLWITMAGVALIPTLYNVIFLSSMWDYPGNTKNLPVAVVNQDKSAKLNKGTISIGKDMEDNLSKN
DSLDFHFTTAKRAEKELEKGHYMVITFPKDLRSRKATTLMTTEKPERLNITYKTTKGRSFAVASKMSETAANKLKDEVA
ESITGTYTESVFKNMGSMKTGINKAADGSQELLNGSNKLQDGSQTLTSLNLDVLASSSQTFSGGANKLNSGINLYTDG
VGTLNGLTSLSDGVTAYTTGVHKLSEGSQKLDDKSQALVEGSEKLTDLGLQQLSQATQLKPEQERTLQNLSDGLKNL
NQIITNLQSTATTDSDTNSKLFNFLTIESSTKALMNTAAADKQKQMTAVQSTSAFKSLTPEQQSQITSAVTGTPTS
AETIAANISSNIENMKTVLSEASSAPSNNGSQNLQTLSTANNLVLKAISDLDKIQKLPTATKQLYQGSQTLTKGI
TDYTNVAGQLRKGAVTLDKSNQLISGTQKASQGAQTLDSKSDQLRDCAGQLASGSDRIADGSNKLGGGHQLIDGL
TELSGGVSQSLSSSLGKAGDQLSMVSVNKDNANAVSSPVTIKHEYDSVDTNGVGMAPYMISVALMVVALSANVIFAK
ALSGKEPANRFSWAKNKLINGFIATLAATILFFAVQFGLKPDYPGKTYFIILLTAWTLMALVTALVGWDRNRYGSF
LSLLILLFQLGSSAGTYPIELSPKFFQTIQPFPMPTYSVSGLRETISLTGDVNHQWRMLVIFLVSSMILALLIYRQ
ED

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
18 November 2004 (18.11.2004)

PCT

(10) International Publication Number
WO 2004/099242 A3

(51) International Patent Classification⁷: **C07K 14/315**,
A61K 39/09, C12N 15/31, C07K 16/12, C12Q 1/68,
C12N 15/11, G01N 33/50

(21) International Application Number:
PCT/EP2004/004856

(22) International Filing Date: 6 May 2004 (06.05.2004)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
03450112.2 7 May 2003 (07.05.2003) EP
03450266.6 28 November 2003 (28.11.2003) EP

(71) Applicant (for all designated States except US): **INTER-CELL AG** [AT/AT]; Campus Vienna Biocenter 6, A-1030 Vienna (AT).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **MEINKE, Andreas** [DE/AT]; Piettegassee 26/1, A-3013 Pressbaum (AT). **NAGY, Eszter** [HU/AT]; Taborstrasse 9, A-1020 Vienna (AT). **HANNER, Markus** [AT/AT]; Jacquingasse 5/6, A-1030 Vienna (AT). **HORKY, Markus** [AT/AT]; Wehlisstrasse 51/2a/20, A-1200 Vienna (AT). **KALLEND, Sabine** [AT/AT]; Roseggergasse 37/1, A-1160 Vienna (AT). **PRUSTOMERSKY, Sonja** [AT/AT]; Kreuzbrunn 10/4, A-3001 Mauerbach (AT).

(74) Agent: **SONN & PARTNER**; Riemergasse 14, A-1010 Vienna (AT).

(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declarations under Rule 4.17:

- as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii)) for all designations
- of inventorship (Rule 4.17(iv)) for US only

Published:

- with international search report

(88) Date of publication of the international search report:
16 June 2005

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: STREPTOCOCCUS AGALACTIAE ANTIGENS I + II

(57) Abstract: The present invention discloses isolated nucleic acid molecules encoding a hyperimmune serum reactive antigen or a fragment thereof as well as hyperimmune serum reactive antigens or fragments thereof from *S. agalactiae*, methods for isolating such antigens and specific uses thereof.



WO 2004/099242 A3

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP2004/004856

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C07K14/315 A61K39/09 C12N15/31 C07K16/12 C12Q1/68
C12N15/11 G01N33/50

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C07K A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS, EMBASE, MEDLINE, WPI Data, Sequence Search

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL 12 September 2002 (2002-09-12), GLASER ET AL.: "Sterptococcus agalactiae NEM316 complete genome, segment 2" XP002304476 Database accession no. AL766844 *page 4 last line- page 5 line 18* *sequence positions 16023-17678 pages 58 and 59*</p> <p style="text-align: center;">----- -/--</p>	<p>1,2, 5-11, 14-16</p>



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *G* document member of the same patent family

Date of the actual completion of the international search

9 November 2004

Date of mailing of the international search report

27. 01. 05

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

Loubradou, G

INTERNATIONAL SEARCH REPORT

International Application No.

PCT/EP2004/004856

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL 2 September 2002 (2002-09-02), TETTELIN ET AL.: "Streptococcus agalactiae 2603V/R section 8 of 100 of the complete genome" XP002304477 Database accession no. AE014198 *page 2 line 43 to line 63* *page 6 sequence positions 4387-6042*</p>	1,2, 5-11, 14-16
Y	<p>WO 02/059148 A (CISTEM BIOTECHNOLOGIES GMBH ; AHSEN UWE (AT); ETZ HILDEGARD (AT); HAFN) 1 August 2002 (2002-08-01) cited in the application page 10, line 20 - line 21; examples 1-7 page 4, line 8 - page 10, line 9</p>	1,2, 5-11, 14-37
Y	<p>ETZ H ET AL: "Identification of in vivo expressed vaccine candidate antigens from Staphylococcus aureus" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, US, vol. 99, no. 10, 14 May 2002 (2002-05-14), pages 6573-6578, XP002222373 ISSN: 0027-8424 the whole document</p>	1,2, 5-11, 14-37
Y	<p>KLADE C S: "PROTEOMICS APPROACHES TOWARDS ANTIGEN DISCOVERY AND VACCINE DEVELOPMENT" CURRENT OPINION IN MOLECULAR THERAPEUTICS, CURRENT DRUGS, LONDON,, GB, vol. 4, no. 3, June 2002 (2002-06), pages 216-223, XP009012456 ISSN: 1464-8431 page 219, left-hand column, paragraph 3 - page 220, right-hand column, paragraph 2</p>	1,2, 5-11, 14-37
Y	<p>TETTELIN H ET AL: "Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, US, vol. 99, no. 19, 17 September 2002 (2002-09-17), pages 12391-12396, XP002268223 ISSN: 0027-8424 the whole document</p>	1,2, 5-11, 14-37

-/--

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP2004/004856

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	GLASER P ET AL: "Genome sequence of Streptococcus agalactiae, a pathogen causing invasive neonatal disease" MOLECULAR MICROBIOLOGY, BLACKWELL SCIENTIFIC, OXFORD, GB, vol. 45, no. 6, 27 September 2002 (2002-09-27), pages 1499-1513, XP002268222 ISSN: 0950-382X cited in the application the whole document	1,2, 5-11, 14-37
A	MOYO S R ET AL: "THE PUTATIVE R1 PROTEIN OF STREPTOCOCCUS AGALACTIAE AS SEROTYPE MARKER AND TARGET OF PROTECTIVE ANTIBODIES" APMIS, COPENHAGEN, DK, vol. 109, no. 12, 2001, pages 842-848, XP001053581 ISSN: 0903-4641 abstract	
A	BRODEUR B R ET AL: "Identification of group B streptococcal Sip protein, which elicits cross-protective immunity" INFECTION AND IMMUNITY, AMERICAN SOCIETY FOR MICROBIOLOGY, WASHINGTON, US, vol. 68, no. 10, October 2000 (2000-10), pages 5610-5618, XP002219117 ISSN: 0019-9567 cited in the application abstract	
A	MICHEL J L ET AL: "Cloned alpha and beta C-protein antigens of group B Streptococci elicit protective immunity" INFECTION AND IMMUNITY, AMERICAN SOCIETY FOR MICROBIOLOGY, WASHINGTON, US, vol. 59, no. 6, June 1991 (1991-06), pages 2023-2028, XP002107260 ISSN: 0019-9567 cited in the application abstract	
A	LARSSON C ET AL: "Protection against experimental infection with group B streptococcus by immunization with a bivalent protein vaccine" VACCINE, BUTTERWORTH SCIENTIFIC, GUILDFORD, GB, vol. 17, no. 5, February 1999 (1999-02), pages 454-458, XP004153828 ISSN: 0264-410X abstract	

-/--

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP2004/004856

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,A	<p>HUGHES MARTIN J G ET AL: "Novel protein vaccine candidates against Group B streptococcal infection identified using alkaline phosphatase fusions." FEMS MICROBIOLOGY LETTERS, vol. 222, no. 2, 28 May 2003 (2003-05-28), pages 263-271, XP002304330 ISSN: 0378-1097 *ONLINE PUBLICATION DATE IS 30.04.2004, see the first line above the abstract* abstract</p> <p>-----</p>	
P,A	<p>HENICS T ET AL: "Small-fragment genomic libraries for the display of putative epitopes from clinically significant pathogens" BIOTECHNIQUES, EATON PUBLISHING, NATICK, US, vol. 35, no. 1, July 2003 (2003-07), pages 196-200,202,20, XP002293668 ISSN: 0736-6205 the whole document</p> <p>-----</p>	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP2004/004856

Box II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Although claims 26 and 27 are directed to a method of treatment by surgery of the animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-2, 5-11, 14-37 (partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-2, 5-11, 14-37 (partially)

Subject-matter related to SEQ ID N°14 and the corresponding polypeptide having the SEQ ID N°231

Inventions 2-229: claims 1-37 (partially)

Each of the nucleic acid having the SEQ IDs 1, 3, 5-15, 18-25, 27-30, 32-36, 39-68, 70-86, 90-101, 103-145, 147, 149-217, 435-448, 463-474 and the related subject-matter defines a separate invention.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/EP2004/004856

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 02059148	A	01-08-2002	AT 410798 B 25-07-2003
		AT 1302001 A	15-12-2002
		BR 0207067 A	15-06-2004
		CA 2436057 A1	01-08-2002
		CZ 20032201 A3	17-03-2004
		WO 02059148 A2	01-08-2002
		EP 1355930 A2	29-10-2003
		JP 2004531476 T	14-10-2004
		NO 20033364 A	24-09-2003
<hr/>			